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(54) Title: SECRETED EXPRESSED SEQUENCE TAGS (SESTS)

(57) Abstract

Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.

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SECRETED EXPRESSED SEQUENCE TAGS (SESTS)

FIELD OF THE INVENTION

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The present invention provides novel polynucleotides which are expressed sequence tags (ESTs) for secreted proteins.

BACKGROUND OF THE INVENTION

Gargantuan efforts have been employed by various investigational projects to randomly sequence portions of naturally-occurring cDNAs. The rationale behind this approach to identification and sequencing genes is founded in two basic principles: (1) that transcribed cDNAs represent the product of the most important genes, namely those that are actually expressed *in vivo*, and (2) that efforts to sequence genes and other portions of the genome of target organisms which are not actually expressed wastes substantial effort on areas not likely to yield genetic information of therapeutic importance. Thus, the high-throughput sequencing efforts focus on only those portions of the genome which are expressed. The randomly produced cDNA sequences represent "expressed sequence tags" or "ESTs", which identify and can be used as probes for the longer, full-length cDNA or genomic sequence from which they were transcribed.

Although this "shortcut" approach to genomic sequencing presents savings of effort compared to sequencing of the complete genome, it still produced a vast array of ESTs which may not be directly useful as protein therapeutics. To date, the majority of protein-related drug discovery has focused on the use of secreted proteins to produce a desired therapeutic effect. Since the EST approach theoretically identifies all expressed proteins, it produces an EST library which contains a mixture of secreted proteins (such as hormones, cytokines and receptors) and non-secreted proteins (such as, for example, metabolic enzymes and cellular structural proteins), without identifying which ESTs correspond to proteins falling into either category. As a result, these methods are not optimally tailored to the needs of investigators searching for secreted proteins because they must separate the secreted "wheat" from the non-secreted "chaff", wasting effort and resources in the process.

Co-assigned U.S. Patent No. 5,536,637, which is incorporated herein by reference, provides methods for focusing genomic sequencing efforts on sequences encoding the secreted proteins which are of most interest for identification of protein therapeutics. The '637 patent discloses a "signal sequence trap" which selectively identifies ESTs for secreted

proteins, namely "secreted expressed sequence tags" or "sESTs". It is to these sESTs that the present invention is directed.

SUMMARY OF THE INVENTION

The present invention provides for sESTs isolated from a variety of human RNA/cDNA sources.

In preferred embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,

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or a complement of said sequence.

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In other embodiments, the present invention provides an isolated polynucleotide consisting of a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

In further embodiments, the present invention provides an isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ

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ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEO ID NO:196, SEO ID NO:197, SEO ID NO:198, SEO ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,

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30 or a complement of said sequence.

In yet other embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEO ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEO ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEO ID NO:82, SEO ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEO ID NO:101: SEO ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEO ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEO ID NO:128, SEO ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEO ID NO:155, SEO ID NO:156, SEO ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,

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or to a complement of said sequence.

The invention also provides for proteins encoded by the above-described polynucleotides.

10 <u>DETAILED DESCRIPTION</u>

The nucleotide sequences of the sESTs of the present invention are reported in the Sequence Listing below. Table 2 lists the "Clone ID Nos." assigned by applicants to each SEQ ID NO: in the Sequence Listing.

15 <u>Table 2</u>

5

Each pair of entries in this table consists of the SEQ ID NO (e.g., 1, 2, etc.) followed by the Clone ID No. for such sequence (e.g., B11, B18, etc.).

	1	BV31	18	CB302	35	BZ83	52	CD244
	2	BV34	19	CB318	36	BZ87	53	CD265
20	3	BV37	20	CB321	37	CB15	54	BT217
	4	BV45	21	CB96	38	CB2	55	BV278
	5	BV8	22	CB98	39	CB44	56	BV280
	6	BV93	23	BZ42	40	CC11	57	BV282
	7	BV99	24	BZ53	41	CC182	58	BV285
25	8	CB100	25	BZ56	42	CC298	59	BV286
	9	CB107	26	BZ6	43	CC310	60	BV291
	10	CB110	27	BZ607	44	CC323	61	BV295
	11	CB114	28	BZ61	45	CC332	62	BW389
	12	CB118	29	BZ62	46	CC335	63	BX135
30	13	CB123	30	BZ641	47	CC338	64	BX141
	14	CB129	31	BZ644	48	CC41	65	BX148
	15	CB137	32	BZ72	49	CC52	66	BZ1
	16	CB239	33	BZ74	50	CD107	67	BZ16
	17	CB259	34	BZ82	51	CD205	68	BZ187

	69	BZ19	103	CE159	137	CH315	171	CC194
	70	BZ205	104	CE2	138	CH325	172	CC198
	71	BZ222	105	CE347	139	BZ568	173	CC199
	72	BZ230	106	CE36	140	BZ578	174	CC205
5	73	BZ234	107	CE40	141	BZ588	175	CC215
	74	BZ244	108	CE87	142	BZ597	176	CC253
	75	BZ269	109	CG1	143	BZ598	177	CC258
	76	BZ280	110	CG44	144	CH637	178	CC259
	77	BZ288	111	CG60	145	CH644	179	CC265
10	78	BZ304	112	CG68	146	CH699	180	CC288
	79	BZ328	113	BP202	147	CI240	181	CC95
	80	BZ331	114	BP242	148	CI247	182	CC96
	81	BP646	115	BP243	149	CJI	183	CD311
	82	BP652	116	BZ444	150	CJ19	184	CD323
15	83	BP656	117	BZ453	151	CJ24	185	CH338
•	84	BP666	118	CC233	152	CJ27	186	CH355
	85	BP667	119	CC242	153	CJ3	187	CH377
	86	BP674	120	CC247	154	CJ37	188	CH421
	87	BP695	121	CC344	155	CJ42	189	CH425
20	88	BP705	122	CC346	156	C J 44	190	CH522
	89	BP713	123	CC351	157	CJ49	191	CH541
	90	BP720	124	CC359	158	CJ50	192	CH555
	91	BP750	125	CC364	159	CJ55	193	CH558
	92	BP754	126	CC365	160	CJ6	194	CH582
25	93	BW143	127	CC374	161	CJ76	195	CH595
	94	BR307	128	CE303	162	C J 77	196	CH720
	95	BR309	129	CE328	163	CJ84	197	CH723
	96	BR312	130	CG199	164	CJ86	198	CH724
	97	BR318	131	CG209	165	CJ91	199	CH735
30	98	CB187	132	CG210	166	CC111	200	CH742
	99	CB190	133	CG350	167	CC118	201	CI126
	100	CB204	134	CG354	168	CC120	202	CI129
	101	CB213	135	CG426	169	CC126	203	CI133
	102	CE120	136	CH303	170	CC130	204	CI181

	205	CI229	239	CG160	273	C1395	307	CJ397
	206	CI25	240	CG175	274	C1407	308	CJ400
	207	C152	241	CG176	275	C1411	309	CJ404
	208	CI84	242	CG180	276	CI437	310	CJ415
5	209	CI91	243	CG279	277	C1443	311	CJ420
	210	BP163	244	CG292	278	CI444	312	CJ424
	211	BP175	245	CG300	279	CI459	313	CJ434
	212	BP199	246	CG301	280	CI480	314	CJ454
	213	BP272	247	CG314	281	CI490	315	CJ457
10	214	BP284	248	CG315	282	C1492	316	CJ481
	215	BP294	249	CG324	283	C1493	317	CJ493
	216	BP299	250	CG336	284	CI510	318	CJ501
	217	BP300	251	CG99	285	CI522	319	CJ514
	218	BP306	252	CH143	286	CI534	320	CJ539
15	219	BP311	253	CH207	287	C1542	321	CJ540
	220	BP312	254	CH224	288	CI560	322	CJ549
	221	BP327	255	CH227	289	CI561	323	CJ551
	222	BP345	256	CH245	290	CI583	324	CK126
	223	BP368	257	CH246	291	CI586	325	CK151
20	224	BP467	258	CH27	292	CJ145	326	CK181
	225	BP468	259	CH30	293	CJ149	327	CK201
	226	BR375	260	CH4	294	CJ160	328	CK213
	227	BR390	261	CH64	295	CJ164	329	CK218
	228	BR408	262	CH78	296	CJ168	330	CK234
25	229	BR418	263	CH85	297	CJ176	331	CK37
	230	BY66	264	CH87	298	CJ183	332	CK48
	231	CF118	265	CN320	299	CJ194	333	CL104
	232	CF127	266	CN343	300	CJ206	334	CL110
	233	CF22	267	CN344	301	CJ230	335	CL122
30	234	CF235	268	CN395	302	CJ237	336	CL132
	235	CG109	269	CN423	303	CJ257	337	CL147
	236	CG131	270	CI363	304	CJ265	338	CL152
	237	CG153	271	CI386	305	CJ378	339	CL181
	238	CG158	272	CI392	306	CJ389	340	CL182

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	342	CL469	376	CN532	410	CO48	444	CO153
	343	CL470	377	CN552	411	CO444	445	CO145
	344	CL481	378	CN593	412	CO431	446	CO140
5	345	CL493	379	CN619	413	CO391	447	CO139
	346	CM12	380	CN621	414	CO384	448	CO128
	347	CM178	381	CN667	415	CO36	449	CO1254
	348	CM188	382	CN703	416	CO351	450	CO1247
	349	CM194	383	CN718	417	CO337	451	CO1232
10	350	CM246	384	CN729	418	CO327	452	CO1224
	351	CM251	385	CN835	419	CO315	453	CO1223
	352	CM54	386	CN896	420	CO304	454	CO1206
	353	CM62	387	CO933	421	CO270	455	CO1198
	354	CN140	388	CO924	422	CO268	456	CO1196
15	355	CN171	389	CO908	423	CO264	457	CO1194
	356	CN173	390	CO900	424	CO261	458	CO1187
	357	CN238	391	CO889	425	CO257	459	CO1180
	358	CN29	392	CO888	426	CO253	460	CO1178
	359	CN291	393	CO874	427	CO25	461	CO1175
20	360	CN304	394	CO851	428	CO246	462	CO117
	361	CN327	395	CO83	429	CO244	463	CO1168
	362	CN49	396	CO821	430	CO240	464	CO1164
	363	CN50	397	CO806	431	CO228	465	CO1162
	364	CN54	398	CO798	432	CO223	466	CO1161
25	365	CN65	399	CO79	433	CO222	467	CO1159
	366	CJ305	400	CO71	434	CO209	468	CO1153
	367	CJ316	401	CO7	435	CO205	469	CO1151
	368	CJ317	402	CO69	436	CO204	470	CO1137
	369	CJ336	403	CO66	437	CO20	471	CO1123
30	370	CJ347	404	CO639	438	CO197	472	CO1076
	371	CJ360	405	CO638	439	CO185	473	CO1072
	372	CJ365	406	CO625	440	CO170	474	CO1026
	373	CJ366	407	CO62	441	CO17	475	CO1000
	374	CN483	408	CO602	442	CO163	476	CN755

	477	CN736	511	CR1166	545	CR632	579	CO409
	478	CN709	512	CR1186	546	CR641	580	CO474
	479	CO975	513	CR1190	547	CT729	581	CO480
	480	CO990	514	CR329	548	CN922	582	CO500
5	481	CP280	515	CR354	549	CN934	583	CO519
	482	CP283	516	CR377	550	CN951	584	CO522
	483	CP287	517	CR390	551	CN952	585	CO526
	484	CP289	518	CR392	552	CN980	586	CO559
	485	CP294	519	CR422	553	CP111	587	CO595
10	486	CP304	520	CR423	554	CP147	588	CO605
	487	CP307	521	CR466	555	CU13	589	CO618
	488	CP311	522	CR477	556	CP251	590	CO629
	489	CP313	523	CR478	557	CP258	591	CO643
	490	CP314	524	CR482	558	CP33	592	CO653
15	491	CP328	525	CR491	559	CP41	593	CO661
	492	CP352	526	CR494	560	CP91	594	CO667
	493	CQ286	527	CR502	561	CP92	595	CO695
	494	CQ294	528	CR506	562	CQ160	596	CO696
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	497	CQ331	531	CR515	565	CQ30	599	CO718
	498	CQ333	532	CR527	566	CR100	600	CO720
	499	CR1116	533	CR529	567	CR178	601	CO722
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	502	CR1127	536	CR540	570	CR335	604	CO767
	503	CR1135	537	CR541	571	CR4	605	CP116
	504	CR1141	538	CR545	572	CR61	606	CP151
	505	CR1142	539	CR587	573	CR93	607	CI293
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	507	CR1147	541	CR593	575	CO310	609	C1298
	508	CR1155	542	CR594	576	CO334	610	CU14
	509	CR1156	543	CR611	577	CO387	611	CU2
	510	CR1162	544	CR618	578	CO390	612	CU25

	613	CU32	647	CR678	681	CT748	715	CS520
	614	CU39	648	CR726	682	CT738	716	CS524
	615	CU40	649	CR733	683	CT726	717	CS534
	616	DA10	650	CR778	684	CT706	718	CT14
5	617	DA136	651	CR836	685	CT705	719	CT142
	618	DA155	652	CR839	686	CT702	720	CT143
	619	DA16	653	CR872	687	CT693	721	CT149
	620	DA165	654	CR890	688	CT677	722	CT156
	621	DA170	655	CR916	.689	CT658	723	CT159
10	622	DA183	656	CR929	690	CT645	724	CT162
	623	DA223	657	CR930	691	CT636	725	CT188
	624	DA224	658	CR936	692	CT631	726	CT189
	625	DA225	659	CR974	693	CT616	727	CT190
	626	DA227	660	CT747	694	CT611	728	CT193
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	628	DA234	662	CT690	696	CT585	730	CT2
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	638	DA507	672	CT807	706	CS317	740	CT271
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	641	DA84	675	CT785	709	CS353	743	CT284
30	642	CR1003	676	CT783	710	CS366	744	CT293
	643	CR1013	677	CT780	711	CS471	745	CO1020
	644	CR1044	678	CT771	712	. CS475	746	CO1043
	645	CR1056	679	CT754	713	CS485	747	CO1067
	646	CR1063	680	CT750	714	CS516	748	CO1069

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	750	CO1081	784	DB343	818	CW1632	852	CT392
	751	CO1094	785	DB415	819	CW1636	853	CT394
	752	CO956	786	DB53	820	CW1640	854	CT415
5	753	CO973	787	DB85	821	CW169	855	CT421
	754	CJ471	788	CW1000	822	CW172	856	CT423
	755	CJ472	789	CW1038	823	CW173	857	CT434
	756	CJ475	790	CW1087	824	CW175	858	CT440
	757	CJ483	791	CW1100	825	CV123	859	CT443
10	758	CJ484	792	CW1109	826	CV156	860	CT450
	759	CJ485	793	CW1112	827	CV160	861	CT453
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	761	CJ488	795	CW1150	829	CV203	863	CT466
	762	CJ496	796	CW1155	830	CV215	864	CT474
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	764	CJ498	798	CW1195	832	CV263	866	CT479
	765	CJ507	799	CW1200	833	CV275	867	CT489
	766	CJ508	800	CW1201	834	CV305	868	CT51
	767	CJ519	801	CW1214	835	CV328	869	CT519
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	769	CJ521	803	CW1230	837	CV394	871	CT526
	770	CJ522	804	CW1233	838	CV410	872	CT536
	771	CJ534	805	CW1272	839	CV416	873	CT541
	772	CJ536	806	CW1292	840	CV461	874	CT547
25	773	CJ543	807	CW1306	841	CV493	875	CT550
	774	CJ544	808	CW1311	842	CV501	876	CT559
	775	CJ547	809	CW1314	843	CT3	877	CT562
	776	CK53	810	CW1334	844	CT314	878	DE36
	777	CK7	811	CW1365	845	CT317	879	DE37
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	779	CL49	813	CW149	847	CT326	881	DE42
	780	CL63	814	CW152	848	CT340	882	DE63
	781	DB203	815	CW1574	849	CT353	883	DE70
	782	DB208	816	CW1611	850	CT358	884	DE83

	885	DE103	919	CS771	953	CW775	987	DA337
	886	DE105	920	CS773	954	CW795	988	DA348
	887	DE110	921	CS776	955	CW802	989	DA373
	888	DE114	922	CW222	956	CW823	990	DA388
5	889	DE117	923	CW224	957	CW835	991	DA389
	890	DEI19	924	CW226	958	CZ115	992	DA390
	891	DE91	925	CW232	959	CZ122	993	DA391
	892	DE95	926	CW254	960	CZ186	994	DA414
	893	DE96	927	CW272	961	CZ214	995	DA428
10	894	CW420	928	CW280	962	CZ247	996	DA443
	895	CW424	929	CW313	963	CZ251	997	DA451
	896	CW457	930	CW314	964	CZ268	998	CW1458
	897	CW485	931	CW347	965	CZ270	999	CW1475
	898	CS383	932	CW354	966	CZ278	1000	CW1481
15	899	CS384	933	CW363	967	CZ291	1001	CW1506
	900	CS399	934	CW374	968	CZ320	1002	CW1510
	901	CS405	935	CW382	969	CZ326	1003	CW1543
	902	CS409	936	CW383	970	CZ362	1004	CW1550
	903	CS431	937	CW386	971	CW1414	1005	CW1552
20	904	CS438	938	CW388	972	CW1440	1006	C Z 372
	905	CS454	939	CW512	973	CE209	1007	CZ374
	906	CS588	940	CW517	974	CE216	1008	CW902
	907	CS629	941	CW53	9 75	CE232	1009	CW922
	908	CS636	942	CW554	976	CE242	1010	CW924
25	909	CS637	943	CW585	977	CF193	1011	CW976
	910	CS638	944	CW618	978	CH776	1012	CW979
	911	CS645	945	CE197	979	CW1381	1013	CW984
	912	CS679	946	CW662	980	CW1389	1014	CW998
	913	CS682	947	CW675	981	CW1399	1015	CZ1
30	914	CS734	948	CW691	982	CZ653	1016	CW753
	915	CS743	949	CW707	983	CZ681	1017	CW759
	916	CS752	950	CW735	984	CZ711	1018	CW800
	917	CS756	951	CW762	985	CZ719	1019	CW891
	918	CS765	952	CW768	986	DA306	1020	CW960

	1021	CT80	1055	DC14	1089	DH1206	1123	DF478
	1022	DF1115	1056	CW1670	1090	DH1212	1124	DF483
	1023	DF1117	1057	CW1682	1091	DH1213	1125	DF494
	1024	DF1125	1058	DF814	1092	DH190	1126	DF499
5	1025	DF134	1059	DF821	1093	DI191	1127	DF7
	1026	DF14	1060	DF842	1094	DI207	1128	DF706
	1027	DF163	1061	DG1	1095	DI216	1129	DF713
	1028	DF174	1062	DG17	1096	DI243	1130	DF 7 27
	1029	DF175	1063	DG174	1097	DI248	1131	DF737
10	1030	DF180	1064	DG256	1098	DI261	1132	DF756
	1031	DF185	1065	DG26	1099	DF1005	1133	DF757
	1032	DF201	1066	DG266	1100	DF1009	1134	DF762
	1033	DF202	1067	DG326	1101	DF1010	1135	DF776
	1034	DF203	1068	DG327	1102	DF102	1136	DF777
15	1035	DF206	1069	DG329	1103	DF1050	1137	DF780
	1036	DF219	1070	DG330	1104	DF1062	1138	DF783
	1037	DF230	1071	DG331	1105	DF1063	1139	DG12
	1038	DF232	1072	DG44	1106	DF1084	1140	DG121
	1039	DF239	1073	DG65	1107	DF153	1141	DG128
20	1040	DF244	1074	DG69	1108	DF218	1142	DG141
	1041	DF259	1075	DG7	1109	DF251	1143	DG149
	1042	DF266	1076	DG71	1110	DF280	1144	DH28
	1043	DF46	1077	DG76	1111	DF286	1145	DH303
	1044	DF65	1078	DG82	1112	DF316	1146	DH318
25	1045	DF69	1079	DH1086	1113	DF317	1147	DH322
	1046	DB145	1080	DH1098	1114	DF343	1148	DH340
	1047	DB150	1081	DH1135	1115	DF347	1149	DH371
	1048	DB159	1082	DH1145	1116	DF370	1150	DH40
	1049	DB174	1083	DH1153	1117	DF382	1151	DH401
30	1050	DB180	1084	DH1182	1118	DF396	1152	DH432
	1051	CY1	1085	DH1185	1119	DF428	1153	DH451
	1052	CYII	1086	DH1190	1120	DF453	1154	DH496
	1053	CY3	1087	DH1191	1121	DF457	1155	DH502
	1054	CY9	1088	DH1201	1122	DF460	1156	DH529

	1157	DH66	1191	DF915	1225	DH1357	1259	D1501
	1158	DF518	1192	DF948	1226	DH145	1260	D1504
	1159	DF521	1193	DF950	1227	DH999	1261	DKIII
	1160	DF538	1194	DF956	1228	DI160	1262	DK113
5	1161	DF543	1195	DF966	1229	DI386	1263	DK120
	1162	DF545	1196	DF968	1230	DI391	1264	DK122
	1163	DF547	1197	DF971	1231	DI435	1265	DK126
	1164	DF568	1198	DF973	1232	DI448	1266	DK134
	1165	DF587	1199	DF979	1233	DI454	1267	DK136
10	1166	DF589	1200	DF984	1234	DJ109	1268	DK150
	1167	DF591	1201	DF989	1235	DJ146	1269	DK160
	1168	DF601	1202	DH1257	1236	DJ167	1270	DK170
	1169	DF606	1203	DH1308	1237	DF1065	1271	DK182
	1170	DF62	1204	DH1314	1238	DI387	1272	DK185
15	1171	DF620	1205	DI341	1239	DI393	1273	DK197
	1172	DF625	1206	DH1265	1240	DI403	1274	DK206
	1173	DF648	1207	DI349	1241	DI430	1275	DK219
	1174	DF657	1208	DI355	1242	DI438	1276	DK223
	1175	DF659	1209	DI362	1243	DJ2	1277	DK227
20	1176	DF661	1210	DI366	1244	DJ188	1278	DK229
	1177	DF662	1211	DI508	1245	DJ238	1279	DK230
	1178	DF670	1212	DI516	1246	DJ259	1280	DK243
	1179	DF674	1213	DI518	1247	DK64	1281	DK264
	1180	DF682	1214	DF1066	1248	DK70	1282	DK268
25	1181	DF688	1215	DF1069	1249	DK81	1283	DK31
	1182	DF810	1216	DG279	1250	DK84	1284	DK39
	1183	DF823	1217	DH1010	1251	DI462	1285	DK93
	1184	DF835	1218	DH1013	1252	DI466	1286	DL101
	1185	DF860	1219	DH1044	1253	DI474	1287	DL110
30	1186	DF877	1220	DH1045	1254	DI475	1288	DL116
	1187	DF883	1221	DH1073	1255	DI479	1289	DL132
	1188	DF895	1222	DH1078	1256	DI480	1290	DL63
	1189	DF909	1223	DH1340	1257	D1482	1291	DL82
	1190	DF910	1224	DH1349	1258	DI500	1292	DL95

	1293	DL99	1327	DL491	1361	DL547	1395	DO181
	1294	DJ332	1328	DL495	1362	DL550	1396	DO419
	1295	DJ362	1329	DL498	1363	DL551	1397	DO424
	1296	DK290	1330	DL504	1364	DL601	1398	DO440
5	1297	DK321 -	1331	DM118	1365	DL604	1399	DO447
	1298	DK324	1332	DM122	1366	DL605	1400	DO568
	1299	DK329	1333	DM126	1367	DL607	1401	DO575
	1300	DK357	1334	DM128	1368	DL608	1402	DO589
	1301	DK360	1335	DM130	1369	DL616	1403	DO610
10	1302	DL141	1336	DM147	1370	DL619	1404	DO715
	1303	DL146	1337	DM169	1371	DL620	1405	DO722
	1304	DL162	1338	DM26	1372	DL634	1406	DO737
	1305	DL163	1339	DM404	1373	DM194	1407	DO742
	1306	DL169	1340	DM406	1374	DM197	1408	DO755
15	1307	DL181	1341	DM407	1375	DM221	1409	DO765
	1308	DL185	1342	DM420	1376	DM248	1410	DO797
	1309	DL218	1343	DM425	1377	DM250	1411	DO836
	1310	DL220	1344	DM435	1378	DM262	1412	DO884
	1311	DL248	1345	DM445	1379	DM265	1413	DO896
20	1312	DL289	1346	DM449	1380	DM272	1414	CZ549
r	1313	DL290	1347	DM459	1381	DM278	1415	CZ598
	1314	DL291	1348	DM462	1382	DM293	1416	DT431
	1315	DL316	1349	DM469	1383	DM303	1417	DT443
	1316	DL320	1350	DM482	1384	DM340	1418	DT446
25	1317	DL321	1351	DM6	1385	DM360	1419	DT449
	1318	DL425	1352	DM94	1386	DM365	1420	DT450
	1319	DL426	1353	D J279	1387	DM522	1421	DT455
	1320	DL427	1354	DJ284	1388	DM533	1422	DT458
	1321	DL439	1355	DJ299	1389	DM542	1423	DN106
30	1322	DL440	1356	DJ319	1390	DM87	1424	DN153
	1323	DL444	1357	DJ323	1391	DN124	1425	DN176
	1324	DL457	1358	DL531	1392	DN144	1426	DT530
	1325	DL463	1359	DL535	1393	DN 147	1427	DT534
	1326	DL466	1360	DL543	1394	DN167	1428	DT535

	1429	DT544	1463	DWI	1497	BK5
	1430	DT563	1464	DW389	1498	BK504
	1431	DT584	1465	DW398	1499	BK513
	1432	DT590	1466	DW654	1500	BK517
5	1433	DT596	1467	DW659		
	1434	DT597	1468	DW665		
	1435	DT598	1469	DW694		
	1436	DT640	1470	DW705		
	1437	DT655	1471	DW716		
10	1438	DT674	1472	DW749		
	1439	DT719	1473	DW761		
	1440	DT734	1474	DW765		
	1441	DT779	1475	DW771		
	1442	DT801	1476	DW78		
15	1443	DT802	1477	DW780		
	1444	DN696	1478	BK10		
	1445	DN697	1479	BK11		
	1446	DN704	1480	BK2		
	1447	DN710	1481	BK368		
20	1448	DN711	1482	BK373		
	1449	DN714	1483	BK374		
	1450	DN721	1484	BK375		
	1451	DN722	1485	BK384		
	1452	DN732	1486	BK402		
25	1453	DN740	1487	BK410		
	1454	DN746	1488	BK415		
	1455	DN747	1489	BK425		
	1456	DN753	1490	BK427		
	1457	DN756	1491	BK436		
30	1458	DN764	1492	BK445		
	1459	DN770	1493	BK455		
	1460	DN772	1494	BK458		
	1461	DN1120	1495	BK494		
	1462	DU372	1496	BK498		

The "Clone ID No." for a particular clone consists of one or two letters followed by a number. The letters designate the tissue source from which the sEST was isolated. Table 3 below lists the various sources which were run through applicants' signal sequence trap. Thus, the tissue source for a particular sEST sequence can be identified in Table 3 by the one and two letter designations used in the relevant "Clone ID No.". For example, a clone designated as "BA312" would have been isolated from a human placenta (26 yrs.) library (i.e., selection "BA") as indicated in Table 3.

As used herein, "polynucleotide" includes single- and double-stranded RNAs, DNAs and RNA:DNA hybrids.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplpasmic reticulum.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decayalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

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The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides disclosed herein.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions, most preferably under highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in Table 1 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

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Table 1

	Stringenc y Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer†	Wash Temperature and Buffer'
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	В	DNA:DNA	< 50	T _B *; 1xSSC	T _B *; 1xSSC
:	С	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	< 50	T _D *; 1xSSC	T _D *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
10	F	RNA:RNA	< 50	T _F *; 1xSSC	T _F *; 1xSSC
	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	Н	DNA:DNA	< 50	T _H *; 4xSSC	T _H *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	< 50	T,*; 4xSSC	T,*; 4xSSC
15	K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	< 50	T _L *; 2xSSC	T _L *; 2xSSC
	М	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	< 50	T _N *; 6xSSC	T _N *; 6xSSC
	0	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
20	P	DNA:RNA	< 50	T _P *; 6xSSC	T _p *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	< 50	T _R *; 4xSSC	T _R *; 4xSSC

^{\$\frac{1}{2}\$}: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

[†]: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

* T_B - T_R : The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, $T_m(^{\circ}C) = 2(\# \text{ of } A + T \text{ bases}) + 4(\# \text{ of } G + C \text{ bases})$. For hybrids between 18 and 49 base pairs in length, $T_m(^{\circ}C) = 81.5 + 16.6(\log [Na^+]) + 0.41(\%G+C) - (600/N)$, where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, such hybridizing polynucleotides have at least 70% sequence identity (more preferably, at least 80% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which they hybridize, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control

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sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac[®] kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA

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Sepharose[®]; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications

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of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

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USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The primary use of polynucleotides of the invention which are sESTs is as porbes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond (i.e., is a longer polynucleotide sequence of which substantially the entire sEST is a fragment in the case of a full-length cDNA, or which encodes the sEST in the case of a genomic DNA molecule) to such sESTs. Techniques for use of such sequences as probes for larger cDNAs or genomic molecules are well known in the art.

The polynucleotides can also be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise antiprotein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify 10

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polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley

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and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre

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syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-

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blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor: ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral

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infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate. T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I

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or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowmanet al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3,8,1-3,8,16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-

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3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

25 Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for

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example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

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H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

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A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-liketissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-liketissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic

plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

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A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

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A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale

et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

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A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

15 <u>Receptor/Ligand Activity</u>

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A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusioninjury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

20 <u>Tumor Inhibition Activity</u>

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

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Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting

(suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or caricadic cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

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ADMINISTRATION AND DOSING

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A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that

can directly signal T cells. Alternatively antibodies able to bind surface immunolgobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

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Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with

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which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about $0.01~\mu g$ to about 100~mg (preferably about 0.1~mg to about 10~mg, more preferably about $0.1~\mu g$ to about 1~mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem. Soc. 85, 2149-2154 (1963); J.L. Krstenansky, et al., FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a

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pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses(including hydroxyalkylcelluloses),including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

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poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorbtion of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

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Patent and literature references cited herein are incorporated by reference as if fully set forth.

Table 3

Sel.	Species	Tissue	Cell Type
AA	Human	Kidney	19-23wks., M/F pool of 5
AB	Human	Fetal Lung	Fetal Lung
AC	Human	Placenta	26yrs., 1 specimen
AD	Murine	Embryo	Fetal ES cells
AE	Murine	Spleen	Adult spleen
AF	Murine	Fetal Brain	Fetal Brain
AG	Murine	Fetal Brain	Fetal Brain
AH	Murine		Fetal Thymus
AI		Fetal Thymus	Adult PBMC/TH1or2
AI AJ	Human Human	Blood Testes	
			10-61yrs., pool of 11
AK	Human	Kidney	19-23wks., M/F pool of 5
AL	Human	Neural	Adult Glioblastoma line TG-1
AM	Human	Kidney	19-23wks., M/F pool of 5
AN	Murine	Bone Marrow	Adult Stromal cell line FCM-4
AO	Murine	Thymus	Adult Subtr. Adult Thymus
AP	Human	Placenta	26yrs., 1 specimen
AQ	Human	Ovary	PA-1 Teratocarcinoma
AR	Human	Retina	16-75yrs., pool of 76
AS	Human	Brain	19-23wks., M/F pool of 5
AT	Human	Blood	Adult lymphocytes+dend. cells
AU	Human	Testes	10-61yrs., pool of 11
AV	Murine	Spleen	Adult spleen
AW	Human	Ovary	PA-1 Teratocarcinoma
AX	Human	Testes	10-61yrs., pool of 11
AY	Human	Retina	16-75yrs., pool of 76
ΑZ	Human	Colon	Caco-2 Adenocarcinoma
В	Human	Blood	PeripheralBloodMononuclearCell
BA	Human	Placenta	26yrs., 1 specimen
BB	Human	Blood	Adult PBMC/TH1or2
BC	Murine	Embryo	Fetal ES cells
BD	Human	Kidney	19-23wks., M/F pool of 5
BE	Human	Blood	Adult PBMC/TH1or2
BF	Human	Brain	19-23wks., M/F pool of 5
BG	Human	Brain	N/A
BH	Human	Ovary	PA-1 Teratocarcinoma
BI	Human	Kidney	19-23wks., M/F pool of 5
BJ	Human	Ovary	PA-1 Teratocarcinoma
BK	Human	Retina	16-75yrs., pool of 76
BL	Human	Testes	10-61 yrs., pool of 11
BM	Human	Muscle	N/A
BN	Human	Placenta	26yrs., 1 specimen
во	Human	Retina	16-75yrs., pool of 76
BP	Human	Kidney	19-23wks., M/F pool of 5
BQ	Human	Colon	Caco-2 Adenocarcinoma Caco2

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BR	Human	Kidney	19-23wks., M/F pool of 5
BS	Human	Pituitary	Adult Pituitary
BT	Human	Blood	Adult PBMC
BU	Human	Placenta	26yrs., 1 specimen
BV	Human	Brain	N/A
BW	Human	Blood	Adult PBMC
BX	Human		
		Ovary	PA-1 Teratocarcinoma
BY	Human	Blood	Adult PBMC/TH1or2
BZ	Human	Kidney	19-23wks., M/F pool of 5
С	Human	Blood	PeripheralBloodMononuclearCell
CA	Murine	Embryo	Fetal ES cell embryoid bodies
CB	Human	Brain	19-23wks., M/F pool of 5
CC	Human	Brain	N/A
CD	Human	Brain	19-23wks., M/F pool of 5
CE	Human	Blood	Adult lymphocytes+dend. cells
CF	Human	Placenta	
CG	Human		26yrs., 1 specimen
CH		Testes	10-61yrs., pool of 11
	Human	Kidney	19-23wks., M/F pool of 5
CI	Human	Brain	N/A
CJ	Human	Brain	19-23wks., M/F pool of 5
CK	Human	Testes	10-61yrs., pool of 11
CL	Human	Retina	16-75yrs., pool of 76
CM	Human	Adult Lung	Adult Lung
CN	Human	Brain	19-23wks., M/F pool of 5
CO	Human	Brain	N/A
CP	Human	SalivaryGland	N/A
CQ	Human	Heart	
CR	Human	Testes	13-73yrs., pool of 3
CS			10-61yrs., pool of 11
	Human	Brain	19-23wks., M/F pool of 5
CT	Human	Brain	N/A
CU	Human	Pineal Gland	N/A
CV	Human	Mammary	Adult Human Mammary
CW	Human	Brain	19-23wks., M/F pool of 5
CY	Human	Pineal Gland	N/A
CZ	Human	Testes	10-61yrs., pool of 11
D	Human	Blood	PeripheralBloodMononuclearCell
DA	Human	Placenta	26yrs., 1 specimen
DB	Human	Prostate	Adult Prostate
DC	Human	Pineal Gland	Adult Pineal Gland
DD			
	Human	Testes	10-61yrs., pool of 11
DE	Human	Testes	Adult NCCIT TeratoCA
DF	Human	Brain	N/A
DG	Human	Placenta	26yrs., 1 specimen
DH	Human	Brain	19-23wks., M/F pool of 5
DI	Human	Testes	10-61yrs., pool of 11
DJ	Human	Placenta	26yrs., 1 specimen
DK	Human	Fetal Kidney2	Fetal Kidney
			- Juni Island

DI	11	Dania	NI/A
DL DM	Human	Brain	N/A N/A
	Human	Brain	
DN	Human Human	Brain Testes	19-23wks., M/F pool of 5
DO			10-61yrs., pool of 11
DP	Murine	Embryo	Fetal ES cell embryoid bodies
DQ	Human	Placenta	26yrs., 1 specimen
DR	Human	SalivaryGland	N/A
DT	Human	Brain	N/A
DU	Human	Brain	19-23wks., M/F pool of 5
DV	Human	Pineal Gland	Adult Pineal Gland
DW	Human	Brain	N/A
DX	Human	Testes	10-61 yrs., pool of 11
DY	Human	Brain	N/A
DZ	Human	Testes	Adult NCCIT TeratoCA
E	Human	Blood	PeripheralBloodMononuclearCell
EA	Human	Brain	19-23wks., M/F pool of 5
EB	Human	Melanoma	Adult Melanoma
EC	Human	Brain	N/A
ED	Human	Placenta	26yrs., 1 specimen
EE	Human	Testes	10-61 yrs., pool of 11
EF	Human	Liver	Adult Liver
EG	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
EH	Human	Blood	PeripheralBloodMononuclearCell
EI	Human	Brain	19-23wks., M/F pool of 5
EJ	Human	Placenta	26yrs., 1 specimen
EK	Human	Brain	19-23wks., M/F pool of 5
EL	Human	Testes	10-61 yrs., pool of 11
EM	Human	Fetal Kidney2	Fetal Kidney
EN	Human	Brain	19-23wks., M/F pool of 5
EO	Human	Adrenal Gland	Adult Adrenal Gland
EP	Human	Placenta	26yrs., 1 specimen
EQ	Human	Testes	10-61 yrs., pool of 11
ER	Human	Brain	19-23wks., M/F pool of 5
ES	Human	Placenta	26yrs., 1 specimen
ET	Human	Testes	10-61 yrs., pool of 11
EU	Human	Kidney	Adult Kidney
EV	Human	Stomach	Adult Stomach
EW	Human	Placenta	26yrs., 1 specimen
EX	Human	Testes	10-61 yrs., pool of 11
EY	Human	Brain	19-23wks., M/F pool of 5
EZ	Human	Fetal Kidney2	Fetal Kidney
FA	Human	Brain	19-23wks., M/F pool of 5
FB	Human	Placenta	26yrs., 1 specimen
FC	Human	Testes	10-61 yrs., pool of 11
FD	Human	SalivaryGland	N/A
FE	Human	Brain	N/A
FF	Human	Testes	Adult NCCIT TeratoCA

FG	Human	Brain	N/A
FH	Human	Brain	19-23wks., M/F pool of 5
FI	Human	Small Intest	Adult Small Intestine
FJ	Human		
FK	Human	Lung CA	Adult Lung CA
		Kidney	Adult Kidney
FM	Human	Brain	N/A
FN	Human	Brain	19-23wks., M/F pool of 5
FO	Human	Brain	N/A
FP	Human	Placenta	26yrs., 1 specimen
FQ	Human	Testes	10-61yrs., pool of 11
FR	Human	Placenta	26yrs., 1 specimen
FS	Human	Testes	10-61yrs., pool of 11
FT	Chicken	Fetal Lung	Fetal Lung
FU ·	Chicken	Limb Bud	Fetal St. 23 Limb Bud
FV	Human	Testes	Adult NCCIT TeratoCA
FW	Human	Testes	Adult NCCIT TeratoCA
FX	Human	Brain	19-23wks., M/F pool of 5
FY	Human	Placenta	26yrs., 1 specimen
FZ	Human	Placenta	26yrs., 1 specimen
G	Human	Blood	PeripheralBloodMononuclearCell
GA	Human	Testes	10-61yrs., pool of 11
GB	Human	Placenta	26yrs., 1 specimen
GC	Human	Testes	10-61yrs., pool of 11
GD	Human	Placenta	26yrs., 1 specimen
GE	Human	Brain	N/A
GF	Human	Brain	19-23wks., M/F pool of 5
GG	Human	Fetal Kidney2	Fetal Kidney
GH	Human	Placenta	26yrs., 1 specimen
GI	Human	Retinoblastoma	Adult Retinoblastoma Y79
GJ	Murine	Spleen	Adult Spleen
GK	Human	Fetal Kidney2	Fetal Kidney
GL	Murine	Lymph Node	Adult Lymph Node
GM	Human	Uterus	N/A
GN	Human	Blood	PeripheralBloodMononuclearCell
GO	Human	Adrenal Gland	Adult Adrenal Gland
GP	Human	Ovary	PA-1 Teratocarcinoma
GQ	Human	Pineal Gland	N/A
GR	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
GS	Human	Retina	16-75yrs., pool of 76
GT	Human	Brain	N/A
GU	Human	Fetal Kidney2	
GV	Rat	Retina	Fetal Kidney Newborn Retina
GW	Chicken	Limb Bud	
GX	Human		Fetal St.26 Limb Bud
GX GY	Human Human	Brain	N/A
		Testes	10-61 yrs., pool of 11
GZ	Human	Brain	19-23wks., M/F pool of 5
Н	Human	Blood	PeripheralBloodMononuclearCell

HA	Human	Testes	Adult NCCIT TeratoCA
HB	Human	Fetal Kidney2	Fetal Kidney
HC	Human	Brain	19-23wks., M/F pool of 5
HD	Human	Brain	N/A
HE	Human	Testes	10-61yrs., pool of 11
HF	Human	Brain	19-23wks., M/F pool of 5
HG	Human	Fetal Kidney2	Fetal Kidney
HH	Human	Brain	N/A
HI	Human	Testes	10-61yrs., pool of 11
HJ	Human	Brain	N/A
HK	Human	Brain	19-23wks., M/F pool of 5
HL	Human	Fetal Kidney2	Fetal Kidney
HM	Human	Testes	Adult NCCIT TeratoCA
HN	Human	Fetal Kidney2	Fetal Kidney
НО	Human	Brain	N/A
HP	Human	Brain	19-23wks., M/F pool of 5
HQ	Human	Testes	10-61yrs., pool of 11
HR	Human	Brain	N/A
HS	Human	Brain	N/A
HT	Human	Brain	19-23wks., M/F pool of 5
HU	Human	Fetal Kidney2	Fetal Kidney
HV	Human	Testes	10-61 yrs., pool of 11
HW	Human	Brain	N/A
HX	Human	Brain Hippoca	Adult Brain Hippocampus
HY	Human	Trachea	Adult Trachea
HZ	Human	Brain Thalamus	Adult Brain Thalamus
I	Human	Blood	PeripheralBloodMononuclearCell
IA	Human	Thyroid	Adult Thyroid
IB	Human	Embryonal CA	Fetal NT2-D1
IC	Human	WER1-Rb1 line	Adult Retinoblastoma
$\mathbf{I}\!\mathbf{D}$	Human	Muscle	N/A
ΙE	Human	Brain	19-23wks., M/F pool of 5
IF	Human	Uterus	N/A
IG	Human	Testes	10-61 yrs., pool of 11
IH	Human	Muscle	N/A
П	Human	Brain	N/A
П	Human	Blood	PeripheralBloodMononuclearCell
IK	Human	Retinoblastoma	Adult Retinoblastoma Y79
IL	Human	Retina	16-75yrs., pool of 76
IM	Human	Various	Various
IN	Human	Prostate	Adult Prostate
IO	Human	Brain	19-23wks., M/F pool of 5
IΡ	Human	Fetal Kidney2	Fetal Kidney
IQ	Human	Prostate	Adult Prostate
IR	Human	Brain Hippoca	Adult Brain Hippocampus
IS	Human	Trachea	Adult Trachea
IT	Human	Brain Thalamu	Adult Brain Thalamus

SEQUENCE LISTING

(1) GENERAL	INFORMATION:
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- (i) APPLICANT: Jacobs, Kenneth
 McCoy, John
 LaVallie, Edward
 Racie, Lisa
 Merberg, David
 Treacy, Maurice
 Spaulding, Vikki
- Agostino, Michael (ii) TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
- (iii) NUMBER OF SEQUENCES: 1500
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy Disk
 - (B) COMPUTER: IBM PC Compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Scott A.
 - (B) REGISTRATION NUMBER: 32,724
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 498-8224
 - (B) TELEFAX: (617) 876-5851
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCC	TTCATGGCCT	AAGTGTTTAA	ATTATAAGCT	GGTGAAGTGA	AATAACACAA	60
ATCAAGCTCA	CCAATTTTAA	TACTCAGCTG	TTGATAAACA	ACACTGAAGA	GTGACATTTA	120
AATTTGAATT	ATCTTCTTTG	AAGTAGCATT	GCAGCACTTT	TGAATGACTT	CCAAAAGGCT	180
GATCATAAAA	ATCACTTCAA	TCATTTTCAA	ATTTTACTTT	AGCAGCAATG	AAGTTATTTG	240

GTATGACTCA GATGAACCTT CTGCTCTGTC TTGGAGTTAT TATGGTCATT TCATTTTCTG CAACCTGGGA AAACCTCGAG	300 320
(2) INFORMATION FOR SEQ ID NO:2:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 357 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
GAATTCGGCC TTCATGGCCT ACGAGTGGAT CTGGTTGAGA GGAAAGCAGC TAAAAATACA GGAGATGAAA GGGATCATAA CGAACATAAT GAACCATGTT CATTATGGTT CGTGGGGAGG CAGGAAAGCA CAGTATCCAG GGCATAGGCA GAAGAGCTGT CTTTCACGGG AGGAGGGGAA CATATTCTAC TGCAATAAGC AAGGGCGGG TAAGTACGGA TCGGGTACTT TGGGAACTAT GACGGTAGGG AGTTCAGGAA GTTGCTGCCT GAAGGCATAA AGGTTTTTTT TTTTTTTTTT	60 120 180 240 300 357
(2) INFORMATION FOR SEQ ID NO:3:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 249 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
GAATTCTTTA TATAATTGG ATACCTACTC ATTGTCAGTT GTATGCTTTG CAAATATCTT TCCTGACCCT TACTTACCTT TTCACTCTTA ATGGTATCTT TGATGAATCA AAAATTTTTC TTTTTTTGTT GTTTTTTGAG ACAGAGTCTT AACTCTGTCA CCCAGGCTGG AGTGCAGTGC	60 120 180 240 249
(2) INFORMATION FOR SEQ ID NO:4:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 262 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
GAATTCGGCC TTCATGGCCT AGACCTGCCT CTAGCTCCTT TCCTTCTACT CTCCTGCTCA GACCATTAGT AGGTACTTTG TTAAATAAAA AACTAGATTA ACATCAATAT TACTCCAATT TGGTATCTTT TACACCTAGT ATTATACCTA CTTTCTTTTT ATTTCATTTA CAAATAGTTT AAATTACTTT ATCAACCAGC TGTATTGTTT CCCTCTTGTA AAAGTACCAT CAAGTGGGGA AAATGTATGT GGCAGTCTCG AG	60 120 180 240 262
(2) INFORMATION FOR SEC. ID NO. F.	



- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCC TTCATGGCCT A	ATAACTTAC	CCAGTCACGA	ATATTTCTTC	ATAGCAGCAT	60
CAGAGTGGAC TAATACGATT A	TAATTATCA	TCACCTTTTG	ACTGACCAAT	TGATTTACAG	120
TATTGAGTTC AATCTGTTTT T					180
GTGGGGTACA AAAATGTATT T					240
GTACCTCGAG					250

- (2) INFORMATION FOR SEQ ID NO:6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCGGCC	TTCATGGCCT	AGGTGCTGGA	AGTAAGCTGT	GTGAACAAAT	GAGACGATTC	60
				GATACATGCT		120
					AGAGGCTTCG	180
				AGCGACTTGG		240
		AGTTGGAGAG				276

- (2) INFORMATION FOR SEQ ID NO:7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCGGCC	TTCATGGCCT	ACTCATTCCA	AAAAAAAAA	AAAAATTTCC	CATGATCTTA	60
TCTAGCTTCT	CTAGCAGTAC	TTGTATGATT	TCACCTTTCT	TTCTTTATTC	TTTTCTTCCA	120
TATTTTTTT	TTTTGAGACA	GGGTCTCACT	CTATTGTCCA	GGCTAGAGTG	CAGTAGTTTG	180
			GGCCTAAGTA			240
			CATGCCTGGC			284

- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTTGAATTCT	AGACCTGCCT	CGAGGACGCC	AGGGAAGTGA	GTTGAAAATC	TGAAAATGCG	60
GCCATGGACT	GGTTCCTGGC	GTTGGATTAT	GCTCATTCTT	TTTGCCTGGG	GGACCTTGCT	120
GTTTTATATA	GGTGGTCACT	TGGTACGAGA	TAATGACCAT	CCTGATCACT	CTAGCCGAGA	180
ACTGTCCAAG	ATTCTGGCAA	AGCTTGAACG	CTTAAAACAG	CAGAATGAAG	ACTTGAGGCG	240
AATGGCCGAA	TCTCTCCGGA	TACCAGAAGG	CCCTATTGAT	CAGGGGCCAG	CTATAGGAAG	300
AGTGCGCGTT	TTAGAAGAGC	AGCTTGTTAA	GGCCAAAGAA	CAGATTGAAA	ATTACAAGAA	360
ACAGACCAGA	AATGGTCTGG	GGAAGGATCT	CGAG			394

- (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGTGATGA	AAATGCTTTA	TGCTTCAACA	CTGTTGGAGG	ACACAACTGT	GTTTGCAAGC	60
CGGGCTATAC	AGGGAATGGA	ACGACATGCA	AAGCATTTTG	CAAAGATGGC	TGTAGGAATG	120
GAGGAGCCTG	TATTGCCGCT	AATGTGTGTG	CCTGCCCACA	AGGCTTCACT	GGACCCAGCT	180
GTGAAACGGA	CATTGATGAA	TGCTCTGATG	GTTTTGTTCA	ATGTGACAGT	CGTGCTAATT	240
GCATTAACCT	GCCTGGATGG	TACCACTGTG	AGTGCAGAGA	TGGCTACCAT	GACAATGGGA	300
TGTTTTCACC	AAGTGGAGAA	TCGTGTGAAG	ATATTGATGA	GTGTGGGACC	ACTCGAG	357

- (2) INFORMATION FOR SEQ ID NO:10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCGGCC	TTCATGGCCT	ATTTCCGATC	TATGTATCTG	TACTCATACA	GCCTCATCGG	60
GCTAAACAGC	CTTCTTTTCA	GAACAGTAGA	TCACTCAACT	GGGTTTTCAA	GTGACTGTTT	120
ACCTTTCAAG	GCTGGCTTTA	TAGGTCTTGC	CTCACTGTAT	CCAGCAATCC	AAACTTTACC	180
CTATCCCAGT	CAGGACTGCA	CACCTCATAT	TGAAAGACAT	ACCTTAGAAC	CAGACTCCCC	240
AAACCTTACA	AATATCCCAC	CCTTGACTCC	CGTTCTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCTAGA	CCTGCCTCGA	GCGCCACACA	GTGACTGCCG	GGTAAAGTTG	TGGAATTACG	60
TCCCTGGACT	CACCCCTGC	CTTCCTCGCC	GAGTCCTGGC	CATAAAGGGC	CGCGCCACCA	120
CCCTGCCCTG	ACCCTCCCCA	ACTCTCCCTG	TCTCCTCTTT	CATTCTTCCC	CTCTTTCCTT	180
TTCCCTCTCT	TTCCCCACTT	CGATATGAGC	TGCTTCTTAA	CGGTATGAGA	TTATTTNACT	240
CCTTCTTCTT	CCTTTCCCTT	CCTGTCCTGC	CTGGCCTAGA	GAGGTGCCCT	GCCTGTCCCT	300
CCTGCACCCA	CCGTCCTTTT	CCAAGCATGA	ACAGTGGGAC	AGGCCCCAGG	AGATGGGTGC	360
CAGGGAGCAG	AAGGGGGAGC	CTTCAGGCCT	GGACAAAACG	AAACACCCCC	CCAAAAAAAG	420
NAAACCCACG	ACTCGAG					437

- (2) INFORMATION FOR SEQ ID NO:12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTTCTTCTA AGTAGATC	TT CCTTCCCCAT	TAAACTAGGT	TTTCTACTGC	AAGATATTTT	60
GTGCATTGCT GTTTTAAA	CC CTTTTAACAG	CGAATCATAG	CAGTCTAAGA	AGTCTTCTGA	120
ACCATCCTGG ACTCTTGG	AAATTTTAAT	TTGTGTCTAC	AAGTTCTCTG	ACATTCTTCC	180
CACCAAGAGG TAGAGTCT	TTCCCCTCCC	TTTGAACCTA	GGTAGGCCTT	TGTTACTGCC	240
TTGATGAATA CAATGAGA	CT CGAG				264

- (2) INFORMATION FOR SEQ ID NO:13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATTTTTTAC CCAAAGCTCT	GGAATTGTAC	ATTTATTTT	TAAAACTCAA	AGAGGGAAA G	60
AGCCTTGTAT CATATGTGAA	CATTGTATCA	TAGGTAATGT	TGTACAGACC	CTTTTATACA	120
GTGATCTGTC TTGTTCCTGC	AGCAAAAATC	CTCTATGGAC	ATAGGAGGTG	CTGTGTCCCA	180
TGCCCTCTTG CCCTGACAGT	GTCCCATGGG	CCCCCTTCTG	CTCCCTGCCC	CCTCCCTGCT	240
ACTGCTGATG CACTCCCCCC	CCTCGAG				267

- (2) INFORMATION FOR SEQ ID NO:14:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTCGGCC	TTCATGGCCT	ATTTTTTATT	TGTTTTGTTT	TGTTTTGTGG	GGATGGGGTT	60
TTGCCGTGTT	GCCCAGGCTG	GTTTCGAATT	TTTGGGCTTA	TGCAATCCAC	CCACCTTGGC	120
CTCCCAAAGT	GCAGGGATTA	CAGGCATGAG	CCATCTTGCT	GGGCCACCTT	TTTCTTCTCT	180
TTTAACAAAT	TCAGCAATTT	TTCAGTCCCA	GAAATCTGTA	AATACATTTT	TTGTGGAAAA	240
ATACAATGGG	AATGGCATCA	AAAGATGGTT	TCTATTAGGA	ATGGGAACAG	GTAACAGTTT	300
TCCCTGCCAC	CTCAACAATC	TCGAG				325

- (2) INFORMATION FOR SEQ ID NO:15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGGCTGGCAG	GCGGGCCAAA	GGTAATGAAG	CAAAGAGAGA	GGGAAAAGAC	GTGTGAAAAT	60
TGCAGAGGGG	GTGACCGAGG	GAAACACGTG	AGCGTGATAA	TGACAGAAAA	ACCACGGAAG	120
GAGCAAACCT	GGGCAGGGGG	TGGGAAACCC	GGGCCGTTTC	CAGGGAGCAC	AGGCAGACTC	180
AGAGGTAACA	CTCAAAAGCA	ACAACAGAAG	CAAGGAGGAA	GTGGGAAAAT	ATTTTTAATG	240
TGCTACAACG	AAACAGCTGC	CTGAATTCTA	TATACCCTCT	GAAAATAATC	TGCACATAAA	300
ATGGGAAAGC	TTCACCGCAG	CAGACCCCAC	TCGAG			335

- (2) INFORMATION FOR SEQ ID NO:16:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCGGCC	TTCATGGCCT	ATGCTTCTTC	CACGCACCAC	CACCACCACC	ACCACCATCA	60
TGGCCATAGC	CACGGTGGCC	TGGGGGTGCT	GCCTGATGGG	CAGTCCAAGC	TCCAGGCCCT	120
GCATGCCCAG	TATTGCCAAG	GACCGGGCCC	TGCCCCGCCA	CCCTACCTCC	CACCCCAGCA	180
GCCCTCTCTT	CCCCCACCTC	CCCAGCAGCC	CCCACCCTTG	CCCCACCTGG	GCTCCATTCC	240
ACCGCCTCCC	GCCTCAGCCC	CACCTGTGGG	GCCACATCGC	CACTTCCACG	CCCATGGCCC	300
AGTCCCAGGG	CCCCAACACT	ATACCTTGGG	CCGGCCAGGC	AGGGCACCCA	GACGGGGGGC	360
TGGAGGACAC	CCTCAGTTTG	CTCCACATGG	CCGCCACCCC	CTGCACCAGC	CCACATCCCC	420
ACTGCCCCTG	TACAGTCCTG	CCCCCCAGCA	CCCTCCAGCC	CACAAACAGG	GCCCTAAGCA	480
CTTCATCTTC	AGCCACCACC	CATCTCGAG				509

- (2) INFORMATION FOR SEQ ID NO:17:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGGCC	TTCATGGCCT	AAAGATGGCG	GAGAACAGCG	GTCGCGCCGG	CAAGAGCAGC	60
GGGAGCGGCG	CGGGGAAGGG	GGCGGTGTCC	GCAGAGCAGG	TGATTGCTGG	CTTCAACCGC	120
CTTCGGCAGG	AACAGCGAGG	CCTGGCATCC	AAAGCAGCTG	AGTTGGAGAT	GGAGTTGAAT	180
GAGCACAGCC	TAGTGATCGA	TACACTGAAG	GAGGTAGATG	AAACTCGTAA	GTGCTACCGC	240
ATGGTTGGAG	GAGTGCTGGT	GGAGCGAACT	GTCAAAGAGG	TGCTGCCCGC	TTTGGAGAAC	300
AACAAGGAGC	AGATACAGAA	GATCATTGAG	ACACTGACAC	AAGCAACTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:18:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCGGCC	AAAGAGGCCT	AGCTAGGTTC	TGAAGCTTCT	GAGTTCTGCA	GCCTCACCTC	60
TGAGAAAACC	TCTTTGCCAC	CAATACCATG	AAGCTCTGCG	TGACTGTCCT	GTCTCTCCTC	120
GTGCTAGTAG	CTGCCTTCTG	CTCTCTAGCA	CTCTCAGCAC	CAATGGGCTC	AGTCCCCCC	180
CCCGTACACG	CCTCGAGGCA	GGTCGAG				207

- (2) INFORMATION FOR SEQ ID NO:19:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCC	TTCATGGCCT	AGGCGGGACT	AACACAGGGT	TGTCATCTTT	TCCTTTTGCC	60
			TCTGCCATCA			120
GTTCTGTTAG	CAACAGAGTA	GAAACTGTAG	GAAAGCATCT	CAGAACAAAA	CTAAGTTGAA	180
TAAATTCACC	TAATAAAAT	GCCTTGGTCT	AGGATTCCTT	TTCTTCATCA	AAAGCTGCAA	240
GAGAAAGCCA	CTGCTTACCT	GATGCCGATT	TACTGGTCAT	TGGGGTGGGC	AGGTTTGGTT	300
CTCGAG						306

- (2) INFORMATION FOR SEQ ID NO:20:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGTCTCACTT	GTCTCATCCT	GTCGCCCAGG	CTGGAATGCA	GTGGTATGAT	CTCAGCTCAC	60
TGCAACCTCA	GCCTCCTGGG	TTCAAGTGAT	TATCCTGCCT	CAGCCTCCAA	GTANCTGGGA	120
CTATAAGCAC	ACATCACCAC	ACCCAGCCAA	TTTTTTTGAA	TTTTTAATAG	GGTTTCACTA	180
TGTTGGCCAG	GCTGGTTGAA	CTCCTATCCT	CAAGCGATCC	ACCCACCTCG	GCCTCCCGAA	240

GTGCTGGGAT TACCTGAGCC ACCGTGCCCA GCCCATTTCA CAGTACTTTT TATTTAACCC TATCGTGCTA GGGCACCATG CAATATACAG CTATTTCATT TTCCTTTTGT CTCTGTTTCT TAGGTGGTCT CGAG 30	0
(2) INFORMATION FOR SEQ ID NO:21:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 306 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
GCAATGGCAG GAATTCGAAA TATTGGCATA TGGTTCTTTT GGATTAGATT ATATAAAATC AGAAGAGGTA GAACCAGGCC CCAAGCACTC CTTTTTCTCT GCATGATACT TCTGCTTATT GTCCTTCACA CTAGCTACAT GATTTATAGT CTTGCTCCCC AATATGTTAT GTATGGAAGC CAAAATTACT TAATAGAGAC TAATATAACT TCTGATAATC ATAAAGGCAA TTCAACCCTT TCTGTGCCAA AGAGATGTGA TGCAGAAGCT CCTGAAGATC AGTGTACTGT TACCCGGACG CTCGAG	0 0 0
(2) INFORMATION FOR SEQ ID NO:22:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 340 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
GGTAGAGATA ACAAAACAGG ATACCAAAGT TGAGCTGGAG ACTTACAAGC AAACTCGGCA AGGTCTGGAT GAAATGTACA GTGATGTGTG GAAGCAGCTA AAAGAGGAGA AGAAAGTCCG GTTGGAACTG GAAAAAGAAC TGGAGTTACA AATTGGAATG AAAACCGAAA TGGAAATTGC AATGAAGTTA CTGGAAAAGG ACACCCACGA GAAGCAGGAC ACACTAGTTG CCCTCCGCCA GCAGCTGGAA GAAGTCAAAG CGATTAATTT ACAGATGTTT CACAAAGCTC AGAATGCAGA GAGCAGTTTG CAGCAGAAGA ATGAAGCCAT CACGCTCGAG (2) INFORMATION FOR SEQ ID NO:23:	0
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 176 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
ATACCCAGCA CATTGTTGCC CATATTGTTG ACATGTAGTA TGTATTTATT ACAATTATAT 12	6 C 2 C 7 G

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAATTCGGCC	AAAGAGGCCT	ATTCTTTGTC	TTTTGCACAT	GTTCTTTGAG	TCTTAGTATC	60
TGTAACGTGG	CGCTACTCTC	TCTATCATGG	GGGGGCATGT	TTTGACATTA	AATTGACTTT	120
TAAGAAAAAC	ATGTCACTAA	CCTGAAGCTC	AGCCACACAG	TGACTTTTAA	GGTTTTATTT	180
AGACTTTACT	GTTGTTCTCA	TGAGAGTAGG	TACAGACTGC	ATAAGGTTTA	GAATCCCAGC	240
ATATGTCTGA	AACGACGGGA	CTTTCACTGT	GATTTCCACC	AGAGAAATTA	TAGCAGAGTG	300
GCTGAGCATG	TGCTCTGAGG	CCAGGCCCCA	GCTCTGCTGC	TGACGAGCTG	TGTGGTCCTG	360
GGCAGAGTGG	TCTCCGAGTT	CCAGTCCCTC	CTCTGTAAAA	TGGGCTTACT	CGAG	414

- (2) INFORMATION FOR SEQ ID NO:25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 497 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAATTCGGCC	AAAGAGGCCT	AAACATATAC	CTAGTCTATA	CTCTCTCTTA	TCTCTGAACA	60
CTTTTCATCT	GGAGCTATTA	ATGCCCTCTA	GCCTTTATTA	TAATTATCAC	ATATAATTAT	120
GCCTTTTCTC	CTCAAAATTA	TCTGTTGGAG	TCATCTTATA	GTAGAGTCTT	TACAGAACAC	180
AAAGCATTCA	ATCACTTTAT	TTCAGACACC	AACCTTGTTT	TTGATGAACA	TATGTTAGTC	240
TTAAGCCATC	TAAAGTAATG	CTAATGTGGG	ATCTTATGGA	AGACTACTGG	TAATACAGGA	300
AAAAAAGTGG	CAAAGAAATC	TGACACGTTT	GGCAATTATT	CCTGAGGCTC	TGACCTCTCA	360
ATTGTTGAGT	GTTGGAGGTC	ACAGTAAACA	AACCATATAA	AGATCATGTT	GAAAGTCAAC	420
ATTATTAATA	TACCATACTT	GAAGGATATG	TGGTTATTGT	CTCACGTGTC	CATGTGAAGA	480
GACCACCGTC	CCTCGAG					497

- (2) INFORMATION FOR SEQ ID NO:26:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAATTCGGCC AAAGAGGCCT AGTTTTTGAT GAATTTGTGT TATTTACTTA TAACTAGAGT 60
TTGAATGTTT ATTGGGAAAA CTTAATCATG ATCATCTACT GGTGGCTCGA G 111

- (2) INFORMATION FOR SEQ ID NO:27:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAATTCGGCC	AAAGAGGCCT	ATGCAATTCT	GACCAGGAAG	CTCCTCTTTA	ATTGGAAATT	60
CTTAGAAAGG	TATGGAGCAA	AGGAGATCCC	AGCAAACATT	CCGGCATCTA	CTGCTCTTGG	120
GTTTTTTCTG	TGTTGGTTTT	TTTTGTTTTG	TTTTGTTTAT	GAGATGGAGT	CTCACTCTGT	180
CGCCCAGGCT	GGAGTGCAGT	GGCGCAATCT	CAGCTCACTG	CAATCTCCAC	CTCCAGAGTT	240
CAAGTGAATA	TCCTGCCTCA	GCCTCTCAAA	CAGCTGGAAT	TACAGGTATA	CACCACCACA	300
CCGAGCTCGA	G					311

- (2) INFORMATION FOR SEQ ID NO:28:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 597 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCGGCC	AAAGAGGCCT	AAGTGCAGTG	GTGCGATTAT	AGC1 CACTGT	AGCCTCAGAA	60
TCCTGGGCTC	AAGCTGTCCT	CCCACTTAGC	CTCCCAAAGT	GCTGGGACTA	CAGGCGTGTG	120
CCACGGGGCC	CAGCCATTTT	TTCGAATATT	TTCAATCTGC	AGTTGTTTGA	ATCCACAGAT	180
GCAGAACCCA	TTTCTAATGG	AGGGCTGACT	ATACCTTTCT	GATGACCTAA	ATATTTGTGT	240
CCACTATTGG	GACACTCCTT	TCTTAGTGTC	AAGGTTTGTG	AGAAATTGAG	GGCTGTTTGA	300
TGGGCAAAGA	TTATTTATTT	TATTTACTGG	CTTATCTACA	ATTGAGACAG	GGTCTCACTA	360
TGTTTCTCAG	GCTAGTTCTA	ACTCCTGGGC	TGAAGCAGTC	CTCCCATCTC	AGCCTCCCAG	420
AGTGCTGGGA	TTACAGGTGT	GACACACCAT	ACCCGGCAGA	GCAAAGAGTT	AAGAGTACAA	480
GACATTTGAT	CATCTTGAGG	AGTATTTACT	TCAGACTGAA	ACACCACATG	AAATTCTAGA	540
GTCCAACAGA	AAGTGTAATA	ATTTTTTGCT	TTTCCCTTCT	TCCGCTACAT	CCTCGAG	597

- (2) INFORMATION FOR SEQ ID NO:29:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATTCGGCC	AAAGAGGCCT	AATTCTAGAC	ATGCTCAGCT	TTGTGGATAC	GCGGACTTTG	60
TTGCTGCTTG	CAGTAACCTT	ATGCCTAGCA	ACATGCCAAT	CTTTACAAGA	GGAAACTGTA	120
AGAAAGGGCC	CAGCCGGAGA	TAGAGGACCA	CGTGGAGAAA	GGGGTCCACC	AGGCCCCCA	180
GGCAGAGATG	GTGAAGATGG	TCCCACAGGC	CCTCCTGGTC	CACCTGGTCC	TCCTGGCCCC	240
CTGGTCTCGG	TGGGAACTTT	GCTGCTCAGT	ATGATGGAAA	AGGAGTTGGA	CTTGGCCCTG	300
GACCAATGGG	CTTAATGGGA	CCTAGAGGCC	CACCTGGTGC	AGCTGGAGCC	CCAGGCCCTC	360
AAGGTTTCCA	AGGACCTGCT	GGTGAGCCTG	GTGAACCTGG	TCAAACTGGT	CCTGCAGGTG	420
GTCGTGGTCC	AGCTGGCCCT	CCTGGCAAGG	CTGGTGAAGA	TGGTCACCCT	GGAAAACCCG	480
GACGACCTGG	TGAGAGAGGC	CTCGAG				506

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAATTCGGCC	AAAGAGGCCT	AGTCTGTGGT	CATTTTCAAC	TCTCATTTAT	AGGATTCTAA	60
AAGGGCACTA	CATTACTCCA	CTCCCTTATC	TAAAATAAAT	TTAAAATTCA	TCGGAATTTG	120
TCCAGTCCTC	CATCACTGGA	AAATGTACAG	ATTCCTTCTC	TGGAAATATC	TAAAGAAAAG	180
TACAGCTAAT	GTTCCCCCAT	TTCGTGTTGT	TTTGTTGCTG	CTTTAACTAT	GAACTCATCT	240
GGCCGGGCGC	AGTGACCAAG	CCGCCGGGAG	CTGGGGAGAG	ACGCACCGGG	GCGGCGACTG	300
GGCCAGGAGA	CCAGAACACT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:31:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAATTCGGCC	AAAGAGGCCT	AGGAGCAGAT	TCCTCATGGT	GCTTGTTTAT	TATATATATT	60
TAATCCTGCT	TGACACTTTA	CCCAAGGGAG	ATGGTCCCTT	TTATCAGTTG	AATGTTAGCA	120
GCGTTATTTC	AGAGTGTGGT	GACTGGTTAG	AGAAACTCAT	GTACTCAACC	AGCCACAGTT	180
TCAAACAAAA	TTTTTATGTG	CAAAGGACAG	CAACCTTCTT	GTATGTTAAA	CCACCAGTAC	240
TCGAG						245

- (2) INFORMATION FOR SEQ ID NO:32:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATAATAAACT CCATGAGGGC AGCAACTTGG CTGGCCTGTG TGCCAGTGCT GGGGACATCA CTGAGAAATG AAGGCCCATT TGGCAGGCTA TTTTTGAGCA AGATTCCTGA GGCCCAATCG	60
CTGAGAAATG AAGGCCCATT TGGCAGGCTA TTTTTGAGCA AGATTCCTGA GGCCCAATCG	120
	180
TTGGGTGATG AGATGGACCC GAGGTATTTC ACTCCAGCTC TCGAG	225

- (2) INFORMATION FOR SEQ ID NO:33:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCCAAAGAGG	CCTAGAGAGC	TCTGGGGGGC	AACCTGGAGG	TCTGAAAAGA	GGAGCCAGAG	60
AAGGTGGTAC	CAGGCTTCCT	GGTCAGAACC	GGCCTGGAGC	TCCTTCCCTT	CCCCCTGGCC	120
TGAGAGGTTG	CTTTTAAGTC	TTCCACCCCT	TGTTCCATCT	GCCTGCCAAC	CCATCGGAAA	180
GGAATCCACA	TCATATTGGA	GATGACCCCA	TCAACCCCAG	GGCTCCAGCA	CTACCAAGTT	240
GGAATTCCAC	GCCCGGGAGT	GGGGTAGAGG	AAGACGAGAC	AGGACGAGGC	AGAAAAGCAC	300
ATTTTAAAAA	CCAGACAAGA	TGGCTAGGCC	ATCACCAACC	AACGGACTTA	CCTTACATTT	360
TTGTAGGTAA	TTCCCCCCAA	ATCTTGATTT	TTTTTTTCCT	CAATTATCCT	ATAAAAAATT	420
AGAAAACACA	TTCCAAACCC	ACTCGAG				447

- (2) INFORMATION FOR SEQ ID NO:34:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCGATTGAAT	TCTAGACCAT	GCCTGCTCTG	GGCCCAGCTC	TTCTCCAGGC	TCTCTGGGCC	60
GGGTGGGTCC	TCACCCTCCA	GCCCCTTCCA	CCAACTGCAT	TCACTCCCAA	TGGCACGTAT	120
CTGCAGCACC	TGGCAAGGGA	CCCCACCTCA	GGCACCCTCT	ACCTGGGGGC	TACCAACTTC	180
CTGTTCCAGC	TGAGCCCTGG	GCTGCAGCTG	GAGGCCACAG	TGTCCACCGG	CCCTGTGCTA	240
GACAGCAGGG	ACTGCCTGCC	ACCTGTGATG	CCTGATGAGT	GCCCCCAGGC	CCAGCCTACC	300
AACAACCCGA	ATCAGCTGCT	CCTGGTGAGC	CCAGGGGCCC	TGGTGGTATG	CGGGAGCGTG	360
CACCAGGGGG	TCTGTGAACA	GCGGCGCCTG	GGGCAGCTCG	AG		402

- (2) INFORMATION FOR SEQ ID NO:35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAATTCGGCC	AAAGAGGCCT	AGTGGAAGAT	TTGGGTACTG	TCTTTAATAA	ATCAATCAAT	60
CGACTCTTAT	TTCAAGGAGA	AAGTTCTATG	TTATATGTTG	AAGGTGAACA	GATCATATTT	120
AGAGGATATA	ACAATTAGAA	ATCTAGAAAA	TAATTATCAC	AAAATTTT	TTTTTAGTCA	180
ACTGTACAAA	TAATTACATA	AAACATCAAT	TAATTATGCT	TAAAAATCAC	TAATGTTCAT	240
AATATATAAT	CACTATTTGT	AATCAAAAGT	TTAATTTTAT	GCCAAAAAAT	AAAAAATGCT	300
TACTCGA						307

- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAATTCGGCC AAAGAGGCCT	ACTTCCATAA	CCGTGCTTTT	GACGTTAAAA	ATTTTAAAATT	60
CAGCCTTTTG GAGAACACTA	AGTATCTTAG	TGTGTTTTTA	CTTACTATAA	TAATATTATT	120
GACCTAGTGT AATATTACTG	CCATATGGAC	CTCAAGGGTA	CTTTTCTGAT	AAATTTCTGT	180
TATGGTTTCA TAATTAAACA					240
TTTTGTTTTG AGATAGCCTG					300
CACAGACACA CACCAAATCT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAATTCGGCT TCATGGCCTA	CAAGAAGATG	AAGAAGATTG	TGGATGCCGT	GATCAAGTAC	60
AAGGACAGCA GTGGACGTCA					⁻ 120
CTGCCGAGT ACTACGAGCT					. 180
ATTCGCAACC ACAAGTACCG					240
CAGAACGCAC AGACCTTCAA					300
CAGTCGGTCT TCACCAGCGT					360
GAGAGTGAGG AGGAGGAAGA					420
CTCGAG					426

- (2) INFORMATION FOR SEQ ID NO:38:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAATTCGGCC	TTCATGGCCA	ACACATAATC	CACGCTCATC	TTGCAAAGCG	CTATTTCAGG	60
			CACCTGCCAG			120
TGGAAGAGTG	ACCTGGCATC	TTGGAAATCA	TTGTGTGTCT	TCAGGAGAAT	GTGCAGTGTC	180
			GCTACATTGT			240
ATGATAAAAC	AGAATATTGA	CAAGCTAGGA	CACCTGTGGT	ATCTTTAATT	GTATCTCCTT	300
			TATGGAAGAA			360
			AGTTTGTTGA			420
GTACCATGAT	GACACTCACA	GGGAGCCACT	GTTCACTGAC	ACTTGGAAGG	CCCTGCCTCG	480
AG						482

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 363 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
GTGTTTGCCC ACACCCTCCT TGAATTTAAC TGCCACAATC TATCCGCAGA TGTGTTTTGT TCTGTTTCTT GTTTTTCACT AGCGTTTGCG TTGCTTCCTC TGAAGCCAGA GGGTGAAAGG CCCTAGCAAA GTTAGTTATC AGTCAACTGA TGATAACTGT GATCCTTAAA GATGAATTCC CAGCCTGAGG TGACACACAG AGGTTCAGCA GACGTCTCAG GATCTGTCAC ATGTCATGTT GCTTGGTGTG AAGATGGAAG AACAAAGTCC ACATCAGTTT CTGCTCCTTC AAACAGTGTG TCGATATGAA ACATTGAGAT TTGGCAGAAA CATGTGCCTA GTTTGCAGCA CCAAATACTC GAG	0 0 0
(2) INFORMATION FOR SEQ ID NO:40:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 336 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	
GAATTCGGCC TTCATGGCCT AAAGGGATAT TCACTCAAAT CCCTAAGTAT TTCAGAAACA 6 GCCTGAGAGC AAGTCCTTGG CTTCGCTTTC TAGTTTTAAA AGGCTTTTAA CTGTTTAGTC 12 TGAGATTCCC CTAAAAGTTC CAGGAAAGCA AACTCAAAAA GAGCCTAGGT GGTCAATCAT 18 TATTTTTGCT GCGTTTATAT AAATAATCAG GCCAAGTTAA TGAGACTAAA CTTATTTTGC 24 AAGCAAATCA GTCTTTGCTT ATTTTTGGTA GGAATGGGGG TAAATGGAGA GAGAGAAATT 30 ATGTTTCAGA AGAAAACTAT AGCACACCAA CTCGAG 33	0 0 0
(2) INFORMATION FOR SEQ ID NO:41:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 251 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:	
GAATTCGGCC TTCATGGCCT AGTGGGAAAC ATTATTTCAA GACATTAGGG ATAAGAATGC CAGTTGCTAC TGAGTTGGTT ATTGTTTCAA GGATTTATCA ATACATAGAG CAAATAATTA 12 TGTTTTGCTT TGTCTTATTT TTATTTCTTT ACTTTAGAAA CAGTACAGCT ACTTACAAAT 18 CAAGTTTAGA ACTCTCAGGT TATCTTAAAT CTGAAGCTTC TACCTTCCTA AGAACAAAAC ACCGGCTCGA G	8 O 4 O
(2) INFORMATION FOR SEQ ID NO:42:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTTCAACCAG	TTCAAATACT	TTTTCAACCT	CTATTTCTTA	CTTCTTGCCT	GCTCTCAGTT	60
TGTTCCCGAA	ATGAGACTTG	GTGCACTCTA	TACCTACTGG	GTTCCCCTGG	GCTTCGTGCT	120
GGCCGTCACT	GTCATCCGTG	AGGCGGTGGA	GGAGATCCGA	TGCTACGTGC	GGGACAAGGA	180
AGTCAACTCC	CAGGTCTACA	GCCGGCTCAC	AGCACGAGGC	ACAGTGAAGG	TGAAGAGTTC	240
TAACATCCAA	GTTGGAGCCC	TCGAG				265

- (2) INFORMATION FOR SEQ ID NO:43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAATTCGGCC	TTCATGGCCT	AAGATGATTG	TGCTATTATT	GTTTGCCTTG	CTCTGGATGG	60
TGGAAGGAGT	CTTTTCCCAG	CTTCACTACA	CGGTACAGGA	GGAGCAGGAA	CATGGCACTT	120
TCGTGGGGAA	TATCGCTGAA	GATCTGGGTC	TGGACATTAC	AAAACTTTCG	GCTCGCGGGT	180
TTCAGACGGT	GCCCAACTCA	AGGACCCCTT	ACTTAGACCT	CAACCTGGAG	ACAGGGGTGC	240
TGTACGTGAA	CGAGAAAATA	GACCGCGAAC	AAATCTGCAA	ACAGAGCCCC	TCCTGTGTCC	300
TGCACCTGGA	GGTCTTTCTG	GAGAACCCCC	TGGAGCTGTT	CCAGGTGGAG	ATCGAGGTGC	360
TGGACATTAA	TGACAACCCC	CCCTCTTTCC	CGGAGCCAGA	CCTGACGGTG	GAAATCTCTG	420
AGGGCGCCAC	ACTCGAG					437

- (2) INFORMATION FOR SEQ ID NO:44:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAATTCGGCC	TTCATGGCCT	AGTACCTTAA	AAACTTTGGA	ATAATAATA	ATAATAATAA	60
ACAAAAAATA	ATCCCAAACC	CCGTAAGTTT	AACTTTCTAT	GCTTTGGCTG	TTTTTGGTTT	120
ATTTTTTGTT	TTTTAGAAGG	GGTCTCGCTC	TGTCGCCCAG	AATGGAGTGC	AGTGGCTTAA	180
TCAGGGCTCA	TTGCAGCCTC	GACCTCCTTG	GTTCGGGCGA	TCCTCCTCCC	TCCACACTCG	240
AG						242

- (2) INFORMATION FOR SEQ ID NO:45:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATTAAATTA	AATTAAAATC	TTTGTTACAA	ACTATGAAAA	TGAATATAAG	TAAATTTCAT	60
ATCATTTCTT	TTCTAGATTT	ATTATCTAGG	ATAGATTTGG	ATGAACTAAT	GAAAAAAGAT	120
GAACCGCCTC	TTGATTTTCC	TGATACCCTG	GAAGGATTTG	AATATGCTTT	TAATGAAAAG	180
GGACAGTTAA	GACACATAAA	AACTGGGGAA	CCATTTGTTT	TTAACTACCG	GGAAGATTTA	240
CACAGATGGA	ACCAGAAGCT	CGAG				264

- (2) INFORMATION FOR SEQ ID NO:46:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAATTCGGCC TI	CATGGCCT A	AACCTGGAGA	AACTATTTAA	GTTGGATGAA	GCAAGTGCCC	60
AGCTCCTTGC TT	'ATAAGGAA A	AAAGGCCATT	CTCAGAGTTC	ACAATTTTCC	TCTGATCAAG	120
AAATAGCTCA TO	TGCTGCCT (GAAAATGTGA	GTGCGCTCCC	AGCTACGGTG	GCAGTTGCTT	180
CTCCACATAC CA	CCTCGGCT A	ACTCCAAAGC	CCGCCACCCT	TCTACCCACC	AATGCTTCAG	240
TGACACCTTC TG	GGACTTCC (CAGCCACAGC	TGGCCACCAC	AGCTCCACCT	GTAACCACTG	300
TCACTTCTCA GO	CTCCCACG A	ACCCTCATTT	CTACAGTTTT	TACACGGGCT	GCGGCTACAC	360
TCCAAGCAAT GO						420
AG						422

- (2) INFORMATION FOR SEQ ID NO:47:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GAATTCGGCC	TTCATGGCCT	ACCGAAGGGC	ATCCCATCGG	TTGGGTAGGT	CATGGTTAAA	60
AAATCATCTC	CTTTGGTTGC	ATATTTAATT	ATTTTCCACT	ATTTTTTCCT	CACACAAAAT	120
GATTTTGCCC	GGTACCCTTT	TTGGGGGTGC	ACAGTCCATG	AGATGAATAT	TGAATGGGGA	180
GACCTGGGTT	CTAGTCTCGC	ATTTACCAGT	CAGGTTACAA	TGCGACCTTG	AGCAAGTCAC	240
TTCACCTCCC	AGCGCCTCAG	TTTCCTCATT	GTAAGATAGG	AAAAGCCTTG	TCATTTTTAA	300
AATTTTATTT	TTTGCATATA	CCTCATGGCG	AACTCGAG			338

- (2) INFORMATION FOR SEQ ID NO:48:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GAATTCGGCC	TTCATGGCCT	ACTATGCTCT	GCACGTGGGT	CATTTCTTAC	TGGTTTCTAA	60
AAGCCTTTCA	TTTTCTGCCT	GTACACAATA	GCCCCCTTCC	TCCATTGTTT	TTAGGATCCT	120
TTTTCCTCTT	ACCAGCTGTT	AACCTGGAAG	TATTTCTTCT	TCATCCCGAA	TCTCCCATGT	180
CCTCCCCACT	TCTATTTGTT	TCCATCCAAT	GTGGATTCAT	GATCATTTTA	TGGATTTTAA	240
ACTACTCTGG	GGCTACCCTC	GAG				263

- (2) INFORMATION FOR SEQ ID NO:49:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAATTCGGCC	TTCATGGCCT	AGAAACACAT	GTGATCTGTA	CTCATGAGAA	CCTGTAGTTA	60
ACTATACGAG	CCTTGCTGTG	CATTTTGTTT	TTATCTGAGC	CTGTCTTTCA	ATGTCCTATC	120
CCTTGAGAGA	ACTGAGGGCT	GAGAACCAAG	CTTTCCGAAG	CGGTCTGAGT	GTCAGCGGTG	180
GTAGTGGTCT	CTGGAGAAAA	GAATGGAGAC	AGGATAGGAC	TTGGAGAAGA	GTGAGTCATT	240
CTTACCCAGA	AACCCTGGAG	AACACTGGAC	TCGAG			275

- (2) INFORMATION FOR SEQ ID NO:50:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGGCGTTCTC	ACGCCCGCAA	CAATTCCTGA	GTAGGGCCTT	GCTTGAGTTC	TTCGGAAAGT	60
CTCATCCACC	CCCACATCGC	CTCTTTAGGA	AGTCACTTAA	TGTTGGGCTT	CATTATTCCC	120
ACATCCCTTT	CCTTACTACT	TGCCTGCACT	TCTTGAGAAA	AAGACTGCAG	AAAGGAGAGG	180
TGGGGCTTTC	AGTAGAAACA	AGCAAACCGC	AGGTCCCTGT	GGGGGGACTC	TCCAGGAAGA	240
AGGGTAATTT	CCTGCCTCCT	TAAATTGGCT	GCTACTGTCA	GTTATTTTGC	TCCCAACCCC	300
AGAGCTTCAC	TTGCTCCTTC	ACTTCCCAGT	TCCGCAAGAA	CCGTGGGCGA	CAGTTATGGA	360
GAAGCGTCTG	CAGGAGGCTC	AGCTGTACAA	GGAGGAAGGG	AACCAGCGCT	ACCGGGAAGG	420
GAAGTACCGA	GATGCTGTGA	GTAGGTACCA	TCGAGCTCTG	CTTCAGCTGC	GGGGTCTGGA	480
TCCGAGTCTG	CCCTCTCCGT	TACCTAATCT	CGGACCTCAG	GGCCCGGCCC	TCACGCCTGA	540
ACGACCTGCC	TCGAG					555

- (2) INFORMATION FOR SEQ ID NO:51:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTGAAGATGG	ACTGCTCTGG	GGCCCATGTG	CAAGTGACCT	GTGCCAAGCT	CATCTCCAGG	60
ACAGGCCACC	TGATGAAGCT	TCTCAGTGGG	CAGCAGGAAG	TAAAGGCATC	CAAGATAGAA	120
TGGGATACGG	ACCAATGGAA	GATTGAGAAC	TACATTAATG	AGAGCACAGA	AGCCCAGAGT	180
GAACAGAAAG	AGAAGTCGCT	TGAGCTCAAA	AAAGAAGTTC	CAGGATATGG	CTATACTGAC	240
AAACTCATCT	TGGCATTAAT	TGTTACTGGA	ATACTAACGA	TTTTGATTAT	ACTTTTCTGC	300
CTCATTGTGA	TATGTTGTCA	CCGAAGGTCA	TTACAAGAAG	ATGAAGAAGG	ATCACTCGAG	360

- (2) INFORMATION FOR SEQ ID NO:52:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 621 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GAATTCGGCC	TTCATGGCCT	AGCTCCTGCG	TAAAGGAGCA	TGAGAGCGTG	GGAGTTTTGC	60
AGTGGCCGTG	GGGTTCTTCG	TCGCGTCTCG	GTCGGGCGTC	GCTTTCTGCA	GCTCCTGTCA	120
GGGAGCGCGA	GGCCTGTTAT	TAACCGCGGA	GCGCTTTGTC	ACGAANTCCC	TGTGGCGTCT	180
TGAAGAAGGC	ATTCCCCACC	CGCCAAATGG	CGTCCATGCC	CCCGACGCCC	GAGGCCCAGG	240
AGAGTCGAGG	TACCTTTTTC	GTCCAAGTTT	ATNGCTGCTT	TCGGTCTCTG	CCTGACCCCN	300
TCCTTTGGAG	GAGAGTTGGG	CATGCCTGTT	GTGGTAGGAG	TGCTCNTGAG	CCCCAAATAG	360
CCCTTTGACC	AAGTGTTCTT	CGTTCCAAGA	CCACACACAT	AATGGTTTAC	CAACTTCNTT	420
CTTTCAGAAC	TACCAACTGG	GAGCAGGGAC	CTGTGGAGGA	ATCTCTGAGA	GAGTTTCTCA	480
ATGTCTTATC	TGTTTGTTTT	GTTTTGTTTG	GAGATAGGGT	CTGGCCTTGT	CGCTGGAGTG	540
TTGCTTGTCT	GGCTGGAGTG	CAGTGCTGAT	ATCATAGCTC	CGTCTGGAAC	TCAGGGAATC	600
CTTACGCCTC	AGCCTCTCGA	G				621

- (2) INFORMATION FOR SEQ ID NO:53:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAATTCGGCC	TTCATGGCCT	ACAATTTGGA	GCAAGGCTTA	GCAGAAGACG	GCGGCATGAG	60
CAGCGTGACT	CAGGAGGGCA	GACAAGCCTC	TATCCGGCTG	TGGAGGTCAC	GTCTGGGCCG	120
GGTGATGTAC	TCCATGGCAA	ACTGTCTGCT	CCTGATGAAG	GATTATGTGC	TGGCCGTGGA	180
GGCGTATCAT	TCGGTTATCA	AGTATTACCC	AGAGCAAGAG	CCCCAGCTGC	TCAGCGGCAT	240
CGGCCGGATT	TCCCTGCAGA	TTGGAGACAT	AAAAACAGCT	GAAAAGTATT	TTCAAGACGT	300
TGAGAAAGTA	ACACAGAAAT	TAGACGGACC	TCTCGAG			337

- (2) INFORMATION FOR SEQ ID NO:54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GAATTCGGCC	AAAGAGGCCT	ACATTACTGG	GTTAGAAAAC	AAAGAGGGAG	TGCCCTGCAC	60
ATTTTCTTTT	GTGCTTTTAA	ATGTTTCTTA	AGTTGGAACA	GGTTTCCTCG	GGCCTGTTTT	120
GACTGATTGC	TGGAGTGCAT	TTGATAGTTA	AAAATTACTA	ATTGGTTTTA	TTTCCCTTCA	180
CACTCTGCCT	CCCCTATTTC	CCCCAATTGA	CCCTAAACCT	CGAG		224

- (2) INFORMATION FOR SEQ ID NO:55:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATTTAATGC	ATGCTAGCAA	CAGCCTTAAC	TTTGGATTCA	GTTATTTGAA	ACACTTTTCC	60
GGCATCTTTC	CCTTTCTAAT	GTTGTGGGGT	GGAAACCGGA	TGGCAAATCA	CTGTGAGCCG	120
GATACCTCAG	CACAGTCCAC	CTTGTGTGTG	ACTTCACAAA	TGGGGGACTT	CACAAATGGG	180
GTAACTGAAT	GTTATTACTT	TCAAATTTTG	ACATGGAGCA	TTATGATCAA	GGAAATGGAG	240
CAACTCGAG						249

- (2) INFORMATION FOR SEQ ID NO:56:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCTGCGCCGC	ACCCTGAGAG	ATGGTTGGTG	CCATGTGGAA	GGTGATTGTT	TCGCTGGTCC	60
TGTTGATGCC	TGGCCCCTGT	GATGGGCTGT	TTCACTCCCT	ATACAGAAGT	GTTTCCATGC	120
CACCTAAGGG	AGACTCAGGA	CAGCCATTAT	TTCTCACCCC	TTACATTGAA	GCTGGGAAGA	180
TCCAAAAAGG	AAGAGAATTG	AGTTTGGTCG	GTCCTTTCCC	AGGACTGAAC	ATGAAGAGTT	240
ATGCCGGCTA	CCTCGAG					257

- (2) INFORMATION FOR SEQ ID NO:57:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATAATTCAAA CITIGICIC AGAGCATIGC CITIATAAGC AGATIGGCAC CAACAGTICC ATAGTTTAAC ATCTAGTTAA GCTACAAATA TAGTATAAGC ATTATTAGCA GCTGGTACTT CTGCTAGGGG TTGTAAATTC CAGGTGTTAC ACTGACCTCA ATCCAATTTA CATAATTTAC ATAAATGCAT CTCGGTGGAA AAATAATCAT TTTCTTGGCA TATCTCGAG	120 180 229
(2) INFORMATION FOR SEQ ID NO:58:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 257 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
GAATTCGGCC TTCATGGCCT ACACTGCTAT GTATGTTTTC TCCTTAATGA TGAAGAGTGT AGATGATGCT AATAATAGTA GCTGATGTAC TGACTTTTAG CTGTGTGCAA AGCCATGTTC AAAATACTTT ACAAGTGTTA ACTTGTTTGA TCTTCACAAC AACCCTAAGA AGTGGATATT ATTAAAGTAG ATTTTGGAAG ACTGATCTAT TTAATTATTA ATAGATCTGT CTCATTCCTT TTTTCCCCCA ACTCGAG	60 120 180 240 257
(2) INFORMATION FOR SEQ ID NO:59:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 223 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
GAATTCGGCC TTCATGGCCT ACGCGTCTGC TTCGGAGACC GTAAGGATAT TGATGACCAT GAGATCCCTG CTCAGAACCC CCTTCCTGTG TGGCCTGCTC TGGGCCTTTT GTGCCCCAGG CGCCAGGGCC TTTTGTGCCC CAGGCGCCAG GGCTGAGGAG CCTGCAGCCA GCTTCTCCCA ACCCGGCAGC ATGGGCCTGG ATAAGAACAC AGTATCACTC GAG	60 120 180 223
(2) INFORMATION FOR SEQ ID NO:60:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 171 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
GAATTCTAGA CCTGCATGTC CCAGTGTGAA ATTTCAGCAC GGCATTTTCT GCATCCTTTC ATGGCCATCC AAAGGATTCC GCTGCAGAAA TTATTGATGT GCTATTTTTG CTGTCTTGTG ATGCAGGCTG CTTTGGGCCC CTGGGTCACT CTTCCAAGGC TGCAACTCGA G	60 120 17:
(2) INFORMATION FOR SEQ ID NO:61:	

(A) LENGTH: 336 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(i) SEQUENCE CHARACTERISTICS:

	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:61:	
AAAAAAGATT A CTGTTTATGC ' AATGTGGAAA A AGAATAGAAG	TTCATGGCCT AAAAAGCAAA AGAAAAGTAA AAGGAAGAAA CAAGAACAAG ATATTGATTT TAAAATCATG CAAAAACTGC AACTCTGTGT TTATATTTAC TGATTGTTGC TGGTCCAGTG GATCTAAATG AGAACAGTGA GCAAAAAGAA AAGAGGGGCT GTGTAATGCA TGTACTTGGA GACAAAACAC TAAATCTTCA CCATTAAGAT ACAAATCCTC AGTAAACTTC GTCTGGAAAC AGCTCCTAAC ATGTTATAAG ACAACTTTTA CTCGAG	60 120 180 240 300 336
(2) INFORMA	TION FOR SEQ ID NO:62:	
(i) S	SEQUENCE CHARACTERISTICS: (A) LENGTH: 212 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:62:	
CATCCCTCTT . CGCCCAATGG	AAAGAGGCCT AGAAGAGCAA GCGCCATGTT GAAGCCATCA TTACCATTCA ATTCCTGCAG CTGCCCCTGC TGGGAGTGGG GCTGAACACG ACAATTCTGA GAATGAAGAC ACCACAGCTG ATTTCTTCCT GACCACTATG CCCACTGACT TTCCACTCTG CACGCTCTCG AG	60 120 180 212
(2) INFORMA	TION FOR SEQ ID NO:63:	
(i) :	SEQUENCE CHARACTERISTICS: (A) LENGTH: 349 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:63:	
TGAGCAGTTG GAAAGCTGCT TGAAGAAGCA GCTAACAGAG	TTCATGGTCT ATGCTACTCA GTTGGATCTA GCAGAAACAA AAGCTGAGTC GCGCGAGGCC TTCTGGAAGA ACAGTATTTT GAATTGACGC AAGAAAGCAA TCAAGAAATA GACAAGAGAT TACAGATAAA GATCACACTG TTAGTCGGCT AACAGCATGC TAACCAAAGA TATTGAAATA TTAAGAAGAG AGAATGAAGA AAAATGAAGA AGGCAGAGGA AGAATATAAA CTGGAGAAGG AGGAGGAGAT AAGGCTGCCT TTGAAAAGAA TATCAACACT AAACTCGAG	60 120 180 240 300 349
(2) INFORMA	ATION FOR SEQ ID NO:64:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 391 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCGGGCTAGT	CATGGCGTCC	CCGTCTCGGA	GACTGCAGAC	TAAACCAGTC	ATTACTTGTT	60
TCAAGAGCGT	TCTGCTAATC	TACACTTTTA	TTTCTGGATC	ACTGGCGTTA	TCCTTCTTGC	120
AGTTGGCATT	TGGGGCAAGG	TGAGCCTGGA	GAATTACTTT	TCTCTTTTAA	ATGAGAAGGC	180
CACCAATGTC	CCCTTCGTGC	TCATTGCTAC	TGGTACCGTC	ATTATTCTTT	TGGGCACCTT	240
TGGTTGTTTT	GCTACCTGCC	GAGCTTCTGC	ATGGATGCTA	AAACTGTATG	CAATGTTTCT	300
GACTCTCGTT	TTTTTGGTCG	AACTGGTCGC	TGCCATCGTA	GGATTTGTTT	TCAGACATGA	360
GATTAAGAAC	AGCTTTAAGA	ATAATCTCGA	G			391

- (2) INFORMATION FOR SEQ ID NO:65:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GAATTCGGCC	TTCATGGCCT	AGGGAGTCTG	AAGCAATTTC	TGAAGAAGAC	CAAAAAGAAC	60
CACAAGACGA	TGAATGAAAA	GGCATGGAAG	CGTTGGTGCA	CACAAATCCT	CTCTGCCCTA	120
AGCTACCTGC	ACTCCTGTGA	CCCCCCATC	ATCCATGGGA	ACCTGACCTG	TGACACCATC	180
TTCATCCAGC	ACAACGGACT	CATCAAGATT	GGCTCTGTGG	CTCCTGACAC	TATCAACAAT	240
CATGTGAAGA	CTTGTCGAGA	AGAGCAGAAG	AATCTACACT	TCTTTGCACC	AGAGTATGGA	300
GAAGTCACTA	ATGTGACAAC	AGCAGTGGAC	ATCTACTCCT	TTGGCATGTG	TGCACTGGAG	360
ATGGCAGTGC	TGGAGATTCA	GGGCAATGGA	GAGTCCTCAT	ATGTGCCACA	GGAAGCCATC	420
AGCAGTGCCA	TCCAGCTTCT	AGAAGACCCA	TTACAGAGGG	AGTTCATTCA	AAAGTGCCTG	480
С						481

- (2) INFORMATION FOR SEQ ID NO:66:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 583 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GAATTCGGCC	AAAGAGGCCT	ACGATTGAAT	TCTAGATCTG	CCCGTCTTGG	CCTCGCAAAG	60
TGCTGGGATT	ACAGGCGTGA	ACCACTGTGC	CTGGCATATT	TGTCTATTAA	TTTGCTTTTC	120
TTTAGATGTA	TTCTAGAGGG	GGGAAAATCA	GTAGAAGAAC	AGTTATGTAA	TTCTAACAAG	180
TTCTCCATGT	GTCTTGCCAT	CTNGCTTTTT	CTCATCCTAT	CAGTACTGGA	TGAGAATGTT	240
TATTTCACTG	AACTTTGCCA	AAGAGTTTCA	ACATTTTTTT	GTTTAATCAT	AGGAGAAAA	300
GGTTTATCTT	ATTTTTAAAA	ATTTTTATTT	AATTCTTTCA	TTACAAATGA	AGTCCCAGAA	360
GTTGTATTTG	TTTCTTTAGG	CTGTTCTTAA	TTGTTCATTG	GAACAGGCAG	GGTTTGAAGG	420
AGTGGGGATA	CTGGGAAAGC	CAGGGTGATG	AGAAAATAGG	AAAGGGGTCT	TGTCATTGGG	480
AGGCCACTAT	ACCAGTGGCC	CTTGTACCAG	GACTAATATG	GTACTTTGAA	GCTTTAAATT	540
CATTTCTTTA	TTCAATAATT	TTAGGCATCC	CAGGATACTC	GAG		583

- (2) INFORMATION FOR SEQ ID NO:67:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GAATTCGGCC	AAAGAGGCCT	AGCTATCCGC	TTTGCTATTT	TAGTGGCATT	ATCAAAATCA	60
CTGGAAGCAC	CTGTNGTAAT	ATGGTCGGTT	CCAAATATAA	GCTCCTCTGC	CACTCTTCCT	120
CCCATACTAA	CATCCATTTG	TGCAAGCAGC	TGGGCTCTAG	TTTCATTCCA	TCTGTCATTC	180
TCAGGTAACA	GGGACACATG	TCCAAGTGTT	GGCCCCCGTG	${\tt GCATGATTGT}$	AGCTTTGTTG	240
ATAGGCATTG	CATCTTTTGT	GTAATATGCA	ATAATGGCAT	GACCAGATTC	ATGATATGCT	300
GTGATGGTTT	TGTTTTTGTT	ATCAATTTCC	ACACTTCTTC	TTTCAGGCCC	CATTAGAATT	360
TTGTCTTTGG	AAAACTCCAG	CTCCTTCATG	GTAACCATTT	CTTTTCCATC	AACAGCTGCT	420
TTTAATGCAG	CCTGGTTCAC	AAGATTCTCC	AACTCTGCTC	CGGAAAAGCC	AACAGTACCT	480
CGAG						484

- (2) INFORMATION FOR SEQ ID NO:68:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GAATTCGGCC	AAAGAGCCTA	ATTGAATTCT	AGACCGGCCT	CATCGTTCTT	TGCCTTCCTG	60
GTCACCATCT	GCTACGCTGG	AAATACATAT	TTCAGTTTTA	TAGCATGGAG	ATCCAGGACC	120
ATACAGTGAT	TTACCATTTT	GATAATTAAA	AGGAAAAAA	AAGGAAGACT	CTCACTGTAA	180
AAACAGCTGT	AGGTATAATG	TATATTCCCA	GAGAATTGTA	TTTAACTAAT	TAATGTTTTT	240
TATATTCTTA	AATTTGCTCA	CAAATTGTGG	TTTGTTACAA	TTAAACTGGA	TACTTATTTG	300
CAAAGTGTTG	TAGCTTATAA	TGAACTCTTA	AGTATCTTAT	TAATGTATTA	ATGTCTTCAT	360
AGATCATATT	TTCTTAGACA	ATGTTTAAAT	AGATAAATTG	CTAATATTGA	GAATGTGTCA	420
AGTTTGTAAA	CCTAACTTTT	AAGATGCCAG	AACTCGAG			458

- (2) INFORMATION FOR SEQ ID NO:69:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GAATTCGGCC	AAAGAGGCCT	ACGGCCAAAG	AGGCCTAGGT	GGTGATTGAC	CTAAGAAAAA	60
AGTGTCTTAA	ATATCTGGAT	TCTATGGGAC	AAAAGGGCCA	CAGGATCTGT	GAGATTCTCC	120
TTCAGTATTT	ACAGGATGAA	AGTAAGAACC	GCTCGAG			157

- (2) INFORMATION FOR SEQ ID NO:70:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 331 base pairs(B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GAATTCGGCC	AAAGAGGCCT	AGTGGACTGC	TACTTCCCTT	TAGCACTATA	TACAAACATA	60
ACTGCTACTT	CCCTTTAGCC	CAGGATCAAA	ATAATGATTC	AGTTAAAAGT	TGCTTGCCTA	120
ACAAAATTTC	AAAATATGGA	CTTCTGTGAA	TTGCTAAAAC	ACATCCTTTT	AACTAGGCAT	180
CTTTAAGTCT	ATAGTATCTT	TAAAGTTAAT	TTCAAAATTT	AGCAGAGCCT	GGAACACAAA	240
TTATTCAGGA	AATAATTCCT	GAACCTACCT	CTATCTTCAT	AAAACGTATT	GGGGCAAGAA	300
CTATTCTATT	GAATTCTAGA	CCTGACTCGA	G			331

- (2) INFORMATION FOR SEQ ID NO:71:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GAATTCGGCC	AAAGAGGCCT	ACCATCTGTC	ACTAATATCA	AAGGAGGCC	AAGGACACAG	60
CCCTGGGGGA	ACTTACCAGG	TCAACCCACA	ATGGGTGAAT	TTATAGTTTG	TTAGTTAGTG	120
GTCAGTTACC	AACTTCTCTG	TCTGTCTAAT	GCTTTGACTA	AAATGTCCAG	ATTATTTACC	180
TAGTTAACAA	AATTAAAGAA	GATTCTAAGA	CCAGTTTAGC	ATCATTTTCT	CTGAAGTCCA	240
TAATGAATGT	CTGTTAAACT	CTCGTCACTC	TTATTTAGGT	GCTTTTGGGT	CATTTGTTGT	300
AGGTTCATTC	TCCCAAATCA	ATGTCACATA	TACGTCTGTA	ACTTGTGTTA	TCAGCTTCCT	360
TCCTAGGGCT	TTAACTTCTT	TTCAGTCTTA	TAGCATTCCT	TCCATTTTCC	TTTCAGTTCA	420
CTCCAATAAA	AGCTCGACAA	ACTCCTGGGA	GCCCCTTGGT	GCTCGAG		467

- (2) INFORMATION FOR SEQ ID NO:72:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GAATTCGGCC AAAGAGG	CCT ACGATTGAAG	TCTAGATGCA	CACATTCAGC	TTCTGTCTCA	60
GTCCTGAGAG TGGTTGT	GTT TTATTGGCTG	ATGAGTTATT	TCCACATATC	ACATGTATAA	120
GGTATTTGAA TGAAGGT	GCT TTGTAGTCAT	GACACACTAC	TCTTTTACTA	ATTATTAATA	180
TCTTAAGATT ACAATTT	GAG AGGTAGAGAT	GGTATTGTTT	TTAATGGGTG	TGGGGGGTGG	240
TGATGATAGG TATTTTT	ACC CTGGTAAGTG	ACCTACTAGG	TTTTATTAAG	TGTTGCAACT	300
TGTCCAGTGT GTGGATG	GGA TCTCGAG				327

(2) IN	FORMATION	FOR	SEQ	ID	NO:73:
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAATTCGGCC	AAAGAGGCCT	AGTGGTGGTA	TGTATTTGAG	TTCACAGTAT	TTGTTTTATA	60
GCAGTTTTGC	AAGCACATAC	TGTGCCACGG	ATTTTCCCAC	ATTATTTTA	GACAAGGGAA	120
CACAGCCATC	AAAACTGATA	CCATGGCCGG	GCGTGGTGGT	GGGTGCCTGT	AGTCCCAGCT	180
ACTTGGGAAC	TCGGGACATT	CTCGAG				206

- (2) INFORMATION FOR SEQ ID NO:74:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 184 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GAATTCGGCC	AAAGAGGCCT	CCACCATGCC	CGGCCTCAAC	GATATTGATT	CTTTGGGCTG	60
TAGTCAGTAT	TGGATTATGA	TCAATATTAT	CACCATTTAT	TTTGTTGCTC	CAGTTCTTCC	120
AGCTGTGGCC	AATCCTTCAG	TTGGATTCTT	GTGCCCCATC	AACATTCTCC	ATCCTTCTCT	180
CGAG						184

- (2) INFORMATION FOR SEQ ID NO:75:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GAATTCGGCC	AAAGAGGCCG	ACTTTATTAT	ACCATACATA	CTATAGGTAC	CTGGGCACAA	60
GATAGGTCAG	GGGGTACTGT	ACCCCTATTT	ACATGCTTAA	TCACATCATA	AGGTTGCAGG	120
TGGTACTTGA	AATCATCACT	AATGAGACAG	CAAATATGTT	AGACTTGCTG	GCCCAGCAAG	180
CCACAGAAAT	AAGGATCACC	ATCTATTAGA	ATAGACTGGC	TTCAAACTCG	AG	232

- (2) INFORMATION FOR SEQ ID NO:76:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GAATTCGGCC AAAGAGCCTA CTAAAATTCC TTGTTTTGTG TTTTTAATAT TCCATCGTTG 60
ATAGTTAATA TTCTTTTNGA GGTTTTGTTT TAGACAAAGT AATGTTTTC TGAAATGATT 120
CTAAGACAAT TGGTCAGAAA TAGTCTCTGC TTGTTTGGTT TATGTTTGGT CAGTTGTGCT 180
TTGATTATAG ATGGTTCCTC ATCTGAGATT AAAGTGGGAC AGAACTTCAA AAGTAAAAGG 240
GTAAATGTTC GCTGAATGC TTATGTGGCA CATGTGCTAG TCCTTGATAG TGGCGAGAAA 300
GATCTTAATT GCTCAAAGGA AGTACTCGAG 330

- (2) INFORMATION FOR SEQ ID NO:77:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 507 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GAATTCGGCC AAAGAGGCCT ACAGTGCATT ATGTTATTTT GTTATCTCTG CAGTAACTTT 60 CTATCATGTT ATTTATTTC TTTGTCTTAT TTAAAGCTTC TGAGATTATG GATTTTTGTT 120 TCCTTCCCTG AAGTTAAGTG TTATCATTCC TATATAGTAC TAAGCTGTCT ACAGAATAGT 180 GGGAGTCTGC CCTCTTGAGT TGGGAAGATC CTAGTTTGAA TCTTGGCTGT GCGACTTTAA 240 AGTTCATTAA CTTCTCTTAG CCTCAGTCAC CTGAACTCTG CAGTGGGGAT CCTTATGCCT 300 CAGAGTGTCA TTGGGAGGAC TCACGAAAAT ACGCTTGTAC TTTGAGTTCA GTACCTAGCC 360 TGTATGAGCC AGCATTAAGA GGGACAGTCA TCACGCAGCG CTTTGCACAC AGCTCTCACG 420 CCACATCCTT TGGCTACTGT TTTGGTAAAT CTTTACTAGT AAATGTTTCT TAAAAGCATT 480 TACATTCATG GACATGATTC CCTCGAG 507

- (2) INFORMATION FOR SEQ ID NO:78:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GAATTCGGCC AAAGAGGCCT AGATTGAATC TAACCTTTTT GCCTCTTCCC AAGTAGCCTA

TTTGAGCTAG AACAAAACTT TGTTAGCCAT TTTGGGAGAG AATAGGGAAT CTAGAGAATG

AAGATCTGCC CGACCTGCCT CGAG

144

- (2) INFORMATION FOR SEQ ID NO:79:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GAATTCGGCC	AAAGAGGCCT	AACGACGGTA	ATCAAGTTTT	GCTCCAGAAG	CATCAAGAAA	60
CTTAGCTACT	GCTTCCAAAT	CAGTACCGGT	TTCAGTTAAG	CCTTGAATAA	TACAGTCTTG	120
AAACTGAGTA	GGGTCAAACC	TCTCTTTTTC	ATCTCTTTTT	CTAGTTTTAA	AACGCTGGCC	180
TGATAGCGTT	GGCTTTTGCT	GCTTTTGATT	ATTCATAAAA	GACACCCGAA	TTTAAGGCGA	240
AGAGGAAAGA	GCCAGAAATC	CCCGATGTAC	CGGCAACTGC	GGCGCTATCT	CCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:80:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GAATTCGGCC AAAGAGGCCT AGACTGCTGG TGGTGAACTG CTTTTCTTGT AGGTTGTGAG 60 GGCTGAAAAA GCCAATCTTA ATAGACATGA GGCTCATGTT TGCACAGTGT GCTCTCGAG 119

- (2) INFORMATION FOR SEQ ID NO:81:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GAATTCGGCC	AAAGAGGCCT	ACTCAGCTGC	AAAAAAGCAT	ATTTTCTGTG	TTTCTGGACT	60
GCACTGTNGT	CCTTGCCCTC	ACATAGACAC	TCAGACACCC	TCACAAACAC	AGTAGTCTAT	120
AGTTAGGATT	AAAATAGGAT	CTGAACATTC	AAAAGAAAGC	TTTGGAAAAA	AAGAGCTGGC	180
TGGCCTAAAA	ACCTAAATAT	ATGATGAAGA	TTGTAGGACT	GTCTTCCCAA	GCCCCATGTT	240
CATGGTGGGG	CAATGGTTAT	TTGGTTATTT	TACTCAATTG	GTTACTCTCA	TTTGAAATGA	300
GGGAGGGACA	TACAGAACTC	GAG				323

- (2) INFORMATION FOR SEQ ID NO:82:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAATTCGGCC	AAAGAGGCCT	AGGCAAATCA	GAACTCTTAA	GTTGTTTCAT	CCTTATTTTA	60
TTCTTAAAAT	AAAGAATTTC	ATTTCAAATA	CGGATTAATT	TTTTTTCTGG	GAAAAAACAC	120
ACTGTAAAAC	ATAATTTTCT	ACCTTTTAAA	ACGTTTTACA	ATTTATCCCA	TCTTCTAACA	180
AGTTATGATA	CTCATACCTG	CCGAGGTTTC	TCTAAATTTG	TCGCTGGTCT	TCTTTTTCCT	240

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AGGTGTTTGG GAACCTGCTG TGGGGCCATC TGAGTTTGCT ATAGAAGCTT TGTCCAGTCC	300 350 409
(2) INFORMATION FOR SEQ ID NO:83:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 463 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	
GAATTCGGCC AAAGAGGCCT ATAAATATAT AATTGACTTA TTTATTAAAT TTAGGAGAAA AAAAAAGTTT TCCTTGACAT TCAGCTCTAT TGGATTTATT TCCATTTAAT TGCATCATGT GTTATGTCTT GGTAAACACT CCATTTCCTG TCTTGGTGGG CATCCTGTCT GTGTACCTGT GCAGTACACT TTAATCATCA AGACTTCAAA GTGCTTTTGA GCTATCAAAT CTTGGGAGAG TCCCATCTAG CATCTTAATA ATTATTTTTC CAAGTTCGTT ATAATTAACT CCTTTAACCT CATCTCATTA AATCAATTTT GTATTATCAT TCTGTTGTTC TCTGGAAAGC AGCCAATTGT TCAGCTCTTG AATCAGAATT TTCAAAGACT CACCTCTCTT ACCTGGGCTT GCACATATTT GTCCTAAGTA ATTCTCTATC CCTTAAACCT CTGAGCCCTC GAG (2) INFORMATION FOR SEQ ID NO:84:	60 120 180 240 300 360 420 463
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 316 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
GAATTCGGCC AAAGAGGCCT AATTTTGTAA AAAGGAATAT CATTCTTTGA TTTTAGATCT TAGACATCAG GCACTGACAT AGAGCTTAGA TATGTTCTTA AGGTAGCTAA GCCATTTATT ATAGGATAGT CAGATAGGAT AGTTCTAGGA TTTATAGACC TTTTCAGATA CTCTTTATCC AGTGAGAGAT GACCTATTTT TATTAAAACT TGGGTTTGGT ATCTTGGAAT TGGCTTGAAA ATGATTTGTT TTTACATTGG ATGTGAACGG AAAGTTTGTA TCTCAAATGT TTTACCACCT GAAGGGACAG CTCGAG	60 120 180 240 300 316
(2) INFORMATION FOR SEQ ID NO:85:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 494 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGGACATGG	AAGTAGGTGA	GGTTGGGGGA	CCTATGAAGA	AAAAAAGAGC	CTTTCCACTG	60
GGCAGTGAAG	TGTGTACACA	CACACTGGGG	GCAGAGCAGT	GTGAAAACAT	TCTGCACCAG	120
CACACAAATG	ACTTTTGGCA	AATCATCTNC	CTGATCTGTC	GGATGTTACG	TCTCTGCAGA	180

ATCTGGAGAA	AACCAGAAAA	CCCAGCTTGT	TTGCCCTCAT	TTTGGCAGTT	TAATTTAGGA	240
ATCACACTGG	CTTTACATAA	ACTCTTTACC	AAAAAAACTG	TATTCTGTAT	TTTGAAGGCA	300
CAAGTTAACA	TGGGCCCAAG	GGAAGGAAGC	ATTGTATACA	ATTACATAAT	AGCTACTCTA	360
TTACTTTAAA	ACCTAATGGC	AGCCTCGGGC	AGAAAAGTCA	AAAGGGGAGA	GAAACCATTT	420
CTGTGAAATT	ATCTGATGCA	ATCATCTCTT	TGGAGACATT	GTCAGTTGAC	AATGGTTCTG	480
CTTTTTCTCT	CGAG					494

- (2) INFORMATION FOR SEQ ID NO:86:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 507 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAATTCGGCC	AAAGAGGCCT	ACGGGAGCAG	TTCATGCAGC	ACCTCTACCC	ACAGAGAAAA	60
CCTCTTGTGT	TGGAAGGGAT	TGATTTGGGG	CCATGTACAA	GCAAATGGAC	AGTGGATTAC	120
CTAAGCCAAG	TTGGAGGGAA	GAAAGAAGTA	AAGATTCATG	TTGCTGCAGT	TGCACAGATG	180
GACTTCATTA	AACTTTACCT	TTTGACCAGT	TGGTCCAGAG	GGCAGCTGAA	GAGAAACATA	240
AAGAATTCTT	TGTTTCAGAG	GATGAGAAAT	ACTACTTACG	GTCACTTGGA	GAAGACCCTA	300
GAAAGGATGT	TGCAGATATC	AGAAAGCAGT	TTCCTTTGTT	GAAAGGAGAT	ATTAAGTTTC	360
CAGAATTCTT	CAAAGAGGAA	CAGTTCTTTT	CCAGTGTTTT	TCGAATTAGT	TCACCAGGAT	420
TACAACTATG	GACTCATTAT	GATGTAATGG	ATAATTTGTT	AATACAAGTG	ACAGGAAAAA	480
AGCGTGTTGT	ACTCTTCAGT	CCTCGAG				507

- (2) INFORMATION FOR SEQ ID NO:87:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GAATTCGGCC AAAG	SAGGCCT AGCTTATCCA	GTCTAGTAAT	TTTTTTTGTA	TGTGTGCACA	60
GCACAAATAG TTAC	CAATAGT TCCCTTTTTT	GACATCAAAT	TCAACAATAC	CTGGCATATA	120
ATTGCTAAAT ACTG	TCATCA TTTTCATTAT	CATTATCCCC	CACATAGTCA	TAAATAAGCA	180
CACATGCTAA TCTT	CAACTC TTCTTCTATT	ATTTGCTGCC	TTCTTACCTG	CGTTAGTGAG	240
AAAGTGCCTT CAAA	TAGATT GCCAACAGTT	ATATGGCTCG	AG		282

- (2) INFORMATION FOR SEQ ID NO:88:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

60	TTCAGTACAG	CTTTTAAGTT	TCACGTGTAA	AGTGCAGTAT	AAAGAGGCCT	GAATTCGGCC
120	AGTATTTAGG	ACTATTGTGT	TCATTTGGGT	AATGTTGTAT	CCTTTAATGC	TGCTTTTATA
180	TGCTACCTTT	TTCGCTTTTG	GGTTGGTGCT	ATGTAAGCTT	GTTTGTTTAT	ATGTATGCAT
240	AGTTTCCATC	ACATTGAGAA	CTGATGAAAT	ATGTGCTAAA	TGTACCAGAG	CTTGGATTTT
300	CAGAGTTTGG	ACTGCTCCTG	GTTGGGGTAG	GATGATGTGT	ATATGGGACT	TTATTCTTTT
333			GAG	GGCCAATCTC	CAGCAAAGCC	AAGAAGTCAC

- (2) INFORMATION FOR SEQ ID NO:89:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTCGGCC	AAAGAGGCCT	AGGTTTCTAG	ACTGGAAGAA	CAAATGAATG	GCTTAAAAAC	60
ATCAAATGAA	CATCTTCAAA	AGCATGTGGA	GGATCTGTTG	ACCAAATTAA	AAGAGGCCAA	120
GGAACAACAG	GCCAGTATGG	AAGAGAAATT	CCACAATGAA	TTAAATGCCC	ACATAAAACT	180
TTCTAATTTG	TACAAGAGTG	CCGCTGATGA	CTCAGAAGCA	AAGAGCAATG	AACTAACCCG	240
GGCAGTAGAG	GAACTACACA	AACTTTTGAA	GGAAGACAAG	GAACGCNAGA	AAAAAGACGA	300
AGAAAAGGTG	AAGGCAGAGG	AAGAATCAAA	GAAAAAAGAA	GAGGAAGAAA	AAAAGAAACA	360
TCAAGAGGAA	GAGAGAAAGA	AGCAACTCGA	G			391

- (2) INFORMATION FOR SEQ ID NO:90:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GAATTCGGCC	AAAGAGGCCT	AGCTTCTCTG	CTTTATTTAT	TCATTTATTT	TTAATTTTTT	60
GAGATGAAGT	CTCGCTCTGT	CATCCAGGCT	GGAGTGTGGT	AGCGCCATCT	CAGCTCACTG	120
CAACTTCCAC	CTCCCAGGTT	CAAGTGCATT	GTCTTTTTAA	TGTCTATGTG	AAGGATTCTG	180
AGCTGTACGA	GTTCTGCCCC	AAATCTGCAC	TTGGGCCTCA	GGATCAGGCC	GCCTCCCCAT	240
CAATCTGGTG	GATGCCAGTT	ATAACCTTTG	CCCTGCACCC	CATCCACACT	GTAGTTCAGA	300
GAAAATCAAC	AGTCAGCAAT	CATATCACAA	GCACTCGAG			339

- (2) INFORMATION FOR SEQ ID NO:91:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 203 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAATTCGGCC AAAGAGGCCT ACGAGTCAGC ATCTAGACTC AGCTCCTTCT TCCCGCCTGC 60

CCTCACACAT GCGTGCATTC ACTCTCCTGT CCAGGCTCAT GTCCTTGTGC CCGCTTGCTG CTTTGCCTCC TTGCTTGTTT CTGACTTGCT CACCCACTCT CTGTCATTGT CTTGCTTACT CAGGCTCACC CTATCAACTC GAG	120 180 203
(2) INFORMATION FOR SEQ ID NO:92:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:	
GAATTCGGCC AAAGAGGCCT AGTTGAATTA TTGCCACATG TTAGGAATGT GGAAGGTTGC TTGGATAAAT GAGAAAAGAA AGAAAAGAAT GCAAGTAATG TCCTGCTGGG GTAGTGCAGT CCTCGAG	60 120 127
(2) INFORMATION FOR SEQ ID NO:93:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 179 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:	
GAATTCGGCC AAAGAGGCCT AGATCCCACG AATTTAGGCT CAGAAGCATC GCTCCTCTCC AGCCCTGCAG CTATTCACCA ATATCAGTCC TCGCGGCTCT CCAGGGCTCC CTGCCCTGAC CTCTTCCCTG GGTTTTCTGC CCCAGGCCTCC TCCTTCCCCC CCCCCCTATA TCCCTCGAG	60 120 179
(2) INFORMATION FOR SEQ ID NO:94:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 326 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:	
GAATTCGGCC AAAGAGGCCT ACTGGAATCA CTAAACTTTG TCTCATTTTT TTTCTCTTCC ATCAAATATC AATTTTGGAT TCAGATCCAG TTTTTTTCTT TCAATTATTT CTGCCTTTTA AAATAATACT ACTCCTTCC TCCCACAATT CATTTCAGCT TGTTTTAGTT CCTTGGGTTC TATATTTTTT CTTCCTAGTA TTACAATATA TGCACAAATA TTAGGTTATA AAACTTCCAA TACAACTTTT ACTGCCACTC ACAGGTTTTT CAATTGTTTT CATTTTCATG TACATTTAAA TAATGTATAT ATTAGGGATA CTCGAG	60 120 180 240 300 326
(2) INFORMATION FOR SEQ ID NO:95:	

- - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 340 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GAATTCGGCC	AAAGAGGCCT	AAATATGAAA	AGCTGTCTAT	ATCTACCCAG	CCAAACCATC	60
TCCAGCTTTT	ACTTTTATTG	AGCAAGTATA	CGTTATTTAT	TTAGTCATCC	ATTCATTCAT	120
TTACTCATTT	ATTTATTTT	TTTTCAGCTT	ATTTCTGCTT	TCATCTTAAT	TCCTCTCTTA	180
AACTTTTTGG	TATCACATTG	GTTCTCCCTG	ACCTCCACCA	CTGTAACCTG	ACTTAAGTTA	240
AATGTTTAAT	TTATTTTTTT	TTTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	300
TTTAGGTAGA	GAAGATGTCT	CACCATGCTG	CCCACTCGAG			340

- (2) INFORMATION FOR SEQ ID NO:96:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GAATTCGGCC	AAAGAGGCCT	ACTITICITIC	TTATTCTACT	TCTCTTTTTT	TCTTTTGTTC	60
AACATCATGT	TTGTGAAAGT	TTCATGCATA	TCGTTGCAAG	TATTTGTATT	TCATTCATTT	120
CTATTGTTGT	ATAATGTTAC	ATTGCATGAA	TATGCAGCAA	TTTGTTCTAC	TGTAAAAAGC	180
AATAAGGATT	TAGTTATTTC	CAGGTTGGAC	ACAAATAATT	TTGCTATGAA	GGGTCTCGAG	240

- (2) INFORMATION FOR SEQ ID NO:97:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GAATTCGGCC	AAAGAGGCCT	ATAACTATAT	AGCCTAGAAT	TTTTCCTATT	CTGTTATTAA	60
GCCTCTATCA	CTATTCTTTG	ATTCTAGGTT	TTATAATCCA	TTCTTTTTTA	TAACAACCTG	120
TTCTTGTTTT	ACTTTTCCCT	ATTTTTGTTT	TATACCCATC	TATTCTTTTT	TAGGATCTAT	180
TCTCCACTTT	TAACTTTGAG	GATTCTAAAA	TACTTACTTT	AAAGTTATTT	TTAACTTGTT	240
CTATTTTTGT	TTTTGTCAGG	AGCGAATTTG	CCTTTTTTAT	TTGGCTGTTC	TACCATGCTT	300
TTTGGAATTT	TGTTTTGTAG	GCTTCTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:98:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GAATTCGGCC	TTCATGGCCT	ACTCTACTCC	AAGTAGGAAA	AGGCCAGGAG	GTCCTGTTAA	60
AGGATGCACT	CAGAGCCCGG	GCTCCCTAAC	GTATGAGAGT	GCTAACCAGC	AGGTGTAGAC	120
TTTTCAGGAG	TGAAGAATGA	GGCAGGCATT	CCAAACCTGG	ACCTTCATCA	CCTTTTGTTT	180
CATCTCAAGA	CAATTCTGAG	GGACTGTTTT	GGAGCGTGTC	TGGAAGGTGA	ACGTTGAAGA	240
AGAGTGTGGG	CTTTGATGTG	ACTCAGTTGA	ATACTCGAG			279

- (2) INFORMATION FOR SEQ ID NO:99:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GAATTCTCAT	GAAACTCTCA	GCGGAAAGCT	ACAAGGAAAC	ACAGATGGTG	AAGATTAAAG	60
AGGAACCCAT	GGAGGTTGAC	ATCCAGGACT	CCCATGTCTC	GATATCACCC	AGCCGGAATG	120
TTGGCTACAG	CACTTTAATC	GGGCGAGAGA	AAACCGAACC	CTTACAGAAG	ATGCCAGAGG	180
GCAGAGTACC	CCCAGAGAGA	AACCTCTTCA	GTCAGGATAT	CTCTGTGAAA	ATGGCTTCCG	240
AGCTCCTCTT	TCAACTGTCA	GAAAAAGTGA	GCAAAGAGCA	CAATCATACA	AAAGAAAACA	300
CCATCCGGAC	CAATCTCGAG					320

- (2) INFORMATION FOR SEQ ID NO:100:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GAATTCGGCC	TTCATGGCCT	AGAGCAACAT	AGTGAGACCT	CATCTCTACA	AAAAATAAAG	60
AGAAAATTAG	TTGGGGGTGG	TGGCGTGCAC	CTATAGTCCC	AGCTACTCAG	GAGGTTGAGG	120
TGGGAGGATC	ACTTGAGCCC	AGGAGTTTGA	GGCTGCAGTG	AGCTGTGGTC	ATGCCACTGC	180
ACTCTAGCCT	GAGTGACAGA	GCAAGATCCT	GTCTCAAAAA	ATAAAGTAAA	TAATAAATA	240
CAGTCAACAA	CAGTGATTTG	TCTTCAAGCT	GCCCTCCTCT	TCGGCTCTCA	AGGCAGTTTG	300
TGAAGTGTCT	AGGATAGGAA	TTTTCCAGAA	GGGCTTGCTC	GAG		343

- (2) INFORMATION FOR SEQ ID NO:101:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

60	GATCACAACT	TCAGATTAAA	TCTTATCTGA	GAAAACATAA	CCAAAGTTCA	GGAAGATGTG
120	TCAGATAATG	GCGATTAGCA	TTAAGGATTT	TCAAAGAATA	CAGATTTTCT	CCAGTGAAGC
180	TCTGATGTTA	ATCTGTTAGT	ATGAACCTGA	AGAAAAAGAC	TCAGTTTTTG	TAAGCATTGA
240	GAGTATGAAG	CGAGGTACTT	TGACTCCATC	TTGGAACCTC	CAGTATTCAT	GCGAGCAAGG
300	GAAGTAGTGT	CAAGACTGAT	ATCCTTCAGC	GGTAGTGGTG	TCTTCAGAAA	CCACAGAGAT
350		CACTCTCGAG	ATAACCCCNA	CCTGGAGGAA	AGATGACATT	CTGATCAAAC

- (2) INFORMATION FOR SEQ ID NO:102:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

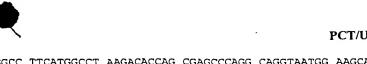
GAATTCGGCC	TTCATGGCCT	ACTCGCGGTC	TGTTAGTAGT	ATAGTGATGC	CAGCAGCTAG	60
GACTGGGAGA	GATAGGAGAA	GTAGGACTGC	TGTGATTAGG	ACGGATCAGA	CGAAGAGGGG	120
CGTTTGGTAT	TGGGTTATGG	CAGGGGGTTT	TATATTGATA	ATTGTTGTGA	TGAAATTGAT	180
GGCCCCTAAG	ATAGAGGAGA	CACCTGCTAG	GTGTAAGGAG	AAGATGGTTA	GGTCTACGGA	240
GGCTCCAGGG	TGGGATGAGC	GGGCCAAGAT	CGATGATCCC	ACAGACTCCA	AGCCTGAGGA	300
CTGGGACAAG	CCCGAGCATA	TCCCTGACCC	TGATGCTAAG	AAGCCCGAGG	ACTGGGATGA	360
AGAGATGGAC	GGAGAGTGGG	AACCCCCAGT	GATTCAGAAC	CCTGAGTACA	AGGGTGAGTG	420
GAAGCCCCGG	CAGCGTCTCG	AG				442

- (2) INFORMATION FOR SEQ ID NO:103:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GAATTCGGCC	TTCATGGCCT	ACAGAAAGTA	AGTTGGAACC	ATGTAAGAAA	AAAAGACACA	60
AATAAAACTA	GGAAAGTGGC	ATGGAGCTAG	GCGTGAAGTT	GCTGCTCAGT	TTACATGTAT	120
GAAGTTCTGT	GTGGACTTAA	GCTCCTACTT	CAGTCATTTA	TTGTATGACT	TGGACAAGTT	180
GCCAAACATC	TCTAATATTC	ATTCATATTT	GTAGGGTAAA	AGGATGAGTA	ATATGTATCT	240
TTAGTGTATA	AAACATTTAC	AGACAACTCG	AG			272

- (2) INFORMATION FOR SEQ ID NO:104:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

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GAATTCGGCC	TTCATGGCCT	AAGACACCAG	CGAGCCCAGG	CAGGTAATGG	AAGCAACTGT	60
AGCTGACTGG	ACCTAAGAAG	CAGTGGCACG	GGTGCCAGGC	ACCCCAGCTG	ACCTGCCTTG	120
GTGCTCAGAG	CAGCAGGGCT	GGCCATGGTC	AGGGAGTCTG	GGGAGGTCAT	GCTCTGTCCA	180
CAGGGTTCTA	GCCAGCTTCT	GCCAAATTGT	CTGTTTTTTC	TCAAGAGAAG	CTGGGAAGGC	240
CAGTTGTGGT	GTCTCATACC	TGCAATCATA	GCACTATGGG	AGGACTCGAG		290

- (2) INFORMATION FOR SEQ ID NO:105:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GAATTCGGCC	TTCATGGCCT	ATGAAAATTT	GGAAGAAGAA	TCCAATGAAA	GTGGTAGCCC	60
TTTTGACCCT	GTTTTTGAAG	TTGAACCTAA	TCTCTAACGA	TAACCCAGAG	GAACATGTAC	120
TGAAGGTAAT	TCCTGAGGAT	GCTTCAGAAT	CTGAGGAGAA	GCTAGACCAA	AAAGAGGATG	180
GTTCAAAATA	CGAAACTATT	CATTTGACTG	AGGAACCAAC	CAAACTAATG	CACAATGCAT	240
CTGATAGTGA	GGTTGACCAA	GACGATGTTG	TTGAGTGGAA	AGACGGTGCT	TCTCCATCTG	300
AGAGTGGGCC	TGGATCCCAA	CTCGAG				326

- (2) INFORMATION FOR SEQ ID NO:106:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAATTCGGCC	TTCATGGCCT	ATGGCAATGG	TGGTCGTGGT	GCTGGGTGGG	ATGNGGTCTT	60
CATCCTCTTC	CTCCAGGAAG	GATGCCTCTG	GGATATGGCT	GAAGGCCTCT	GGGTGCAGCC	120
TGGCCAGTTT	CCCTTTCAGC	GTCCTGATAC	GGCGGAAGAT	GATGTCCAGG	TCCCGTTTCA	180
TCTCTACTAG	GGTCCTCGTG	TGGTGCAGGA	AGCGTTCGCT	CATCTGCTGC	AGGCGGGCAT	240
TGGACAGGTT	GTTGAAGTTG	AGCAGCATCT	CATTGGTCTT	CTCAAAGCGG	TCCAGCATGT	300
TCTTCTGGGA	CAGGATGATG	GCGTTGACAT	CATCTGTGTT	CACCATGCTC	AGGATGCGGC	360
CGCAGAAGAC	CCTCGAG					377

- (2) INFORMATION FOR SEQ ID NO:107:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GAATTCGGCC TTCATGGCCT ACATGACACC ACCTGAACGT CTCTTCCTCC CAAGGGTGTG 60 TGGCACCACC CTACACCTCC TCCTTCTGGG GCTGCTGCTG GTTCTGCTGC CTGGGGCCCA 120

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GGGGCTCCCT	GGTGTTGGCC	TCACACCTTC	AGCTGCCCAG	ACTGCCCGTC	AGCACCCCAA	180
GATGCATCTT	GCCCACAGCA	ACCTCAAACC	TGCTGCTCAC	CTCATTGGAG	ACCCCAGCAA	240
GCAGAACTCA	CTGCTCTGGA	GAGCAAACAC	GGACCGTGCC	TTCCTCCAGG	ATGGTTTCTC	300
CTTGAGCAAC	AATTCTCTCC	TGGTCCCCAC	CAGTGGCATC	TACTTCGTCT	ACTCCCAGGT	360
GGTCTTCTCT	GGGAAAGCCT	ACTCTCCCAA	GGCCACCTCC	TCCCCACTCT	ACCTGGCCCA	420
TGAGGTCCAG	CTCTTCTCCT	CCCAGTACCC	CTTCCATGTG	CCTCTCCTCA	GCTCCCAGAA	480
GATGGTGTAT	CCAGGGCTGC	AGGAACCCTG	GCTGCACTCG	ATGTACCACG	GGGCTGCGTT	540
CCAGCTCACC	CAGGGAGACC	AGCTATCCAC	CCACACAGAT	GGCATCCCCC	ACGCACTCGA	600
G						601

- (2) INFORMATION FOR SEQ ID NO:108:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAATTCGGCC TTCATGGCCT ATTTTTTTT TTTTTATCAA AAGTTTGTTT TATTTCAAT 60 ACAAGATAAA TACCATGCTT GTTACTAGTG CAGTTCTCGA G 101

- (2) INFORMATION FOR SEQ ID NO:109:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GAATTCGGCC	TTCATGGCCT	ACAGAATTGG	AGGCATGATG	AAGACTCTGC	TGCTGTTTGT	60
GGGGCTGCTG	CTGACCTGGG	AGAGTGGGCA	GGTCCTGGGG	GACCAGACGG	TCTCAGACAA	120
TGAGCTCCAG	GAAATGTCCA	ATCAGGGAAG	TAAGTACGTC	AATAAGGAAA	TTCAAAATGC	180
TGTCAACGGG	GTGAAACAGA	TAAAGACTCT	CATAGAAAAA	ACAAACGAAG	AGCGCAAGAC	240
ACTGCTCAGC	AACCTAGAAG	AAGCCAAGAA	GAAGAAAGAG	GATGCCCTAA	ATGAGACCAG	300
GGAATCAGAG	ACAAAGCTGA	AGGAGCTCCC	AGGAGTGTGC	AATGAGACCA	TGATGGCCCT	360
CTGGGAAGAG	TGTAAGCCCT	GCCTGAAACA	GACCTGCATG	AAGTTCTACG	CACGCGTCTG	420
CAGAAGTGGC	TCAGGCCTGG	TTGGCCGCCA	GCTTGAGGAG	TTCCTGAACC	AGAGCTCGCC	480
CTTCTACTTC	TGGATGAATG	GTGACACTCG	AG			512

- (2) INFORMATION FOR SEQ ID NO:110:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GAATTCGGCC TTCATGGCCT AAATTATTAA AGGTGACAGT ACACAGGAAA CATTACAATT 60 GAACAATGCC TCAGCTATAC ATTTACATCA GATTATTGGG TGCCTATTTG TTCATCATTT 120 CTCGTGTTCA AGGACAGAAT CTGGATAGTA TGCTTCATGG CACTGGGATG AAATCAGACT 180 CCGACCAGAA AAAGTCAGAA AATGGAGTAA CCTTAGCACC AGAGGATACC TTGCCTTTTT 240 TAAAGTGCTA TTGCTCAGGG CACTGTCCAG ATGATGCTAT TAATAACACA TGCATAACTA 300 ATGGACATTG CTTTGCCATC ATAGAAGAAG ATGACCAGGG AGAAACCACA TTAGCTTCAG 360 GGTGTATGAA ATATGAAGGA TCTGATTTTC AGTGCAAAGA TTCTCCAAAA GCCCAGCTAC 420 GCCGGACAAT AGAATGTTGT CGGACCAATT TATGTAACCA GTATTTGCAA CCCACACCGC 480 TCGAG 485

(2) INFORMATION FOR SEQ ID NO:111:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAATTCGGCC	TTCATGGCCT	ACACACATTG	TGAGCTGTAT	ACGTTAACCC	AAAGTCTGCA	60
TTCAAAGTGG	AATTATAACT	GGGCAGTGAA	TGAGTTGCTC	AGTCCATCTA	TTAACCATAC	120
TCTTTTAGGC	TTTTTATTGC	CTCTAATTGT	TGTAATAATT	AACATTTTCC	CAGGAAGTTG	180
TTTTACAGAA	GAAGGGGCCT	TAGCGGCTTT	CAACTCTTTA	GAGATAAGTT	CAACTTTGTG	240
GATTGACCAC	AGCACATCTT	GTTTAGTAGT	GAGCGGGAGC	CATATGAATC	CTCTAGAGAC	300
ACAGCCGTGT	CTGAGATGGA	CATTGCCAAC	ACAGCTCGAG			340

- (2) INFORMATION FOR SEQ ID NO:112:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

TTCGGNCTTC	ATGGCCTACT	CTCATAAAAA	TATTCAAAGA	TCAACCCCAA	ACGTGCCTGC	60
ANTTTGGACA	ATGTNAGCTA	AAGCTATAAA	TGGAACAGCA	GTGGTCATGG	ATGATAAAGA	120
TCAATTATTT	CACCCAATTC	CAGAGTCTGA	TGTGAATGCT	ACACAGGGAG	AAAATCAGCC	180
AGATCTAGAG	GATCTGAAGA	TCAAAATAAT	GCTGGGAATC	TCGTTGANGA	CCCTCCTCCT	240
CTTTGTGGTC	CNTCTTGGCA	TTCTGTAGTG	CTACACTGTA	CAAACTGAGG	CATCTGAGTT	300
ATAAAAGTTG	TGAGAGTCAG	TACTCTGTCA	ACCCAGAGCT	GGCCACGATG	TCTTACTTTC	360
ATCCATCAGA	AGGTGTTTCA	GATACATCCT	TTTCCAAGAG	TGCAGAGAGC	AGCACATTTT	420
TGGGTACCAC	TTCTTCAGAT	ATGAGAAGAT	CAGGCACAAG	AACATCAGAA	TCTAAGATAA	480
TGACGGATAT	CATTTCCATA	GGCTCAGATA	ATGAGATGCA	TGAAACACTC	GAG	533

- (2) INFORMATION FOR SEQ ID NO:113:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GAATTCGGCC	AAAGAGGCCT	AGAAAATAGA	AAATCAGGTA	GCTATGTCAT	TTTATAAGCA	60
TCAGTCCTCA	CCAGATTTGT	CAAGTGAAGA	AAGTGAAACA	GAAAAGGAAA	TTAAAAGGAA	120
AGCTGAAGTT	AAGAAAACCA	AAGCAGGAAA	CACCAAAGAA	GCAGTGGTTC	ACCTGAGAAA	180
GAGCACAAGA	AACACAAGTA	ATATTCCAGT	GATTTTGGAA	CCTGAAACTG	AAGAAAGTGA	240
AACAGAAAAG	GAAATTAAAA	GGAAAGCTGA	AGTTAAGAAA	ACCAAAGCAG	GAAACACCAA	300
AGAAGCAGTG	GTTCACCTGA	GAAAGAGCAC	AAGAAACACC	CTCGAG		346

- (2) INFORMATION FOR SEQ ID NO:114:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GAATTCGGCC	AAAGAGGCCT	AGGCAGGTAT	TCTTTGCTTT	GGGAAATTCT	TCTTTCTGTC	60
CTCCCTTCCC	TCACTTTTTC	CAAATTCTGG	GCACAACAGC	AGCTCTCTCT	CTTCTGTGGC	120
AGGTGTGCAT	CCTATTGGCT	GGCTGGTATT	TCTTGTTTTT	TTTCCCCCTT	ATTCTTTTTA	180
AATGGGGGTG	GGGGTATAAA	AATATGTGTA	TGGGGTACAT	GCAATAATGT	TGTAATGTTT	240
CTTGTTGTTT	AATGGATAAT	TAATTGCAAA	ATAATTGTTT	TAAITATAAC	ATGTTTGAGT	300
AAATGCTAAA	TTAGTATTTT	TTTCTAATAT	AATAATGAAT	TTGAAATCTA	GCATTCCTGT	360
AACAATGTGT	CTATGTTTGT	CTGTCTGTGT	CTGTCTAATA	GTAATTAATA	TCTGTGGTCC	420
GCACCCACTC	GAG					433

- (2) INFORMATION FOR SEQ ID NO:115:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAATTCGGCC	AAAGAGGCCT	AAGCAAAGCT	TAGCTTACGG	GGAAAAAAAA	ААААААААА	60
AAGTAGAGCT	TNCCTTGAAT	CTGGAGAAAT	TAAGCACACA	GGTGTCCTGC	AATATTAGTT	120
AAGAGACTAC	TGCACCCATC	ATACTGTAGC	TTAAGACAGT	TTCTTCTTTT	AGTTTTTTCT	180
AAAATGTCTC	CATGTCTGTG	TTATGCCACA	AATAACACAG	CCTTGGTTAA	CTTTTGGACT	240
AAAAAAAATC	AACTTATTGG	CCAAGCATGG	TGGCTTACAC	CTATGATTGT	AGCACTTTGG	300
ATAGGTCTCG	AG					312

- (2) INFORMATION FOR SEQ ID NO:116:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAATTCGGCC	AAAGAGGCCT	AATTTTCCTA	ACTGTGTGCT	GCCTTTTGGG	TTAATTAGAA	60
TTGTAGCATT	TCGTTTTGAT	TATTTTTTG	GCTCTTTAGC	TGTTCTCTCA	CATTTTTTAA	120
AATGGTAACT	CTAGGGATTA	TAATATGCAT	CTTTAATTTA	TCAAAGTCTG	TTTTTACTAC	180
TTCGTGTAAA	ATAAACGAAC	CTTGCATTTA	TAGTTACATT	TATTCCTCTC	ATCTCGAG	238

- (2) INFORMATION FOR SEQ ID NO:117:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 184 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GAATTCGGCC	AAAGAGGCCT	ACTCAAAAGT	AGATGAGCAA	TTGGTCAGAA	TTGTTAGAGG	60
ATATTATTTG	AGCTAAATGT	TTCCTCTCTC	TGTTTCAGTG	GTGTATGTGC	AAGTGTGTGT	120
ATATGTTTTT	TGTTGGGGAC	AGTTTCAGGT	AGATGGTATG	AAGAGGCAGC	AGGAGACTCT	180
CGAG						184

- (2) INFORMATION FOR SEQ ID NO:118:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GAATTCCGCC	TTCATGGCCT	AATTTTCTAA	AACCTGGAGA	CAAACCACAT	AAATACAAAA	60
CAAGTCTGCT	TCTTCAAAAT	TCTGCTGGTG	AGAACTCAGA	TATCAGTGAT	CTTATTAGCT	120
TTTTCACAAG	CCAGAACATA	ATGGTGACGA	TGATTAATGA	CAGTGACTAT	GTATCCGTGG	180
CTCCCCATAG	TGCGGCTTTA	AATGTGATGC	ATTCAGAAAA	GGACTATGTT	TTTGCAGCTG	240
TTTTCAACAG	TACTATGGTT	TATTCTTTAC	CTATATTAGT	GAATATCATT	AGTAACTACT	300
ATCTTTATCA	TTTAAATGTG	ACTGAAACCA	TCCAGCTCGA	G		341

- (2) INFORMATION FOR SEQ ID NO:119:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GAATTATGCT	GTGCTGTTTT	CCTGGACACT	CAGAATCAAA	CAGGCCTTCC	ACCCCATCCC	60
ATCATGTTGA	ATTACAAAGT	ATTTTGAGCA	TCGTTTGGTT	TGTTTCTTTC	CACCCATACC	120
TGTGTAGGGC	AGCGGTAGCA	GTCTTCAACA	ATGCATCCTC	TTGGACAATG	CATTGTAATA	180

AAATTCATTC CACACTGTCA TCCCTTTGTC CTAACCAGAA TCTCGAG	287
(2) INFORMATION FOR SEQ ID NO:120:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 196 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:	
GAATTCGGCC TTCATGGCCT AATGTATGGT AGACAATTTT TTTTTAAGAC ACAGAGATAA ACGTTTTCCT GCTTTGGTTA CCTTTCCTTT	60 120 180 196
(2) INFORMATION FOR SEQ ID NO:121:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:	
GAATTCGGCC TTCATGGCCT AGTGATTGGG TGCAGAGGAA ACAGGAACCA GAGAAGGGTC ATCTCAGCTG CCTGTCCCAC TCCCTATGCT TGGTGTTACC TGCGCCATAG TCTCGAG	60 117
(2) INFORMATION FOR SEQ ID NO:122:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 234 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:	
GAATTCGGCC TTCATGGCCT AGTAAGTGCT CTGAGTATAT TAGGAAAAGG AAATCTTATA CATAAAAATC AAAGCTGTTG CTAATTTTTC CACTAGTGAG TCAGTCTATT AACATTACTC ATGGTAGGTT TTGCCATACA GAATTTTAAT TTTTTTATAT TATTTTTTGGC TTTGTTATTA TGCTTAGAAG TCCATGGGGA CCCAAAGATC AGAAAAGATT CATCTGTACT CGAG	60 120 180 234
(2) INFORMATION FOR SEQ ID NO:123:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 265 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAATTCGGCC TTCATGGCC	I ACGGAACGAA	CATTGGCTCG	GCGGTGGTGA	TGCTAATTCC	60
CACTGTCATG TTCACAGTG	A TGGCCGTCTT	TTCCTTCATC	GCCCTCAGCA	TGGTTCATAA	120
ATTTTACCGG GGAAGTGGG	G GGAGTTTCAG	CAAAGCTCAG	GAGGAGTGGA	CCACAGGGGC	180
CTGGAAGAAT CCACATGTG	C AGCAGGCAGC	CCAGAACGCA	GCCATGGGGG	CAGCCCAGGG	240
TGCCATGAAT CAGCCAAGA	C TCGAG				265

- (2) INFORMATION FOR SEQ ID NO:124:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GAATTTGCCA	CACCATGAAG	CTCTTGTGGC	AGGTAACTGT	GCACCACCAC	ACCTGGAATG	60
CCATCCTGCT	CCCGTTCGTC	TACCTCACGG	CGCAAGTGTG	GATTCTGTGT	GCAGCCATCG	120
CTGCTGCCGC	CTCAGCCGGG	CCCCAGAACT	GCCCCTCCGT	CTGCTCGTGC	AGTAACCAGT	180
TCAGCAAGGT	GGTGTGCACG	CGCCGGGGCC	TCTCCGAGGT	CCCGCAGGGT	ATTCCCTCGA	240
ACACCCGGTT	CCTCGAG					257

- (2) INFORMATION FOR SEQ ID NO:125:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GAATTCGGCC	TTCATGGCCT	AGGAAAGATT	CGTGTTTTAC	TTTAATAAAC	CTGAAAGAAC	. 60
TGTCGTTTTT	CACTGCCTAT	AGGACCACTA	CAAAGCCGCA	AAGAAAAATT	AGACTTGTTT	120
CATTTTATAA	CAACAACAAC	TGCTACTACT	GCTACTAGTT	AGATACCGTT	TGCTCATTTA	180
TAACAATCTC	AGTTGGTAGG	ATGAAGCTTA	AACACTTGGC	ATTCATCGTC	TTTTTCAGTC	240
CTCTCGAG						248

- (2) INFORMATION FOR SEQ ID NO:126:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GAATTCGGCC	TTCATGGCCT	ACTGTCTTTT	CATGCAGATT	TCATATTGTC	TTTGTCCTTT	60
TCATTGCTTC	TTGACCTTCC	TGGCAGGTGT	CGCTCAGTTT	CTTCCTGTTT	CCCTTCCTGT	120
CCTCTCCACA	CCTGCTATCC	CGTCCCACTC	CCATCTACCT	CCCGGGAAGC	CAGCCCTGCA	180
TGCTGAGTTT	GTGACCTGCT	TCATTCCCAT	TTCATTTCTA	GAGGGTTTAG	AGGTGACCTG	240
GAACCGTTCC	CTTTCCCTCT	CCTACCCCCT	CCTCTGCAAC	ACCAAGAGGC	CTGGAGGGGC	300
AGACAGAAAG	CAGCCAGCCA	CGGCGGGAAG	TCTCGAG			33.

- (2) INFORMATION FOR SEQ ID NO:127:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs(B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GAATTCGGCC	TTCATGGCCT	AACTTATTTC	TTTTGTTGAT	TGCCTGTCTT	TCTTTTTCTT	60
TCCTTCCCTC	CCTCCCTCCT	TCCCTTCCTT	CCTTCCTTCT	GTAGAGATGA	GGTTTCACCA	120
TGTGGCCAGG	TTGGTCCTGA	GCTTAAGTGG	TCCTCGCACC	TCAGCCTGGC	AAACTGCTGG	180
GATTACAGGT	GTGGGCCATC	ACGCCTGGCC	TTACAGTAAA	TTCTTGATAA	ACAACCCAGC	240
AACACACCTC	GAG					253

- (2) INFORMATION FOR SEQ ID NO:128:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GAATTCGGCC	TTCATGGCCT	AGGACGGGGG	ACTCAGGTTC	TACACTGGAA	CCTGGGGTCA	60
TGTATCATGT	ACCAGGTGGG	GAGAAGTGTA	GCAAATCTCA	GTGCCAATTT	GAGGGGAAGC	120
CAGTCATTCC	AGGAGAAGAG	CTGAGGGGAA	AGAGCTGTTG	ACTTTCATAA	TGCAGTCTTA	180
ATTATCCAGT	CACCCTCCTG	CCACATGGCA	GAAGCCAGGT	GGCAGTGATG	GTGGTGGGG	240
AAACAAAACA	CACAGTCTCT	GGCAAGCCCC	ACCGGGAAAG	GAGGGCTCAG	AAGGCGTAGC	300
GGGTCCGGAT	ATCCTCGAG					319

- (2) INFORMATION FOR SEQ ID NO:129:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GAATTCGGCC TTCAT	GGCCT ACAATAAAA	G CCCATAGGGA	AGAGAGAGAG	GATATAGGGA	60
AACAGAATCA GATGT	GTAAT ATACTTGGC	A CAGCGAAAAA	ATGGATTTAA	AAGACAAAAA	120
TGGAGGTCCA GGTAG	ATGTA ATTCACACA	G ACTGAAAGTG	AGTTCGGGCT	TGTGTAAAAC	180

ACATGAGATT	GGATTTGACC	CCTTGGCTCT	CAAGTGTCCC	CTTAGATCTA	GAACTGCTCC	240
TTGGTGGCCA	TTAGATCGAG	TCAGTTTTGA	TCTGCATCAC	TTAGTTATTG	GGAATTTCTT	300
TGTTGGAAAC	AGGAAAATTT	TTTTAGATTA	TTTGGCGTAC	GGCTCGAG		348

- (2) INFORMATION FOR SEQ ID NO:130:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GAATTCGGCC	TTCATGGCCT	AGGCACAGTG	AAACCCGTGG	AAATTCAAAG	GTGAGCAGGA	60
CAGTGGGTCC	TGTATCTTGA	TCTTTACGGA	TCTTTCTCTT	CTTGAATCCT	CACAGCACCC	120
ATTTTATAGA	CAGGAAGACT	GAGGCCCGAA	AGTTCTGTCT	GACTCTGAGC	CTGGCCTCTT	180
TGCTGCCTCC	CGTTGTCCTG	TGAGGCTGTG	TGGTCACAGC	ACCCAGGACT	TGAGAGGAGT	240
GAAGTTCTTC	CTCACCCCGC	AAAGGCTTCA	TGAGCCCTAC	TGTGTGCCAG	GCCAGCCCTG	300
CTCAGTCTGG	GGCGATAAAC	ACAGGGCAGA	TTCTGAAAGC	CTGTGTGAGG	GAAGTTCTAG	360
GCCTGCAGGA	GCTGAGAGGA	GACCCTGGAG	AGGAAGGGAG	TCAGGGCCAG	CTTCCTCGAG	420

- (2) INFORMATION FOR SEQ ID NO:131:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GAATTCGGCC	TTCATGCCTA	AGCTGATGGA	GACTGTAAAT	GAACCAGAAA	CAGGTGAAGT	60
GAGCAAAGAT	GCAGTCATTG	TAAAGCAGGA	GAAAAATAAT	GAATATTGCC	TTCAGGATAT	120
TGATGATAAA	TTGTCAGAAT	CAGCAGAGGA	TGATGGTGAA	GATGATACCA	ATGATGAAGA	180
TGATGATGAA	GATAGTAACC	CTAAAAAGAA	TACTCAGGCC	CCACTAGAGT	TAATGGCAGA	240
ATTTCTGAGA	GCAGAAATGG	CCCGAGAGTA	CCAGCTGGCA	TATTAAAAAA	GTCAGATGAT	300
CCTAATCTAT	GAACCAGAAA	ATCCTGAGGC	CAAGGAGTTT	TTCACACTTA	TTGAAGAAAT	360
GTTGCTGATG	GAGAAAACTC	AGAATCATGA	GCAAGACGGT	GAAAACAGTG	ATGAAGACAG	420
CAGCGGGCTC	GAG					433

- (2) INFORMATION FOR SEQ ID NO:132:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GAATTCGGCC TTCATGGTCT ACAAAATCAA CTGCAAGCAG CCATCATCAG TTTGGAAGAA
GCTTTGGGAA GCCTTCAAAG AAAAACCTCG GTATCCACCA AGTCAGGCTC AAGCAGCTCT
120

WO 98/45436

PCT/US98/06955 TCAAGACAGT CCCCCTGAAG AGTACTCCTA TAAGAAATCA ATAAGAAACC TGTTTAAAAA 180 CATTCCTTTT GTCCTTCTGT TGATCACTTA TGGTATCATG ACTGGTGCCT TTTATTCAGT 240 CTCAACGTTA TTAAATCAAA TGATATTGAC ACAACTCGAG 280 (2) INFORMATION FOR SEQ ID NO:133: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 398 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133: GAATTCGGCC TTCATGGCCT ACGCGAGCGG CAGGTGTGCA CAGGAGGTTC TCCACTTTGT 60 NCTCTGAACT CGCGGTCAGG ATGGTTTTCT CTGTCAGGCA GTGTGGCCAT GTTGGCAGAA 120 CTGAAGAAGT TTTACTGACG TTCAAGATAT TCCTTGTCAT CATTTGTCTT CATGTCGTTC 180 TGGTAACATC CCTGGAAGAA GATACTGATA ATTCCAGTTT GTCACCACCA CCTGCTAAAT 240 TATCTGTTGT CAGTTTTGCC CCCTCCTCCA ATGGTACTCC AGAGGTTGAA ACAACAAGCC 300 TCAATGATGT TACTTTAAGC TTACTCCCTT CAAACGAAAC AGAAAAAACT AAAATCACTA 360 TAGTAAAAAC CTTCAATGCA TCAGGCGTCA ATCTCGAG 398 (2) INFORMATION FOR SEQ ID NO:134: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 403 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134: GAATTCGGCC TTCATGGCCT AGGGCGATGG TGGGCAGAGG ATCCTTAGTG CTCAGTCGGG 60 CTCCACCAGA ACCACGGACT TGAAGGAGAA GAGACTCTCG GTTCCAGGTA GCAGAAAACG 120 TGGAGTTTTG GACACAGATC CTCCTGGCCA GAGAAGGATG CTTGAGAATC TGAGATTTAC ACAGCTGTAT TAGGTTGTCC ACGATGACCG GGCAGTAGGT CTCTCTCTTG GGGATTTCCT 240 CAGTGGTCTG CCAGAGACGG GCGTGAGAGA TCACATTCAG AACGCACTCG TCTTGGTTCT 300 CTATGTGGTT CCTTGGATCA TCAACAAGGC TAAGCACTTT CTCGGGAAGG CCTTCTATTA 360 ACTTGGTCTT GGTGAGCCAG AGGGCCTGCT TTACACCCTC GAG 403 (2) INFORMATION FOR SEQ ID NO:135: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 205 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

60

120

180

GAATTCGGCC TTCATGGCCT ACTCCATTTT TCGAATGGCT TATTTAGGCC CAGCTCTTGC

GTTTGCATTG TCCCTTCAGG CCCAGAACTT TCTCACGTCA TCGTCACCAG GCCTAGCTTC

TGCATCTGGT CAGCCTTTTA AGGCCCAGCT TTTGCCTCAT AAACTCAGCT CCTGTTTAAT

GGCGGCCTCC CGGGTCCCAC	TCGAG	205

- (2) INFORMATION FOR SEQ ID NO:136:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAATTCGGCC AAAGAGGCCT AGTTTTATTA CTTTGGTTAA GACATCAGTT ATTTTAGTCT
TTGATAATTC ATTATCTAGA TAATGGTTAC TTTGTATTGT CTGTTTCTCG AG
112

- (2) INFORMATION FOR SEQ ID NO:137:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GAATTCGGCC AAAGAGGCCT ACACAGAGCC CTTCAGTACT TTTAATTCTT CTTAAATTGG 60
TGGTTCATGT TAATTAAATT ATTATTATT TTTTTTGAGA CGGAACTCGA G 111

- (2) INFORMATION FOR SEQ ID NO:138:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GAATTCGGCC AAAGAGGCCT AAAGATGTTT TCCATGAGGA TCGTCTGCCT GGTCCTAAGT 60
GTGGTGGGCA CAGCATGGAC TGCAGATAGT GGTGAAGGTG ACTTTCTAGC TGAAGGAGGA 120
GGCGTGCGTG GCCCAAGGGT TGTGGAAAGA CATCAATCTG CCTGCAAAGA TTCAGACTGG 180
CCCTTCTGCT CTGATGAAGA CTGGAACTAC AAATGCCCTT CTGGCTGCAG GATGAAAGGG 240
TTGATTGATG AAGTCAATCA AGATTTTACA AACAGAATAA ATAAGCTCAA AAATTCACTA 300
TTTTGAATATC AGAAGAATCT CGAG 324

- (2) INFORMATION FOR SEQ ID NO:139:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEO ID NO:139:

GAATTCGGCC AAAGAGGCCT AGGTCCAGAA ACATTTAAAA AAAAAAAAA GGGGGCTTGA 60
GAAAAGGGCT TCCAGTGCCA GGCAGAAATA TGTTTTTCTT AATAGGGC 108

- (2) INFORMATION FOR SEQ ID NO:140:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAATTCGGCC AAAGAGGCCT ATGAAAACGT GGATTTGCTT TGTAAACTT AGAATACATT
TTGTTGCCAA CAAAAAGAG GAAGAAAGA GGAAGATATT GAAGAGAAGA AATCGATTAA
GAAAAAAATT AAAGAACTTA AGTTTTTAGA TTCTAAAATT GCCCAGAACC TTTGTAAGTA
TCATATTCCA ATACCATTCA AAGACAGTGG AAATATTTCT TTAAATGATT TCATTTTCTT
TAAGACCGAT TATTCATTAT TTGCTATTTT CATTTTGTTA TTATATGCAT GATAAATTCA
300
CAGATACTCT CGAG

- (2) INFORMATION FOR SEO ID NO:141:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GAATTCGGCC AAAGAGGCCT AGGGTAAGAC TAGAGTGTTT TAAATCATCA ATAAAAAGTG 60
GAGAAAACAA AGGTTATTCA GCGATTGAAT TCTAGACCTG CCTCGAGCCC TGCCTTTCCT 120
TTACTTTTAC TTTTTTTTT TTTTTCTTTG GAAGAGAGAA GAACAGAGTG TTCGATTNTG 180
CCCTATTTAT GTTTNTANTC GGGAACAAAC GTTGGTTGTG TGTGTGTGTG TTTTCTTGTG 240
TTGGTTTTTT AAAGAAATGG GNAGAAGAAA AAAAAAATTC TCCGCCCCTT TCCTCGATCT 300
CGCTCCCCCC TTCGGTTCTT TCGACCGGTC CCCCCTCAAC CTGCCTCGAG 350

- (2) INFORMATION FOR SEQ ID NO:142:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GAATTCGGCC AAAGAGGCCT AGAGAGTCTG GATGACAAGC AAAGCTCAAT CTCAAAACAA

TAATTTTTAA AGTAATGATT ATCTTAACCA TTCTTAAATC CTTCTGTCTA GTAGGAATCT TATTCATGGG AGTGTCTGGA AAAGGGACAA AGAGCGGCTA TCTCGAG 167	
(2) INFORMATION FOR SEQ ID NO:143:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 216 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:	
GAATTCGGCC AAAGAGGCCT AGTGTTTCAC AAAAGAATTG GAAACCATAG TCCTGAACTC TCCCTAAGTA GTATAAGCTT TAAATAGCAC TCAATCCATA TTAAGTCTTC TTAGTGTAGC ATGGTTGCTC TCATGCGTCT TTCTTATGTT TTAAATGGTG TAAATTTTAG TCGTTTGTCA TTCAGAAGTG GCTTTGCAAA TACAAAATAT CTCGAG	0
(2) INFORMATION FOR SEQ ID NO:144:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 301 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:	
TAATCTTTAC TGGTGAAAAG GATGGAAAAA TAAATCAACA AATGCAACCA GTTTGTGAGA 6 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA CCTGAATGCG GAAGAGCTCG 12 GCTCCCGTTT AGCATTTTGT ACTTAAGGAA ATAAAAAAACC AACAAAGGAT CTCACATTTT 18 CTTAAAAAGT GAAGATTGCT GTATACTATT TATTCAACTT ATAATTATG TTACTCCTTG 24 ATCTTTGTCT TTTGTCATGA CAAAGCATTT ATTTAATAAA GTTATGCATT CAGTTCTCGA 30 G	10
(2) INFORMATION FOR SEQ ID NO:145:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:	
AGTATTTTAT TTCTATTTTA TATATTGAGA TTTCTTCTAA CATTTCCTTT GATAAAAATC 12	60 20 77

- (2) INFORMATION FOR SEQ ID NO:146:
 - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 310 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAATTCGGCC	AAAGAGNCGT	AGGGAAAGAT	TTCAGCTATT	AATCAACTGG	AGGAAATTCA	60
AAGCCAGCTG	GCTTCTCGGG	AAATGGATGT	CACAAAGGTG	TGTGGAGAAA	TGCGCTATCA	120
GCTGAATAAA	ACCAACATGG	AGAAGGATGA	GGCAGAAAAG	GAGCACAGAG	AGTTCAGAGC	180
AAAAACTAAC	AGGGATNTTG	AAATTAAAGA	TCAGGAAATA	GAGAAATTGA	GAATAGAACT	240
GGATGAAAGC	AAACAACACT	TGGAACAGGA	GCAGCAGAAG	GCANCCCTGG	CCAGAGAGGA	300
GATTCTCGAG						310

- (2) INFORMATION FOR SEQ ID NO:147:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGTGGCCTTG	GGTCAAGATT	CGCACCATGG	TGGGCACAAA	CCCAGGAGAA	CACTTTCCTG	60
TAAACGTGTT	TTCATGCTGG	AGCCAAGGTT	TTGACTTGGG	TTTGGATTTT	ATTTATTTAT	120
TTTATTATTA	TTATTACCAG	GTTGCATCTA	AAGGATGTTT	TGGAGGAGCA	CAGAGTTTGT	180
CTGGTGAGGG	TAGGCTCTGG	GCAGATTTTT	CTGTGAGTCT	CCCCTGCCTG	CGGCATCAGG	240
ATCATCCCTG	GTGCCCTGTG	GTGGCACCAG	GTGGCTGCCC	ACCCACAGGC	GTGGCCTTCA	300
CAGTGGGGGC	CATCTCAGCC	TGGGGTAGCG	ATCTGCCTCC	GACCTGCCTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:148:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 283 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGCCTGCATC	GCAACAGCCA	GGAGGGCCAG	GCCACCCCAG	GCAGGAGGCA	GTGGGCTGGC	60
AGCCACCCTG	GGCACAGAAG	AGCAGACGCA	GACAGTGCTG	GGCAACGAGG	GGCTTTCTTC	120
ATGGGCCCGC	CTGCCCTGTC	CCTCCCCCA	GGTCCCCACC	TTCTAGGGTT	AAAGTGCAGC	180
TGGGAGGGAG	GAGGCAGGCA	GAATTGGGGA	GCTAGAGAGA	GCCCAAGTGA	ACCCTGACTG	240
TCCACGCAAG	TCCCATGTCC	TCCTCGTCCT	GGAGTTCCTC	GAG		283

- (2) INFORMATION FOR SEQ ID NO:149:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GAATTCGGCC	TTCATGGCCT	AGACCTGCCT	CGAGTTCCTT	TTGTTATTTC	CCTGCATCTT	60
ACAACGTTAA	GGCCTTGGTC	CCTGCTAATA	TAAAAATA	AATCAACTTT	ATAAAGAGCT	120
TACAATATGC	CAGATACTGT	ACTAAGTGCT	TTATATTTT	TTTTTGGGTG	GGGGGTGGCT	180
GTTGGGCAGT	GTCTCGCTCT	GTCACCCAGG	CTGGAGGGCA	GTGGCACAGT	CATGGCTCAC	240
TGCGGCCTTG	ACCTCCTGGG	CTCAGGCCTC	CCGCCTCAGC	CTCCCAGGTG	GCTGGGGCTA	300
CGGGCGTGCA	ACATTCTCGA	G				321

- (2) INFORMATION FOR SEQ ID NO:150:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GAATTCGGCC	TTCATGGCCT	ACGTAATTCT	GGAAAAGTGA	ATACTTGTGA	AGAGTCGTCT	60
TGAATGATTT	GTAAAAAATC	CTGTTCTTAT	ATTCAACGAG	TTTCGAATCT	TTGTCAGAGG	120
AGTATTACCA	TTAGATTGAA	AAAAAGGAAA	ATAAATA	AACACTTTTA	AAAAAACTCC	180
CCATTCTCTT	ATTCTCACTT	TTAGGAAAAG	AGACTGACTA	ATATCTTCTG	CCACAAATAC	240
CGATGTTCTT	TTTATAAAAA	ATGGGACTGC	TTTTGGCAAC	CAGCCCTATT	TTGTTTTCAT	300.
ATCCCTTTTT	GCTCCCATCT	TTCCAAACTC	ATAAACTCGA	G		341

- (2) INFORMATION FOR SEQ ID NO:151:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CNATTCGGCC	TTCATCCCCT	א ההנה ההנה הנה	ACTAAAAATA	CAAAAATTAG	CCAGGCACGC	60
GCCAGGTGGT	GCGCACCTGT	AATCCCAGCT	ACTAGGGAGA	CTGAGGCGGG	AGAATTGCTT	120
GAACCTGAGA	GGTAGAGGTT	GCACATAGCG	CCACTGCGCT	CCAGCCTGGG	CAACAAGAGT	180
GAGACTCTGT	CTCAAAAAAA	TATATAAATA	AATAAATGAA	TAAAAAAT	TGTATAACAT	240
CTATACTATA	GCCTCGTAAG	CATTAGCTAC	TTAATATTT	TGGTATATTT	ATTTTAATAA	300
ATACAGCATT	TTTGATTACT	AGTGAACATG	AATATTTTCC	CATATTTGTT	AATTATACTT	360
TCCTCTTACA	GAAATTCTGT	TTGTGTCCTT	CACCCTTCAC	TCGAG		405

- (2) INFORMATION FOR SEQ ID NO:152:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAATTCGGCC	TTCAGGGCTC	CTTCTTCCTA	GGCTAGTATT	TATCCCACTA	CATCTGACTC	60
ATTCTCTACT	ATCGCTGTTG	ATTTCCTCTT	GGGTACTAAA	TCTGTTGAAC	ATGTTGCCAG	120
GCTTACTGCT	GGTATTATGG	GATAGCATTT	GCCTGATGGC	AGCTTCTAAA	GGAGACTCCG	180
ATGGCACTAA	GCAGTTTCCA	AAAGTTTATC	TTGCAAGTTC	AACCCAATTC	GAG	233

- (2) INFORMATION FOR SEQ ID NO:153:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GAATTCTAGA	CCTGCCTCGA	GATGTTTTTT	TCGTTATTTG	AAATCTTTGC	TCTTTTATTT	60
TTCAGCTCCC	AGATCCTCTC	CCTCTCTTTA	GCTTTCACTG	TGTTTGATAT	CAAGAATATG	120
AAATGTGAAT	TCCACGGACT	CGAG				144

- (2) INFORMATION FOR SEQ ID NO:154:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATGGCCT AGGCAGGAAG GA	AGGCTGGAA TAAATAAAAA	TAAAAATAGA	60
ATAAATA ATACATTTTT AA	AACATGTCA ACATTGATAA	TACAATGAAG	120
AGTATCA TATCTAACCA AG	GATATGCAA AAGATGCATI	CAGTAAGCTG	180
rgtaact gtgaaatcag c	TCACCAGTT CAAGTCACTA	GGTTTGCCAC	240
STTTCAG CGAGCATAGC GA	AGTGGCTGT AAGAAATTGT	CCATGCCACC	300
CTTGCCC AGGTGGTCTC G	AG		333
	TAAATA ATACATTTTT A GTATCA TATCTAACCA A GTAACT GTGAAATCAG C TTTCAG CGAGCATAGC G	TAAATA ATACATTTTT AAACATGTCA ACATTGATAA GTATCA TATCTAACCA AGATATGCAA AAGATGCATT GTAACT GTGAAATCAG CTCACCAGTT CAAGTCACTA	TGGCCT AGGCAGGAAG GAGGCTGGAA TAAATAAAA TAAAAATAGA TAAATA ATACATTTTT AAACATGTCA ACATTGATAA TACAATGAAG GTATCA TATCTAACCA AGATATGCAA AAGATGCATT CAGTAAGCTG GTAACT GTGAAATCAG CTCACCAGTT CAAGTCACTA GGTTTGCCAC GTTTCAG CGAGCATAGC GAGTGGCTGT AAGAAATTGT CCATGCCACC TTTGCCC AGGTGGTCTC GAG

- (2) INFORMATION FOR SEQ ID NO:155:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAATTCGGCC	TTCATGGCCT	AGGAAGTGGA	GGGAAGCTGG	GTCGCTGCTG	GAAGGGAGGG	60
AGGCTGACTC	TCTACCCCTC	ACCTCTGCAA	GGAACTGAGG	CCTGTAGGGT	TGCGGCTGTC	120
ACTGGCTACA	GGCGGCATCT	TTCTGTAAAA	AGCTTTTCAG	GCATGAAACC	CATTTCTGTA	180
TGGACTGGGC	TGTGTTGACG	GTGGTGCTTG	GGCCTTGTGT	GCCAGGCCTC	TCTGGGTCCC	240

CTCCCTGGCC TTTGCCTTCC TCTCACCTTC TCGAG

275

- (2) INFORMATION FOR SEQ ID NO:156:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 244 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GAATTCGGCC	TTCATGGCCT	AGAGTCATAG	GTCAGACCAC	TTTCTAGGAG	CTGTTCAGTG	60
ATAAAATTAA	TAACAGTGAC	TTTTGAGTCA	AAATAGATTT	TTAAAGTACT	TGATTTTCTC	120
TTTGATTTGG	AAACATCTTT	GTTTAGCTTA	ATTGAAATGA	TCTAAAATAT	TTGAAGGATT	180
TTATACTTTA	CACAGAGGCA	TGTATTTGGA	TAATTAGCTT	TTATTAAACC	CAGGCTTCCT	240
CGAG						244

- (2) INFORMATION FOR SEQ ID NO:157:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GCGATTGAAT	TCTAGACCTG	CCTGAACCCC	ACCCTTCACG	TCCTACTTGG	GCTGCCAAAG	60
TCATCTTCCC	AAAACATGAC	TTTTCCTCAG	TCACTTTTCT	TATTAGATTT	TATCATATTC	120
CACATCCCTT	CCCTGGCCCT	CAAGGGTGCC	TGTAACCTAG	AACCATCTTA	CCTTTCCACC	180
CTTGTTTCCA	AACCTTCCGC	TTTACTTAGA	CATGCCTTCC	CATTTCCCTC	CCGACCCACC	240
CCCCTCGAG						249

- (2) INFORMATION FOR SEQ ID NO:158:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GAATTCGGCC	TTCATGGCCT	AGAAAAAAC	AAGTAGTTTG	GCAAGGAGAG	CAGAAAAATA	60
AAATTCCACT	GTGTAGGCAT	TTGGAGATTT	AGCAAGAGCA	ACCTAGAGTC	TGCCCCCAGA	120
GACACTGCAC	GTTGTTTCTG	ACACAGAGGA	TGCACTAATT	CTATTTCCTG	TGCCACCTGA	180
AAAAATCATA	ATTTGAGAAG	AGAAACTGTT	AGGCCATTTC	TAGTGAACTA	TTTTTCCAAA	240
CCCTCACGGA	ACCCTGAACA	GGGCGTGTCT	CGAG			274

- (2) INFORMATION FOR SEQ ID NO:159:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GAATTCGGCC	TTCATGGCCT	AAGCTTGCTC	ACTCTTCTGT	GTGTTTGAAA	TAATGGTAAA	60
ATACAATAAT	ATTGTCAAGC	ACAGTGGATC	GGAGATTTTT	CTTCTCAGGA	CTATTCTGCT	120
TATAGGTCTA	CTTCCTATAG	CTATTTGTCA	TTGTCCTCCT	GGTCCTTCTC	TTTTCTTCTC	180
TCCTGTGCTA	GATGCTCTCT	CTTCCTATCC	CTCCCTCTCT	TCCCACCCCC	ACCTCCCACT	240
TCTCTGTTTA	TATCCTGATT	TTGGTGGAAC	ACATCCTCCA	GGCTCCCTGG	CACTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:160:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ATGGCCTAAG	GTGCCCNAGC	TTGCCAATTA	ATTCCCAGTA	GAAATTTTTA	AATGTTAAAG	60
ACAGTAATTA	ааааааааа	AAAACCACAC	TGTTTTGACA	TTTTACCTCG	TGCTTTGTGT	120
GTGACTAGAT	TATGCACTAG	AATTTCATTC	AGTATTCTTC	CAAATAAGTT	ATTTCCCAGG	180
TGTTCGCTGG	TATCTAACCA	ANTANTCAAT	AAAGTATTCT	TGCTAAGTNG	GCCATGAAG	239

- (2) INFORMATION FOR SEQ ID NO:161:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GAATTCGGCC	TTCATGGCCT	AATATCATGA	TCACTGAAAT	TACATCTAGT	GAAACACACA	60
CGTGCTTATC	TGCACGTGTG	TGTAAGTTAG	AAAGAAAAA	CAAAGGCCTA	ACAGTGATTG	120
TCTTAGGTTG	ATAGGATAGT	GGGTGGGATT	TGCAGAATTT	TTGTATCTGC	AGAATTTTTG	180
CAAAGTGCCC	ATTAGTTTTG	TAAAGAAAAA	AACCTAAATG	TATAACTTCT	AAAGAGATAA	240
TTTTTTTTTT	CATGTTTTTG	CTACCTATAT	CTAGGAAAAT	AACTTAGAAT	TGTAATTATT	300
TTGAAGCTCT	GGAATTATTA	TGTTCAAAAA	TTACAGAACC	AAAAAGTCTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:162:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 469 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GAATTCGGCC	TTCATGGCCT	ACTTGCTGTG	GCTGACTCGG	TTATTGACTT	TACTTCTTTT	60
CTTTTCAGGT	TTTTATGGGA	CTGTTTCTAG	CCCTGATTCA	GGTGTGTATG	AAATGAAGAT	120
TGGCTCCATC	ATCTTCCAGG	TGGCTTCTGG	AGATATCACG	AAAGAAGAGG	CAGATGTGAT	180
TGTAAATTCA	ACATCAAACT	CATTCAATCT	CAAAGCAGGG	GTCTCCAAAG	CAATTTTAGA	240
ATGTGCTGGA	CAAAATGTAG	AAAGGGAATG	TTCTCAGCAA	GCTCAGCAGC	GCAAAAATGA	300
TTATATAATC	ACCGGAGGTG	GATTTTTGAG	GTGCAAGAAT	ATCATTCATG	TAATTGGTGG	360
AAATGATGTC	AAGAGTTCAG	TTTCCTCTGT	TTTGCAGGAG	TGTGAAAAAA	AAAATTACTC	420
ATCCATTTGC	CTCCCAGCCA	TTGGGACAGG	AAATGCCAAA	CAACTCGAG		469

- (2) INFORMATION FOR SEQ ID NO:163:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

G	ATTTATTCA	TTCTTGATTA	AATGCACTGA	AAAGTAAAGG	GTCTGTTTGT	GTCATGTTCA	60
7	GAAAATGCG	GTTAGAGAGG	TGCTATTCAA	GTGATTCTGA	AGGCACCCCA	AGGTATATCT	120
C	AAATTTAAA	GATTACTGCA	AATATCTTTA	CTTTACTGTG	GGTTTTTAGT	ACATCTGTTA	180
Į	TTTAGTGTT	TCTTTGTGTG	TTTTGTAGAC	TAGTGTTCTT	CCATCCTTCA	ACTGAGCTCG	240
7	\G						242

- (2) INFORMATION FOR SEQ ID NO:164:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

GAATTCGGCC	TTCATGGCCT	AGCATTTTTT	TTCTTTAAAT	TATTGTATCC	ACTAGTTCTT	60
GCCAGTATAA	AGGAATACAA	TTGACTTTTG	TGTGTTTCAT	ACCCTACAAC	CTTTCTAAAT	120
TCACTTATCA	GGTCCAGAAC	TCTTCTACTA	ACAATGCACT	TTTATAAAGC	CCTAACACCT	180
CTCCTGATCT	CTGTCTCACC	CTCCCACCTA	TCTCACTGTG	GGATGGGAAG	GAAGTCAATG	240
GAAAACACAG	GAGCGCATTC	TAATAATAGC	CCACATGGTA	TACTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:165:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 199 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GAATTCGGCC	TTCATGGCCT	AGCTCGATCC	AAGAAGAAAA	ATTAAAATGA	CAGCTTTTCC	60
CATTGATATA	ATCATCTTAC	TTTGCTCTCT	ACAAGAAATA	TGCATTAGGA	ACCTTCATTA	120
TAGGTCCACA	GAAATAGCAG	AACACAAAAG	CGCCCCCTA	CCCCCCCCCC	CCGGTAACCA	180
GAAATACACA	GAGGCAGAG					199

- (2) INFORMATION FOR SEQ ID NO:166:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE TESCRIPTION: SEQ ID NO:166:

GAATTCGGCC	TCATGGCCTA	GAATTAACCA	ATTAAGAATT	AATAAATTAC	TTAAAAATT	60
AAAAATCAGG	AATACCAGGC	TTAATGCATT	CATTTATTCT	ATTTAGCAAA	CTTTTTTTT	120
TTTTTTGAAT	GCCCACAATG	TCCTAGGTTC	TGGAAATACA	AAATTACTTG	GTACCAGTAA	180
CTCGACTGTC	ACCTTTCCAG	CCATGGACTT	GGTTĆAGACA	AACCCCCAGT	CCACGGTTGT	240
CGTCCACTTG	CAGTGCCCGC	CGACTGTGGA	TATATGCTGG	GGATCCCAAC	ACAACGCAGC	300
TACTCTCGAG						310

- (2) INFORMATION FOR SEQ ID NO:167:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GAATTCGGCC	TTCATGGCCT	AGTAAATATT	TTCTTCTACT	TTGTGTTTTG	CCTTTTTGTT	60
TTCTCAGCAT	TATTTTTTGA	AGACAAAAAG	ATTGATTTTG	AAGAAGTCTA	ATTTATCAGG	120
TTTTTTCTAG	TAGTTTGTAG	CGGATTTNTG	CATGCTGCTT	TTAAAAAAAT	CTTTGCTAAC	180
CCTCGAG						187

- (2) INFORMATION FOR SEQ ID NO:168:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GAATTCTAGA	CCTGCCTCGA	GCCTTGCCCA	GAATCAGCAA	GTAAACTGCA	CTAATTTGTC	60
TTATATTTGA	CTTTCTAACA	CTGATTTTTC	TGATTTTTCC	CTGTTCGACC	CTCCAATTTA	120
TAAAAATGTG	TATAATTGTT	CTGCTGCTTC	TGCTTTTGCC	TGCTTTGGCT	GCTGCATATA	180

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436	PCT/US98/06955	
430	CAGGTGAAGA TCTGGAAAGA AATGATGGAT CTACAGAAAA ACCCTACTTC GTAACCCCTA ACCTGCATGG AATTCTGATC AAGAAGCAAC TCGAG	240 275
	(2) INFORMATION FOR SEQ ID NO:169:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 287 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:	
	GAATTCGGCC TTCATGGCCT AGTTTCACAT TGTCTGTACT GTGTTGTGCA GTACCAGAAG TTGCTGGTAG CTACTTGGTC TTCTGGGACC TGCCATTGCA GACGTGGTA TTGTAATCTT AATCTTGTTG AAACAGGATG GATTTATGAC TGGGATGGCC GGAAGCCACA CCAGACACCC AGTCACCTGG TCATGGGAGA GGTACTTTGT TGGCTTTTCA TAGTACTTAA CACTGTGAGC TGCTTCCTGA AGTGGCACTC TTAAGGCCAG GTGCCCCCAC CCTCGAG	60 120 180 240 287
	(2) INFORMATION FOR SEQ ID NO:170:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 314 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
•	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:	
	GAATTCGGCC TTCATGGCCT AAGACAGACA TTTTTGGCAG AGCATAGATG AAAATGGCAA GTTCCCTGGC TTTCCTTCTG CTCAACTTC ATGTCTCCCT CCTCTTGGTC CAGCTGCTCA CTCCTTGCTC AGCTCAGTTT TCTGTGCTTG GACCCTCTGG GCCCATCCTG GCCATGGTGG GTGAAGACGC TGATCTGCCC TGTCACCTGT TCCCGACCAT GAGTGCAGAG ACCATGGAGC TGGAAGACGCT CGAG TGGAAGACCT CGAG	60 120 180 240 300 314
	(2) INFORMATION FOR SEQ ID NO:171:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 195 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:	

60 GAATTCGCCT TCATGGCCTA CACCAAGTTG AATCCCTATG CAGGAGGAGA CGGCCTTCAG AACAACCTGT CCCCCAAGAC AAAGGGCACT CCTGTGCACC TGGGCACCAT CGTGGGCATC 120 GTGCTGGCAG TCCTCCTCGT GGCGGCCATC ATCCTGGCTG GAATTTACAT CAATGGCCAC 180 CCCACATCCC TCGAG 195

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 238 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:	
GAATTCGGCC TTCATGGCCT ACACTCCTGG TCATTTTGCA TTTTATCCAG CTTTTTTCA TCAACCATGT TATCCTGACA GACACATTTA TTGGATATTT AGTTGGAAAT ACCTTATGGT TGGTTGCAGT TGGCTATTAT ATCTATGTAA CTTTCCTGGG ATACAGTGCA TTGCCATTTT TGAAAAATAC AGTAATTCTT CTGTATCCAT TTGCACCTCT GATTCTGCTC AACTCGAG	60 120 180 238
(2) INFORMATION FOR SEQ ID NO:173:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 234 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:	
GAATTCGGCC TTCATGGCCT AGGCTAACGT AATTGAGAAA ACCAAATGAA ATATATCTTG ACCAATAATT TAAAACCATA TCAGAGATTC AGTTTGGTTC TGTCTTCTGC TTTACTGATT TTAGGATCAG CCTCATACAA AAGGGTAATG GTGGCAGCAG CTCCAGAACT CATATCATAT	120
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 251 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:	
GAATTCGGCC TTCATGGCCT ACTCAGTTCC ATTGTTAAGC AAGGAAAAAC AAACAATACA TTGAATTTGA CAACCCACTG AAGTTGCAGA TAATGAGGAC TTACCATTGT ATACCATTAT TCATCTGGAC CTATATGTTC CATACAGTTG ACACCATCCT ATTACAAGAA AAACCTAACA GTTATTTATC AAGCAAAAAG ATAGTGGGTC TGACAAAAGA TGACGGTAAA ATGCTACGTC ACACCCTCGA G	60 120 180 240 251
(2) INFORMATION FOR SEQ ID NO:175:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 239 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GAATTCGGCC	TTCATGGCCT	AAACCACTGC	GCACCATATT	TCTTAAGGAT	GTTCTGAAGA	60
CCCATGAATG	TCTGGTCAAG	TCTGCTGATC	TCTTAATGAG	GGACAACCTG	TTTGAAATAA	120
TAACAAGCTC	CAGGACATTC	TACGTACAGG	CAGACAGTCC	AGAAGACATG	CACAGCTGGA	180
TTAAGGAGAT	TGGCGCAGCT	GTCCAGGCCC	TCAAGTGCCA	CTAGGCCATG	AAGGCCGAA	239

- (2) INFORMATION FOR SEQ ID NO:176:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GAAAACCCCA	GATATTCCTT	ATTATGGAAG	AAGAAGCAGG	AAATATGTTT	TTGAATAATG	60
TGGGTCAGAG	AATTGTGCAT	TTATTATTGC	TAGGATGCAT	ATACACATTG	AACTCAGTCA	120
ACTTACTCTC	TCTAAATTAT	CTCACCGGTG	GAGACATTGC	CTCAGGAGTC	GAGCCCTGTG	180
GTGTGCCTCC	TGCTGTCACC	ACATTTGACC	ACCTAACTGA	CCCCACTGTG	GTCACCTTTG	240
CCACCAATCT	CGAG					254

- (2) INFORMATION FOR SEQ ID NO:177:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 175 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GAATTCGGCC	TTGCCAGTAT	TCATGCTGTT	GCTTCAGTCA	AGAATGAATT	CCTCAGCGCT	60
ACCTCTCTTG	ACCTTCACAT	CTTACTTAGT	GCAAATGCTG	TCTCCTCCTG	AGACTTGCCT	120
GACTTCGGAT	ACTCTCCCTG	TGACATCTTA	TCTAAAATGT	CAAGTGAGAC	TCGAG	175

- (2) INFORMATION FOR SEQ ID NO:178:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GAATTCGGCC	TTCATGGCCT	AAGTGGCTGT	GTGGTATTTC	CTAAGTATTT	TTAAAATTT	60
TCTCTCATTG	ATACCCTATA	AAAATGCAAC	TGTTAAAGAA	TTTGTCTTTC	TTTCTCATTA	120
TATTCTTTCC	AGAGTATATA	ACTAATTTAT	TCAGCATTCA	TTCATTCAGC	AGATATTTGT	180
TGAGCACTAA	CTATGTTCAG	GCACTGGGCA	GGGATATCGG	GATACCAAGA	AAGCTCGAG	239

- (2) INFORMATION FOR SEQ ID NO:179:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAATTCGGCC	TTCATGGCCT	AGAAAATAAT	TTAGAGAAAG	AATAGAAAGT	CATGGAAAAT	60
CTCATAGGTA	GGAGACAGAA	GAGAGAACAT	TGTAAATAAG	TTTAAAAAAG	ATAAGAAAAT	120
CAGGATAAAG	TAGTATGGAC	TCTGAGGTGG	GAGAGAATTT	TAAGATTAGC	AGGAAAGTAG	180
TGTAGTTGGT	ACTTTTTAGT	TATTAACAAA	GCACTCACTT	CTTACAGAGT	CTCGAG	236

- (2) INFORMATION FOR SEQ ID NO:180:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 410 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GAATTCGGCC	TTCATGGCCT	ACGAAGATTA	TAATGTATTT	TTATTCTGTT	TTCAGCTTCA	60
TGTTTCCTGT	TGCAGGTGGG	ATAAGACCCC	CTCAAGGCCT	GATGCCGATG	CAGCAACAAG	120
GATTTCCTAT	GGTCTCTGTC	ATGCAGCCTA	ATATGCAAGG	CATTATGGGA	ATGAATTACA	180
GCTCTCAGAT	GTCCCAAGGA	CCTATTGCTA	TGCAGGCAGG	AATACCAATG	GGACCAATGC	240
CAGCAGCGGG	AATGCCTTAC	CTAGGACAAG	CACCCTTCCT	GGGCATGCGT	CCTCCAGGCC	300
CACAGTACAC	TCCAGACATG	CAGAAGCAGT	TTGCCGAAGA	GCAGCAGAAA	CGATTTGAAC	360
AGCAGCAAAA	ACTCTTAGAA	GAAGAAAGAA	AAAGACGCCA	GTATCTCGAG		410

- (2) INFORMATION FOR SEQ ID NO:181:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

(GAATTCGGCC	TTCATGGCCT	ACACATTTGC	ATTGTCTGCC	CATGGACTGG	TTGGAGCAGA	60
i	AACCTCCATA	CCTCAGTCTC	TTGGTATTTG	TCTGCCCCAA	CTGCTGCTTT	TTGTTGGGAT	120
•	GTTTGTGTGT	GCTGGGGTCT	CGGCAGCATC	GGCTGCTTCC	CGGTGCGCAC	TGACATGCAC	180
•	TTGTTCTCCA	CGATGGCTTT	CTCTACCTTC	TGAGATGCTC	CATTATCAGT	CCTGCCTTTG	240
•	TTCCGGAGAG	TTGAGATGGT	ATCACTTCTC	ATCCATCCTT	AGAAATACCC	CTCTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:182:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GAATTCGGCC TTCATGGCCT	AGGGGGCTGG	TAGTGAAATA	TTTGGTACTG	AAAGTGTGAA	60
GACCTCTGCT GGGGACTGAA	CAGAGGGAGT	GTCTTCTGCT	GGTGGTGTGA	AATCTATCTC	120
ATCATCAAAA TTATCTTCAA					180
ACAGTTTGCA ATTAACACTA					240
TCAGGAAACT TCTGCAGCAG					272

- (2) INFORMATION FOR SEQ ID NO:183:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GAATTCGGCC	TTCATGGCCT	ACTACTTATC	ATCCCTGCTC	ACACACCCTT	GTCCAAGGCT	60
TTATGCATCG	GATTTATTTT	TCCAAATCAA	GAGGACAGTG	ATAGATGCAT	TTTCCCCAGG	120
CTCTCTCACA	AACCTCCCTA	AATGTATACT	GTTGTCAGAA	TTGCTGAGAT	CTCCCCCCAC	180
CIGICICAGA	AAGGICGCIA	WIGHT	CCACTCAC	TTOUTUTOTO	TCTCAGGCAG	240
TTTTGGTTTT	TGCAGCAGTA	AAAACICIII	CCACIGIGAC	HAITHCIC	rerendents	250
CAGACTCGAG						250

- (2) INFORMATION FOR SEQ ID NO:184:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

CAATTCGGCC	TTCATGGCCT	AGATCTTCTC	CCCATTCAGC	AAAACTTTCC	CATTCCGGTT	60
AATGGTTTTG	ACAAGCAGGG	CACCACGGGG	CATAAAATTG	TATCATCCAG	CCTCCTTCCA	120
AAIGGIIIIG	CCACTTCTTC	TCTCTCATCA	TCCCTACCTT	GCTCTGCCGC	CTGTGGGTCC	180
					CTCCTGGAGG	240
						300
GTGCCATGTC						360
TAAAAACTGT	GACTATCAGT	GTTTTAAAAA	TTGCCCGGTA	ACTCTAGACT	TCAAAAGTGG	• • •
CATAACTAAT	GATAAACCAA	TAATAAACCC	TGCCTCGAG			399

- (2) INFORMATION FOR SEQ ID NO:185:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 185 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEO ID NO:185:

GAATTCGGCC AAAGAGGCCT AAAAATTAAT ATTACCTTAT GACTGCCTTT ATCATGACTC 60
TCTTAGTGGG GATTTCTGTC CTCCACATGC CCTGGGGGAT GTGCAGCCCC CGTGCACTCC 120
CCGCCTTGGC CGGCCCTTC CCCCATGCCC AGGTAGACTC TGAGCTCTTA GCCCAGCAAC 180
TCGAG 185

- (2) INFORMATION FOR SEQ ID NO:186:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 base pairs(B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAATTCGGCC AAGAGGCCT AGGGAACTAA TCTTAAACAC TGAACCTCTT TTCAGCAAAT 60
TGGCTTTCTA GTTTCTCAGC TCTCTCTTTA CACCTCTAAA TCTCTTTCCT GGCAAGATCA 120
TTTATTTGCC TTGGTTTATG GTGATACTCT TCATTGTTAT ACTGGTGGGT GATTGTTTTA 180
ATTCATAGCT GTTTTTCT ACTTCAGGAA GATGACACTG CTGGCTCTGC TGGCTCTGAT 240
GTTTACCTTG TGGCTAATGC CTGTGTTTGC CTGTGTTCAC ATTTATTCCA CGATTCATTT 300
GTTAACATTT ACTAAGCTCG AG 322

- (2) INFORMATION FOR SEQ ID NO:187:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

	AAAGAGGCCT					60
TTGAGATGAA	GAAAGTTCTC	CTCCTGATCA	CAGCCATCTT	GGCAGTGGCT	GTTGGTTTCC	120
CAGTCTCTCA	AGACCAGGAA	CGAGAAAAAA	GAAGTATCAG	TGACAGCGAT	GAATTAGCTT	180
	TGTGTTCCCT					240
	ATGGTTTAGA					300
CTCCCCACCT						
crecenter	COAC					314

- (2) INFORMATION FOR SEQ ID NO:188:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GAATTCGGCC	AAAGAGGCCT	ATTATGCTGG	TGCTGTCTAC	TAATTTCAAG	AAAAACTACA	60
AGTCTGGCTA	GACTCTGCTA	CCGCCTAGCA	CTGAGGTGTG	GTCCTTTATC	TGTTATTACA	120
	TAATGAAATT					180
GAATAAAGTA	TTTGTTTGTT	GTCTGAAAAG	AGATCTTTGA	AATGTTAAGT	TGCCACAGAC	240
CCAGACCAAG	GAGCCTGCTG	AGAGTTTTAA	AGGCTCTTAT	TGGATGACAG	TAGATTCTTT	300
CCTTGAAATG	TCTATAATGA	ATATTCAAGA	ATGCTCATTC	TGCATGAAAT	TTGCAATTTT	360
AATTATCAGT	GAAAGAAAAG	ATTACACAGT	GCTAAATGAT	TGCCATGGAA	AAGTTATGGC	420
TACCTCTTGG	AGTAGAGAAA	ATCTCAAAGG	CCGCTACTCG	AG		462

- (2) INFORMATION FOR SEQ ID NO:189:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GAATTCGGCC	AAAGAGGCCT	AGTGGGCAAC	TTGGAGAAGA	GTGAAAAACA	CTAAAGAATC	60
		AGTCCCATGA				120
AATTACCTTT	CGGCGGGACA	CCGTCTCAGG	GCAGCTTTTT	CAAGGCTTCG	CTTGACATGA	180
TTTCCTTCCC	TTCATCAGTC	ACTTTGGATC	CAGCTGAATA	TCTCTCTCGG	GTGAGAGCGG	240
		GAAGAAGAGT				300
CTGGCTTCCT	GGTCTCGAG					319

- (2) INFORMATION FOR SEQ ID NO:190:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TAATCCAAAA TACAAGATAC CACTTAACGG	TTCTGTNACC GGAAAGGATC ACTCTTAGTG TTACAGAACA	AGTGAAAAGA TATCTGTCAG TCTTGATGAA ATTTTTGAAC CTTTCACTGA TTGCCATGAT	CTATTCCATA AGTGTTCTGC CCATAATTAT TATTTTCCTT	TCAATAAAGG CATTCTTATT ATTTGTCTGA AGTGAATCTT	ACACAGCTGG AAAGTCAACA TAATAATTGG AACAACAATT	60 120 180 240 300 360
CTACCAGTAA G	TTTCTAATAT	TTGCCATGAT	TAGACTTTCA	AAATTAGTCC	ACGCACTCGA	361

- (2) INFORMATION FOR SEQ ID NO:191:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAATTCGGCC	AAAGAGGCCT	AAGAAACATG	GCGGCCGCGA	CGTTGACTTC	GAAATTGTAC	60
TCCCTGCTGT	TCCGCAGGAC	CTCCACCTTC	GCCCTCACCA	TCATCGTGGG	CGTCATGTTC	120
TTCGAGCGCG	CCTTCGATCA	AGGCGCGGAC	GCTATCTACG	ACCACATCAA	CGAGGGGAAG	180
CTGTGGAAAC	ACATCAAGCA	CAAGTATGAG	AACAAGTAGT	TCCTTGGAGG	CCCCCATCCA	240
GGCCAGAAGG	ACCAGGTCCA	CCCAGCAGCT	GTTTGCCCAG	AGCTGGAGCC	TCAGCTTGAA	300
GATGATGCTC	AAGGTACTCT	TCATGGACCA	CCATTCGCTG	TTGGCAAGAA	ACGGCTTTAC	360
TTACAAAACA	GTCTCGAG					378

- (2) INFORMATION FOR SEQ ID NO:192:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 175 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAATTCGGCC	AAAGAGGCCT	ACTCTGAATT	AATGCAAATT	CCCGTTGTAC	TGTATTTAAT	60
TATGCACAAA	ATGGTGCCCT	TGACTCAGAT	TTCAGTGAAG	AACTTCATTT	TTTTACTTTT	120
AAGTCTCCAA	GTAGGAAATT	CAATTAGCGT	TATGAAAGAA	ACACTAAAAC	TCGAG	175

- (2) INFORMATION FOR SEQ ID NO:193:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 700 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GAATTCGGCC	AAAGAGGCCT	AGGCAGCAAT	GTTATCTGTC	CTTCATTCTT	GCATGTTTTT	60
GGAAATTGCT	TTTGCTTTTA	CTTTTGGTCG	TCATGGCAAT	CACGTGCCTT	CTCTGGTTCA	120
TTTTGCACAG	ACCTGCCTAG	AGCTGGAACG	TTACCTCCAG	AGCGAGCCCT	GCTATGTTTC	180
AGCCTCAGAA	ATCAAATTTG	ACAGCCAGGA	AGATCTGTGG	ACCAAAATCA	TTCTGGCTCG	240
GGAGAAAAAG	GAGGAATCCG	AACTGAAGAT	ATCTTCCAGT	CCTCCAGAGG	ACACTCTCAT	300
CAGCCCGAGC	TTTTGTTACA	ACTTAGAGAC	CAACAGCCTG	AACTCAGATG	TCAGCAGCGA	360
ATCCTCTGAC	AGCTCCGAGG	AACTTTCTCC	CACGGCCAAG	TTTACCTCCG	ACCCCATTGG	420
CGAAGTTTTG	GTCAGCTCGG	GAAAATTGAG	CTCCTCTGTC	ACCTCCACGC	CTCCATCTTC	480
TCCGGAACTG	AGCAGGGAAC	CTTCTCAACT	GTGGGGTTGC	GTGCCCGGGG	AGCTGCCCTC	540
GCCAGGGAAG	GTGCGCAGCG	GGACTTCGGG	GAAGCCAGGT	GACAAGGGAA	ATGGCGATGC	600
CTCCCCGAC	GGCAGGAGGA	GGGTGCACCG	GTGCCACTTT	AACGGCTGCA	GGAAAGTTTA	660
CACCAAAAGC	TCCCACTTGA	AAGCACACCA	ACGGCTCGAG			700

- (2) INFORMATION FOR SEQ ID NO:194:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAATTCGGCC	AAAGAGGCCT	AGAAAAATAC	TTGGGCAGAA	AGAAAATATC	ATCAAATAAC	60
ACCTATTTCT	TTTCAGCTAT	AGAGATGGCT	GGATATCAAA	AGCACCACGG	GAGCTTTGCA	120
ATTTGCTGCC	TCTTTTCAGC	CCTCAGCTTG	ACTCTCAGTT	TTCAAGAGGG	AGAAAATGAA	180
TGTTTCCCAG	CATTCTCTGT	CCTTTGCTCC	AAAGAAGAGA	GCAGGTGTTG	GCTTCCAAAC	240
CTTCCGTATT	TTCTTATTGC	TGTTAGGGGG	ATCAACTGCA	TGTTTCCTGA	GGGAAAAGGG	300
TGGCTCACTG	ACCTACTTGA	AGGCATTCTC	TCAGTGGAAG	CTGGGCAAGA	GAATCCAGGG	360
ATTTCTTTTG	CAGGTTTCTG	CGCAGTGCCC	CTGCCATCAA	GCTGCCTAAA	ATGTGAATAT	420
TGCTTCCCTG	CGTTTCAGAG	GTGGCCGCTC	GAG			453

- (2) INFORMATION FOR SEQ ID NO:195:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

GAATTCGGCC	AAAGAGGCCT	ACAAAATGTG	AATGGAACAA	ACCTGCACGT	GTACCCTTGG	60
ATGTGTGGAT	GTTCTTTGTT	TTTATTTGTT	AAACCTGATG	TCTTGTCTGT	ATGACACATT	120
TATTGGAAAC	GTTTTTTCCC	TATTCTGTGT	CTTGTATTTT	ATTTTCTCGT	GTTCTCCAAA	180
GAGCAGATAT	TTTAAATTTT	TATATAAATC	CAGTTTGTCA	ACATTTTTAA	AGGGTTCATG	240
CTTTTTGTAT	CCTATTTCAG	AAAACTTTGG	CTACTTCAAG	GTCACAAAGA	TTTTGGATTT	300
GTTTTAATCT	ACAAGTTTTA	TAGCTTTGAC	TTTTATATAT	AAGTCTGATT	CATTTGGAGT	360
TAATTTTTGT	GTACAGTGTC	AATTAAGGGT	CTAGGTTCAT	TTATTTTCTT	ATGAATATCC	420
AATGGTTCCT	CGAG					434

- (2) INFORMATION FOR SEQ ID NO:196:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GAATTCGGCC	AAAGAGGCCT	ACAAACACAG	AACATTTCCA	TCGTTGCAGA	GAGTACTATT	60
AGAGAGCAGT	ATTCCAGAGC	CTGTGATCTT	AATCACTACA	CCTAAAGCCT	CCCAGTTGAC	120
AAAGTTACCA	CCTTTTTTTG	GTGTGTGTGC	ACGTGCGTGT	GTGTGTGTGT	AAGTATATAT	180
AATTTAAATC	ATTCCATTAA	ATTTACCTCT	GAAATTCAAA	AGACTGAAAC	AGATCTTCTT	240
TTTATCAAAT	AAGTTGATTG	CAGAGATTAT	ATTGGTGTTT	ACATTTCAGG	CAACCTGCTC	300
ATGAAATTAT	CCATTGCTCT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:197:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GAATTCGGCC	AAAGAGGCCT	ACTCCTCCGC	CTGCAACCAT	TGTTTCCTAC	CACTGGATTA	60
TTCTGAAGCA	AATTTTAGAC	ATCATATATA	TTTATCTCTG	AAAGAGGACT	CTTAAAAACA	120
TGCACTTATA	CCTCTATTAC	ACTGACAAAA	TTGGTAACAA	TTCCTTTATA	TTATCAAATT	180
TCCTTATTGA	GTTCCTGATG	TTCAAATTTC	TGATTCTCCA	GATGCTCCAA	ACTTCCAGAA	240
ACACAGATTC	CCAGATGGAA	TCCTGGGGAA	GGCTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:198:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 448 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GAATTCGGCC	AAAGAGGCCT	ATTTTCTAAT	AAAAACTATT	TTATGGTAGG	TTTTGTGGAT	60
TATTGAATAC	AATCTGGCAT	TCTGTTTAAT	ATGTATGTTT	TCCTGAATGA	GGGGGTACAT	120
TGTAATTTTA	ATTATTAAAC	TCACAATGTT	TTTGGTTTTA	AAAATAAAA	TTTTAGGAGC	180
AAGCAGTGTT	CCTGCCTTCT	TTTCTGAAGA	TGATTCTCAA	TCGAATGACT	CAAGTGATTC	240
TGATAGCAGT	AGTAGTCAGA	GTGACGACAT	AGAACAGGAG	ACCTTTATGC	TTGATGAGCC	300
ATTAGAAAGA	ACCACAAATA	GCTCCCATGC	CAATGGTGCT	GCCCAAGCTC	CCCGTTCAAT	360
GCAGTGGGCT	GTCCGCAACA	CCCAGCATCA	GCGAGCAGCC	AGTACAGCCC	CTTCCAGTAC	420
ATCTACACCA	GCAGCACTCC	ACCTCGAG				448

- (2) INFORMATION FOR SEQ ID NO:199:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GAATTCGGCC	AAAGAGGCCT	AACTTTTGTA	ATTTGAATTG	GGTCCCGCTT	AGTTCTTGAA	60
TTGTTATGAA	AATCCTATAT	CTGTTTGTAT	ATTTGCAAAC	CCTTTGTATT	ATAATTGTTG	120
ATATTTTCCC	TTTTTAAAAA	ATACCATTGA	AATCAGCATG	ACAAAAATAA	CACTGTGGGC	180
ACTCGAG						137

- (2) INFORMATION FOR SEQ ID NO:200:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double :
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

G	AATTCGGCC	AAAGAGGCCT	AGACCAGAAT	AAGCCTTTTA	AGGTAAACCT	CAAAATTATC	60
A	TTTTATGGT	AATACTGACC	ATTTTAGTCC	CCTAGGTTTG	ACATGGGAGA	TAGTGACTAC	120
Α	CTGGTGTCT	GACTTTTTTC	CTAGAGATTT	CTCCCTGAAA	AATACAAGGG	CTGTTGGTGA	180
G	AGCAGACTT	GAGGTGATGA	TAGTTGGCCT	CTGGTCTACA	AAGATTTCAT	AACTCCTTGG	240
Α	AAGCTTCTT	ATAATCATTC	TTAACTTCTT	GGTAGCTAGA	AATTTAGAGT	AGTTGAAATC	300
т	TTAGGAATG	AACTTCTGAG	GGCCAAAAAA	TGTGACTGAC	ACACTCGAG		340

- (2) INFORMATION FOR SEQ ID NO:201:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GAATTCGGCC	TTCATGGCCT	ACATCACCAA	TTCGGCTGGG	TAAGGGTCCC	CATGAAGGCG	60
CAGCCGGGTA	TAGAGGTGCA	GGGGAGAGCA	GCCTGGGGAG	TCCCTATCTG	GATAGGCTCC	120
AGCCTGGGTC	GGGGCGGTCC	TGGTGCCCGG	TGAAGCGTCA	AAAGAGGGAG	CCTGAGCGGG	180
GCAACGCAGA	AGGGTGGAGA	GGAGGGGGTG	GCGAGGGCGG	GCAGCGAGGC	CTGGAGCCGC	240
CAGGAGAGGG	GCGGGGGGCG	GCCCTTCTCC	AGGAATTTCC	GGGGATCGTG	TTACAGCGTT	300
GGCGGAGCCC	GAGCGGAGTG	GGACTCGAG				329

- (2) INFORMATION FOR SEQ ID NO:202:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GAATTCGGCC	TTCATGGCCT	AGAAAGGGGA	GGGAACGTGA	CAGGCAGGTG	TGGGATAGGG	60
ACTTCTCTTC	CGGTCAGAGC	AAGGGTCGTC	CGAAACCAAA	ACAACCCTCT	TCCCTTCATC	120
TCGCCCCGGA	TCCAAAGTCT	TGGGGCTAGG	CTGGGGCGGG	AGTGGCACGG	AGATGTAGGA	180
ACACTGCCTT	TCGTTACTTC	TCCTGCCATG	GCTGACCTTT	TTGTCTCTTG	TTTCATGGTT	240
TTACACGTAT	GAATGGCTTG	AGACTGAGGA	TTTAGGGAAG	AAGCGAAGGC	ATCATCTAGG	300
GCTGTGCTGT	GCCAAGTTGA	GCAGTTGTTT	AAACTGTTAG	AATTTTTGAC	TGGTGTAAAA	360
ACCCTCTATG	CTCGAG					376

- (2) INFORMATION FOR SEQ ID NO:203:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

GAATTCGGCC TTCAAGGCCT ACGTGAAACC CCATCGGCTT CATTGGCTCC TTGATTTAAA 6

CCACGCCCGG CTNTCTGCCC TCTTTGATGC TGCTGGGCCA GGTTGCCCAG CCATATCCCA 120
GCCCCGTCTG CAGGGAGCCG GAGGCNGCTG CTGCTGCTAT TGTGTGGATG CCGCGCGTGT 180
CTTCTCTTCT TTCCAGAGAT GGCTAACAGG GGCCCGAGCT ATGGCTTAAG CCGAGAGGTG 240
CAGGAGAAGA TCGAGCAGAA GATCTCGAG 269

- (2) INFORMATION FOR SEQ ID NO:204:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 197 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GAATTCGGCC TTCATGGCCT AGATGTGTG AACCTTATTC TTGTACATTC ATTCAATCAA
GGCAAACTTT TATAATTTTT CTTTTGTTTC CAATGACCTT GAAATGTTAT AGCATGGTAA
TATTCTATGC AACTATAGTT ATACTTTTTG GTTTGACACT GTATTTTTTC ACATTGATTT
ACTGGTTGAG GCTCGAG
197

- (2) INFORMATION FOR SEQ ID NO:205:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

			•		
	rggcct agcaagacct				60
TATGATCATG ATGCT	rgtagg aaaaaaagg	TATATGTCCA	AGTGTATGTA	CTTGTAAATG	120
TGCCTAAAGA AACCT	rggaag gatacacago	TCTTCCCTGG	GGTACAAGAC	GGAGAACTGG	180
	CTCTAC TCTTCCTTT				240
TGTATACATG GATTA	ACTGTT ACTTAGCAGO	GGCGACCGGT	TGGCCAAAGC	CTTGGTGTGC	300
CCTTGGCACA ATTC	IGCCAA GACCCTTAC	CTCTCCTCTC	CTCANGGCTC	CCTTAACCCC	360
TCTCCCCACA TCTG	GAAAAC CCTGGATAC	TTTTCT			396

- (2) INFORMATION FOR SEQ ID NO:206:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GAATTCGGCC TTCATGGCCT					60
ACCCAGCCCT GCCCCTCACC					120
TCTCAGCCTC TGATCAGTTT	CACAAAGTTT	GTTCCCTAAG	GAAATCAAAT	CCCATTGTCA	180
CCTAACTCTG AAGATCTAAA	TAGCCCTTGG	ATCAGTACGG	GAACCCCAAA	TCCCACAGGG	240
CCAGATGTGG AGTCTGTGTC	TGCCCCCGTC	TTCTCTCCAT	CCTCAAAGCC	CCCACTTCTC	300

TCCAGGCTGC TTCTCGAG

318

- (2) INFORMATION FOR SEQ ID NO:207:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GAATTCTAGA TCCTGCCC	TC GGAACAATGG	GACTCGGCGC	GCGAGGTGCT	TGGGCCGCGC	60
TGCTCCTGGG GACGCTGC					120
TGGCGGCATC TGCAAACA					180
CAGAGACTCT CCAACATG					240
AACCACCAAC TTCAGTTG					296

- (2) INFORMATION FOR SEQ ID NO:208:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GAATTCGGCC	TTCATGGCCT	AGTCTCTTGA	AAAGCCGCAT	TTCCAGGCGC	TTGGCCAGTG	60
GCCTGGGAAG	TAGCCTGTGC	TTGTATTGAG	ACAGTCCCCC	AGCAGCAAAC	CATGTTCCAG	120
					TAAAACAAGC	180
					TAAAAAGAGG	240
					CTCCGTCCCC	300
		1101000100	10.0100			312
TCCTGGCTCG	AG					

- (2) INFORMATION FOR SEQ ID NO:209:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GAATTCGGCC TTCATGG	CT AGGCAGCGTT	TCACCGCTGT	GGAGGACCAG	TATTACTGCG	60
TGGATTGCTA CAAGAAC					120
GGAAAAGGAC TGTGTCA					180
GCACGGGAA ACGCTTG					240
CGGGTGGAGA GAGGACT					300
TAGCAGCTCC TCGAG					315

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 518 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GAATTCGGCC	AAAGAGGCCT	AGGAAGATGG	CGAAGGTCTC	AGAGCTTTAC	GATGTCACTT	60
GGGAAGAAAT	GAGAGATAAA	ATGAGAAAAT	GGAGAGAAGA	AAACTCAAGA	AATAGTGAGC	120
AAATTGTGGA	AGTTGGAGAA	GAATTAATTA	ATGAATATGC	TTCTAAGCTG	GGAGATGATA	180
TTTGGATCAT	ATATGAACAG	GTGATGATTG	CAGCACTAGA	CTATGGTCGG	GATGACTTGG	240
		CTGAGAAGAC				300
		GCCATGGAAA				360
GGATTTTACA	AGAAGATCCA	ACTAACACTG	CTGCAAGAAA	GCGTAAGATT	GCCATTCGAA	420
AAGCCCAGGG	GAAAAATGTG	GAGGCCATTC	GGGAGCTGAA	TGAGTATCTG	GAACAATTTG	480
TTGGAGACCA	AGAAGCCTGG	CATGAACTTG	CACTCGAG			518

- (2) INFORMATION FOR SEQ ID NO:211:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

		AATTGAATTT				60
ATAAATGGGA	ATTTTAAATA	CCTGCATGTT	CTGTTTTTCT	CTTTTTTCTT	TTTTCAGCCA	120
		GCAAACATCC				180
		AGACTGTTGC				240
		AAGCTTCTAA				300
TCCAATGAGC	CCTGTAGGCA	GAACTTCACG	AGCTTCAAAA	AAAGTTCATA	ATTTTGGAAA	360
GAGGTCAAAT	TCAATTAAAA	GGAATCCTAA	TGCACCGGGC	GATCTCGAG		409

- (2) INFORMATION FOR SEQ ID NO:212:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

		AGTACAGTCC				60
GAGGGACTAG	ACTCAGTGTT	GGGTTTGGAG	GATCCACTGG	TGAGGAGCAT	TCAGTCTAGC	120
		TTATTACACA				180
AGGTCTAGGA	ACTGTTCAGA	GGAGCACAAA	TGAATGAGAG	AGAGAGGGAG	AGAGGGAGAT	240
TGAGTGAGTT	AGAGAGTTGT	TGGTGCTCCA	CAAGGAGCAG	TAAAGTATTT	AAAAAATAAA	300
AAATAATAAG	GCTGACTCTG	TGTCCTGCCT	AGGGGTTGGC	CATGCTCCAC	AAAAAGCAGT	360
AAAGTGTTTT	TTGTTTTGTT	TCGTTTTTTT	TTTAAAGACA	GACGTCTCGA	G	411

- (2) INFORMATION FOR SEQ ID NO:213:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GAATTCNGCC	AAAGAGGCCT	AGTTTNATCT	TCTTACCTAT	TTACTGAATG	CNACATTACT	60
GCACACCAAG	ACAAAAGAGC	TCTCCAGGAA	AACATTGGAT	ATATTGAGAG	CATTAAAAGA	120
TACTGCAAAA	GCTCTAATAA	ATTCAGTCTG	CTTATTTTCC	AAATTTCATA	AACTACATAC	180
TTAGGAAACT	GTGCTTTCAG	TGAGCTAAAC	TTCTTTTTTT	AAGTAACTAT	CATAGTTTTA	240
AGAAAAACAT	TTTAAGAAGA	CAAAAAGTAT	TTATTAAGCC	CATCTAAAAG	GCTAATGCAA	300
ATTCCCAAAA	AAGGAGCACA	TAGAGATAGG	CATCTCGAG			339

- (2) INFORMATION FOR SEQ ID NO:214:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

GAATTCGGCC	AAAGAGGCCT	ATTGAATTCT	AGACCTGCCT	CGAGACACTA	GCCCTTTTTT	60
CTGTTGGTTT	AGCACAAATA	CTTCCCTCCT	CCGGCACCTC	CAAACCTACC	CCACAGTCAG	120
TGTACTTGTT	TTATATATAT	TTAATCTTAT	TCAATGGAAA	CCATGCTTTT	GTCGTTTTAT	180
ACTTTGCTAG	GTAGACTTCT	CGAG				204

- (2) INFORMATION FOR SEQ ID NO:215:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

CTCGAGAGGC	GCATCTTCAC	TGGCATATGA	CAGGCTGTCA	CTGCAGCTAA	TGTTGGTACA	60
GTTTTTCCAA	AGACCTACTG	ATGCATCTAC	CGTATTGGAA	ACCAACCAGA	CATTGGCAAT	120
GGTGCTAACA	AATAGCATAA	TAACAGTAGC	GATGTGGACC	ACAAAGATAC	CAGCCAGCAA	180
TACCAACATG	TTGGCTCTTT	TTTTTTTGGT	AACTTGTGAG	CAAAGAGAGT	TCTGAAGGGT	240
CCCAGCGACA	GAGGCACTCG	AGGCAGGTCT	AGAATTCAAT	TAGGCCTCTT	TGGCCGAATT	300
С						301

- (2) INFORMATION FOR SEQ ID NO:216:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GAATTCGGCC	AAAGAGGCCT	AAAATATTTG	AGTCTAAACT	TATAAATTTT	GCATTCTCCC	60
TAACGAAAAA	ATTTCTATTA	CTGTGGTGGA	TTTCTTTAAA	TTTTGAATAT	AGTTACTGAA	120
ATATTAATTC	TTTCAATTAA	ATTTATATTT	ACTCACTGGT	TCCTTCCCCT	TCTTTAAGGA	180
GACAGAAAAC	ATTAACACTT	TTTAACCTCT	CATTTGTTTA	AAAATTTATT	GACCTCTCCT	240
CTGAGACAGT	TTGTATTCCT	AGATCTCTTT	AAACATAAAT	ATGCTTATTT	TCAAGTTTTT	300
GTCACAGTAT	TCACTCGAG					319

- (2) INFORMATION FOR SEQ ID NO:217:
 - (i) SEQUENCE JHARACTERISTICS:
 - (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

				GTAGACATTT		60
					TTGAAAAAGA	120
					AGATTAATGA	180
GCTTCAAGCA	GAGCTACAAG	CTTTTAAGTC	TCAGTTTGGT	GCCTTGCCAG	CTGATTGTAA	240
TATTCCTTTG	CCTCCCTCTA	AAGAAGGTGG	AACTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:218:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GAATTCGGCC	AAAGAGGCCT	ACCTGGCTCA	TTTATAACCT	CCTCGATCCT	ATTACTGATT	60
			AGTGCAACCT			120
			AAAGAAGAAA			180
			CTCTCTGTTT			240
TAAACCTGCT	TCTACATCAG	TTACTGTGGT	TATGGGCGTC	TTGTTGGCTG	AGCTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:219:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GAATTCGGCC	AAAGAGGCCT	ACTTAGCAGA	ATATATTCTT	TAATAGCTCC	CATAAAGCAA	60
ACAAACCCAA	AATATATTCT	CCTGACCCTA	CATTCACTTC	CAACTATCAC	CCTACATCTA	120
CATTCTCCTT	TTCATACCAA	ACTTTTTCCA	AGCAGTTGTC	TATATTTATG	TCTCCACTTC	180
TTTACCTCCT	ATTCTTGCTT	CAGTATGCTT	CAGTTGAGCT	TCGTCCCCCT	GTAGTCCACC	240
ACCAACTCGA	G					251

- (2) INFORMATION FOR SEQ ID NO:220:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GAATTCGGCC	AAAGAGGCCT	AGATTGATTC	TGTGTTGTGG	TATTGGCCCT	TACATACAAC	60
TGGAGGAAGT	GTGAATTTCA	TCATGTTGAT	AAATTGGACT	GTCATGATTC	ATTAATATT	120
CTTCAATGCC	ATGTTTGTCG	GTCCGGGCTT	TGTCCCTCTG	GGGTGGAAAC	CGATGTGTGA	180
TGAAGATGGA	CCATCACTGT	CCTTGGATCA	ACAACTGTTG	TGGTTACCAA	AATCATGCTT	240
CGTTCACACT	GTTTCTCCTT	TTAGCACCAC	TGGGTTGTAT	CCATGCTGCT	TTCATTTTTG	300
TGATGACTAT	GTACACACAG	CTTTATCATC	GGCTCTCCTT	TGGGTGGAAC	ACAGTGAAGA	360
TCGACATGAG	TGCAGCACCC	TCGAG				385

- (2) INFORMATION FOR SEQ ID NO:221:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GAATTCGGCC	AAAGAGGCNT	ACCCNGATTA	TAGTTTTTGT	ATTGTTTTTA	CAATTTTTGT	60
GAATTAGGAT	CCAAATAAGG	TCTGTAAATA	TTACATTGGG	TTTAGGTAAT	CGATACTTTT	120
TTTCTTTTAA	TCTATAAGTT	TTCCTCTATC	TTTTTTATTGT	GGTTATTCCC	ATACAATTGG	180
TTTGTTGAAG	AAGCCAGGTC	TTTGCCCTAT	AATACTTCTC	AGAATCTAGA	TTGTGTTGAT	240
GAGATCCCAG	TGGTTTCATG	TAATATGTTC	TTTTGTCCCT	TGTATTTTCT	GTAAATTTTG	300
TTTATTTTAT	TTTTTTTTTT	TCTATTATTT	GAGATGGAGT	CTTGCACTGT	CACCCAGGCT	360
AGAGTACAGT	GGCATGATCT	CAACTCACCG	CAACCTCGAG			400

- (2) INFORMATION FOR SEQ ID NO:222:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GAATTCGGCC	AAAGAGGCCT	AAGAGCCTAT	AAGGTTTACA	TATTTCACTG	GAGAGAGAAA	60
TAGGGACATA	CAATAAATGA	TTTTATAATA	AATTTCCATG	AAAAGTGAAT	CTGAAAACCC	120
CACCGGAAGG	CAGAGTAGTG	CAGCCAAAGG	AGCATGAATT	GTGGAATCAT	ACAGCTCTAG	180
GTTCAGATCC	TACCTTTACC	ACTTGATAGC	TAGGCAGACT	TCAACAAGTT	AGTCTAATTT	240
GAGCTTCAGT	TCTCTCATCT	GTGAAAAAGA	GAAAATACAG	CCACTTTATA	ACATTATTTT	300
AGATGCCATA	AGGTAGGTAA	AGTGCCAGAC	ACATAGATTC	AAAAATCTCA	DDATAAAATA	360
AAGGCTGGAA	TTTCCAAAAT	TTTTTCTTGC	TTTCACAATC	TGGGTTCTAA	ATTTATTATT	420
ACTCTACCCA	TCACTTCCTC	CTTCTCCCTC	CACAACCTCA	CTATAAGCCC	AACATCTCGA	480
G						481

- (2) INFORMATION FOR SEQ ID NO:223:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GAATTCGGCC	AAAGAGGCCT	AGTGTCATGT	AGAGGTCTCA	GCATTTCTCT	TAGTATTTGA	60
CTGTATTAGT	TTTACATATT	TCTTCTTTTG	TTTAGAGTAT	AACCGCTTCT	TACATTTCCT	120
TCAGTCGTTT	TCTAAAGAAG	AAATTAATCT	TTTTAGAAAT	CCTGGCAGTT	ACCCCGCAAT	180
TGATGTTTTG	GTGGAAAATT	AGAGCACACC	AGTTTGTCAT	AACTTTAAGA	AACATTTTCA	240
CTTTATTGAT	ATTCTGAGGA	TTTTAGTGAT	TTGGGTAATT	TGGGTCTAAT	AAAGAGTAAA	300
TTGTTGAATA	CTCATTTGTT	TTGAGTCATC	TATATTTTA	AACCCTTTCT	TTAGTTGTTT	360
TTTCATCCCT	AATACAAATG	CAACTTTCCC	ACTTGCTCGA	G		401

- (2) INFORMATION FOR SEQ ID NO:224:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GAATTCGGCC	AAAGAGGCCT	AAACTGATGT	CTTCCATTTG	CTGGATAGGA	CATGCTGACT	60
GATGACCTCA	CAGACTGTTC	TTATGCCCTC	ACTACTCACC	TCACCACCTA	CAGTCATAGG	120
CTGACTAGGA	GTTGGTTGTG	TACATTCCTA	AACCTTTTTG	CCCTCTTTAT	TTGTCTTTCT	180
AAGTGTGTAT	TCAGTACTAT	GTAAATTGAT	AAAACATGAG	TGTGAAAATA	TTTTTTTTTG	240
CTATAAAAAT	GTAAATTGAA	TTCTTTGGGG	AAGAGCTGAT	AAAATATGTC	ACTTAAAGAT	300
CTTGTTAAAT	TAGATGAGGG	AGATATAGAT	GACAGAAACT	CTTTCAACAA	ATATCTAAAA	360
AGATGTGCCA	CTCCAATTAT	TTTGTGAGTG	TCTTCAAGTT	TITGTCCCAC	TTTAAAGAAA	420
ACCAAACTGG	CCATCATAGC	CAATGAATTA	TGCAGGAGTC	TCGAG		465

- (2) INFORMATION FOR SEQ ID NO:225:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GAATTCGGCC	AAAGAGGCCT	ACACATTATA	TTAGATTTCA	TAGAAACTGT	TGGAAATATC	60
TAGCACATGT	GCTTTATCCC	ACAATAATTA	CATAGAAAAT	TAAAAAGAAT	TAATTCTAAT	120
GTAACCATCT	TTTTACTTGA	CTTTTTTTTT	TTTTGCTCTG	CTCACAGGTC	TAATTGTTGT	180
TATTCTCACT	TTATTTTTCT	ATAAGGTAGG	AATAATATCC	ACTTCATTAG	CTCATCATGA	240
GGGATAAGTA	GGATTGGAAA	AGATACTTTC	AAAGGGCACC	TAACTGTGAA	GAAGATGCCT	300
TCATTTGCAT	TTCTTTCTTG	GCACATTTCT	TGTTATCCAG	TCATTCATTA	GGACTCCATG	360
TTTATTGAAC	ACCTACTCTG	TGCCAGGCAC	TTTTCTCTGT	TCTGGAAATA	TCACCATGTA	420
AAAACAAATA	GCTGAAGAAT	GCCCTGCCCT	CATAGAGCTT	ACAGACATAG	AGCTCGAG	478

- (2) INFORMATION FOR SEQ ID NO:226:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GAATTCGGCC	AAAGAGGCCT	AGCGTTTCTG	ACTTTATTAC	TGGTAATTTA	TTGCACAGGT	60
TTTTCTGCAT	CAAAAAAGTA	TCTGCTAAAA	TAGAGAAAGT	TGTGTCTGAA	TTCACATTTC	120
CCCCCAACTT	CTAAAAATAT	TTCCCCTAAA	AAAGAATCCA	CTCATCTAAT	TTTAAAGAAA	180
ATATACTTCT	TACACAAGAC	AATCCAAACT	GATGCAAAAT	ATTTATTCCA	AGTTAGTTAT	240
TTTATGCAGT	AGTTTCCCCC	TCGAG				265

- (2) INFORMATION FOR SEQ ID NO:227:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GAATTCGGCC	AAAGAGAGAA	ATTTTAATCT	TGAAAGACTT	TTCAGGGTAT	CTCATTTTTT	60
AGGTGGGGGT	GGCAGGTGTA	TTTCTTTTTT	AACAAATAAA	AGGCATTTAA	GTAAAACTAA	120
AATGAAAAA	GTAGGCCTTC	TGACATTGTG	TACTTGGTGG	TTCTGTCCCT	CTGCCTGTAA	180
CAAATCTCAT	TTTTGTTACC	AAGAACTGTA	TGAAAGAAGT	AAATCCACCC	CTCTCGAG	238

- (2) INFORMATION FOR SEQ ID NO:228:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

GAATTCGGCC	AAAGAGGCCT	ATGCCTGTGT	TGGGTTGACA	GTGAGGGTAA	TAATGACTTG	60
TTGGTTGATT	GTAGATATTG	GGCTGTTAAT	TGGTGTTGTA	GAATATTTGA	GCACAGGTGG	120
AGTAGAAACA	AATCACAAAG	ACTTTAAGGA	GTTGAGGTAT	AATGAAAGTC	TCACAAACTT	180
CAGCTGTCAT	GGGAAGAATG	GAACCACCAA	TGGAAGGATC	ACTCATGGTT	TCAAGTTACA	240
GAGTGCCTAT	GAGAGTGGCC	TGATGCCTTA	CACGAATTAC	ACATTTGATT	TCAAGGGTAT	300
AATAGACTAC	ATTTTCTATT	CTAAACCTCA	GCTGAACACC	TTAGGCATCC	TGGGCCCTCT	360
GGACCACCAC	TGGCTGGTTG	AGAATAACAT	CAGTGGCTGC	CCGCACCCCC	TCATCCCCTC	420
TGACCACTTC	TCACTTTTTG	CACAACTGGA	GCTCTTACTG	CCTTTCCTGC	CCCAAGTCAA	480
CGGCATTCTC	GAG					493

- (2) INFORMATION FOR SEQ ID NO:229:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 572 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GAATTCGGCC	AAAGAGGCCT	AAGAAATCAA	AATTAAAGCA	ATCAAATAAT	ACTCACATTT	60
ATATAAGAAA	TACTTCAATT	TACTTTCCAA	TGAGTAAAGT	TTTATATTTA	ATGTTTTAAT	120
ATTTCATATT	TTAGTTTCTT	GCAATTATTT	ACTTTTTCTA	AAACCTACTT	AAATTAGGTT	180
TAAAAGTCTA	CTATATATAA	TTTGAAATTT	TATTCAGTTT	GCCTACAGGT	GTGTTTTAAC	240
CACTGTGTAC	ATAGTATTTA	ACGGTCTGCT	TTTTTTTTT	TAATAATGGT	TCATGTNTGA	300
ACATCTGTAT	GTTCATACTT	TTCTTGACAA	AGTTCTAAAG	GTTACTGTGT	TGAAGCATAC	360
TGAACGATTA	CTGATAATTT	CTATTTTGAG	GAACAGGTAT	GTCAGTTCTT	TCTCTCTGTT	420
TGATAATTCT	CTCTTTTCCC	CTTAGGAATC	CAAAAATCCT	TGTGGAGTGT	CTTACTCCTG	480
ATTTTCGAGG	TGATCTCAAA	GCAATAGAAA	AAGTTGCTCT	GTCAGGATTA	GATGTGTATG	540
CACATAATGT	AGAAACAGTC	CCATTGCTCG	AG			572

- (2) INFORMATION FOR SEQ ID NO:230:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GAATTCGGCC	TTCATGGCCT	ATCGAGATAC	GCTTTCGCGC	ACCAGGTACG	CCTGGTGTTT	60
CTTTGTGGTT	TTTCGGATTC	TTTTTGGGGA	GTGCGGGGAG	TCACAGTTAG	AAGGCGGCCG	120
GGTGTTGCTG	GAGGAAAGTG	CTGAGGTCCA	GAGCGTAGTC	CGAGGGCTCC	GAAGTCAGAT	180
TAAAGGGCTC	GAG					193

- (2) INFORMATION FOR SEQ ID NO:231:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 608 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GAATTCGGCC	TTCATGGCCT	ACATAATGAT	GCTGCCTCAA	AACTCGTGGC	ATATTGATTT	60
TGGAAGATGC	TGCTGTCATC	AGAACCTTTT	CTCTGCTGTG	GTAACTTGCA	TCCTGCTCCT	120
GAATTCCTGC	TTTCTCATCA	GCAGTTTTAA	TGGAACAGAT	TTGGAGTTGA	GGCTGGTCAA	180
TGGAGACGGT	CCCTGCTCTG	GGACAGTGGA	GGTGAAATTC	CAGGGACAGT	GGGGGACTGT	240
GTGTGATGAT	GGGTGGAACA	CTACTGCCTC	AACTGTCGTG	TGCAAACAGC	TTGGATGTCC	300
ATTTTTCTTT	CGCCATGTTT	CGTTTTGGAC	AAGCCGTGAC	TAGACATGGA	AAAATTTGGC	360
TTGATGATGT	TTCCTGTTAT	GGAAATGAGT	CAGCTCTCTG	GGAATGTCAA	CACCGGGAAT	420
GGGGAAGCCA	TAACTGTTAT	CATGGAGAAG	ATGTTGGTGT	GAACTGTTAT	GGTGAAGCCA	480
ATCTGGGTTT	GAGGCTAGTG	GATGGAAACA	ACTCCTGTTC	AGGGAGAGTG	GAGGTGAAAT	540
TCCAAGAAAG	GTGGGGGACT	ATATGTGATG	ATGGGTGGAA	CTTGAATACT	GCTGCCGTTA	600
TACTCGAG						608

- (2) INFORMATION FOR SEQ ID NO:232:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 518 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

GAATTCGGCC	TTCATCGCCT	ACAGCGCTGC	CTTTCCTTAT	GAAGAAGACA	CAAACTTGGA	60
TTCTCACTTG	CATTTATCTT	CAGCTGCTCC	TATTTAATCC	TTTCGTCAAA	ACTGAAGGGA	120
TCTGCAGGAA	TCGTGTGACT	AATAATGTAA	AAGACGTCAC	TAAATTGGTG	GCAAATCTTC	180
CAAAAGACTA	CATGATAACC	CTCAAATATG	TCCCCGGGAT	GGATGTTTTG	CCAAGTCATT	240
GTTGGATAAG	CGAGATGGTA	GTACAATTGT	CAGACAGCTT	GACTGATCTT	CTGGACAAGT	300
TTTCAAATAT	TTCTGAAGGC	TTGAGTAATT	ATTCCATCAT	AGACAAACTT	GTGAATATAG	360
TGGATGACCT	TGTGGAGTGC	GTGAAAGAAA	ACTCATCTAA	GGATCTAAAA	AAATCATTCA	420
AGAGCCCAGA	ACCCAGGCTC	TTTACTCCTG	AAGAATTCTT	TAGAATTTTT	AATAGATCCA	480
TTGATGCCTT	CAAGGACTTT	GTAGTGGCAA	ATCTCGAG			518

- (2) INFORMATION FOR SEQ ID NO:233:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GAATTCGGCC	TTCATGGCCT	ACCTTGATAC	ATCAGCTGAC	CTCATTTCCG	GATACCTTTT	60
CCCCCCGAA	AAGTACAACA	TCTGGGCCGC	CCCAGCCCGA	AGACAGATCG	TCGCTCCCTG	120
GACAATCAGA	CGAATTCTCC	CCCCCCCCC	AAAAAAAAAG	CCATCCCCC	GCTCTGCCCC	180
GTCGCACATT	CGGCCCCCGC	GACTCGGCCA	GAGCGGCGCT	GGCAGAGGAG	TGTCCGGCAG	240
GAGGGCCAAC	GCCCGCTGTT	CGGTTTGCGA	CACGCAGCAG	GGAGGTGGGC	GGCAGCGTCG	300
CCGGCTTCCA	GACACCAATG	GGAATCCCAA	TGGGGAAGTC	GATGCTGGTG	CTTCTCACCT	360
TCTTGGCCTT	CGCCTCGTGC	TGCATTGCTG	CTTACCGCCC	CAGTGAGACC	CTGTGTCTCG	420
AG						422

- (2) INFORMATION FOR SEQ ID NO:234:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GAATTCGGCC TTCATGGCCT AAGAGATTAA GTGATTTACT CAAGGTCATA TTCCTTGGAA
GTAGCAAAAC TTCTGGACCA GATTTCTGAT TCCAAAGGCG GTACTGCTTG TACAACACTC 120
TGAGAAGTAA TTACTGTGGA GCAAAGCAAA AAGAAGTCTA AAAGCAGGTG ATAGGTGTAG 180
ATTTAGATAG TGTAAGGGTA GGCTAAAGTG TTGTAACAAA TGCACCCTCA AGTAGGTAAT 240
GGCTCAAACA CAATAGATGT TCACTTCCCA CATCTCAGAG CAAATTGGGT TCTCCTCATC 300
AGCTAAAGCT TTCCTACATG GGATGATTTG GGGAGCAAGA CACTCCATCT ATGGCTCCCT 360
TACCCTCCAA GGCCTTCTTA TTGTCTTTAT GTAACCAGTG GAAGAGCTCG AG 412

- (2) INFORMATION FOR SEQ ID NO:235:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GAATTCGCCT	TCATGGCCTA	GGCTTCTTCG	GAGCTGTGTA	NTCTTAATTT	GCTTTGCTGC	60
TGGCTGGCTG	ACAGCTGATG	GGGGACTCCT	CANGACGGAC	TCCCTTCCAG	ATGCACCCAT	120
CTCCATCCTT	CTCAACTCCC	CAACCTTTGT	CCTCCCCACT	CTTCGCTCGC	GCGGCGGTCT	180
GAGACCACCA	GGACCAGTTT	CAGGGGTTTC	CTTCTCCAGC	GAGACTTGGC	AGAACAGGCT	240
TTAAAAGCAA	AGGAGGCAGC	GGAAGACTGT	GAATTCCTTT	GGACAATTGA	TGATATTTAT	300
CATTGTGCCC	AGTTTCTACA	AATAAAAGAT	GGGTGGATTA	TTTTCTCGAT	GGAGGACAAA	360
ACCTTCAACT	GTAGAAGTTC	TAGAAAGTAT	AGATAAGGAA	ATTCAAGCAT	TGGAAGAATT	420
TAGGGAAAAA	AATCAGAGAT	TACAAAAATT	ATGGGTTGGA	AGATTAATTC	TGTATTCCTC	480
AGTTCTCTAT	CTGTTAACAT	GCTTAATTGT	ATATTTGTGG	TATCTTCCTG	ATGAATTTAC	540
AGCAAGACTT	GCCATGACAC	TCCCACATCT	CGAG			574

- (2) INFORMATION FOR SEQ ID NO:236:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

GAATTCGGCC	TTCATGGCCT	AGGCGCGGCC	CGGGTTCCCG	TTCCCCGCGG	AGCCATGCGG	60
TACAACGAGA	AGGAGCTGCA	GGCTCTGTCC	CGGCAGCCGG	CCGAGATGGC	GGCCGAGCTG	120
GGCATGAGGG	GCCCCAAGAA	GGGCAGCGTG	CTGAAGCGGC	GGCTGGTGAA	GCTGGTGGTG	180
AATTTCCTCT	TCTACTTTCG	GACAGACGAG	GCCGAGCCCG	TCGGAGCCCT	GCTGCTGGAG	240

CGCTGCAGAG TCGTCCGGGA AGAGCCCGGC ACCTTCTCCA TCAGCTTCAT TGAGGACCCT GAGAGGAAGT ATCACTTCGA GTTCAGCTCG AG	300 332
(2) INFORMATION FOR SEQ ID NO:237:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 238 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:	
GAATTCGGCC TTCATGGCCT AATTGCAAGA TCACGGAATC TCCTGAATCA TTAAGAAAAG ATAAAATATC ACAAGCATCT TTAGTGTTAT GTGTATTCAG TAATTCTTTG GAGTTGTATT TATTAAGCTT ACCAGATTTT AAAGGCATAT AAAATGTGGT AAGATATGAG ACACATACTG AAATATCAGT GCAAAGGGAG AATGGTAGTT GAATGGTCAG AAACGAAAAA GCCTCGAG	60 120 180 238
(2) INFORMATION FOR SEQ ID NO:238:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 180 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:	
GAATTCGGCC TTCATGGCCT AGAAGCATTT TTTGTTATTG TGAAACATTT TTATACTTTC ATTATAATTT GTTGAGCCTA GAGTTGGGCT ATTTGAATAT TTATTATGAT AATCTTTTGG CTAATGGTAA CAGCATATCT TGTTCTAACA AAATTACTGT TAACAGCAAT CGAACTCGAG	60 120 180
(2) INFORMATION FOR SEQ ID NO:239:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 578 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:	
GAATTCGGCC TTCATGGCCT ACTGAGATCC AGACCAGCTC CTCCCAGACC TCTCCAGAAG AAGCCATGGG AACCCCTCGT ATCCAGCATT TGCTGATCCT CCTGGTCCTA GGAGCCTCCC TCCTGACCTC GGGCCTAGAG CTGTTTTGTC AAAAGGGTCT GTCCATGACT GTGGAAGCAG ATCCAGCCAA TATGTTTAAC TGGACCACAG AGGAAGTGGA GACTTGTGAC AAAGGGGCAC TTTGCCAGGA AACCATACTA ATAATTAAAG CAGGGACTGA GACAGCCATT TTGGCCACGA AGGGCTGCAT CCCGGAAGGG GAGGAGGCCA TAACAATTGT CCAGCACTCT TCACCTCCCG GCCTGATCGT GACCTCCTAC AGTAACTACT GTGAGGATTC CTTCTGTAAT GACAAAGACA	60 120 180 240 300 360 420
GCCTGTCTCA GTTTTGGGAG TTCAGTGAGA CCACAGCTTC CACTGTGTCA ACAACCCTCC ATTGTCCAAC CTGTGTGGCT TTGGGGACCT GTTTCAGTGC TCCTTCTCTT CCCTGTCCCA	480 540
ATGGTACAAC TCGATGCTAT CAAGGAAAAC CTCTCGAG	578

- (2) INFORMATION FOR SEQ ID NO:240:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GAATTCGGCC	TTCATGGCCT	ACATGAATCC	ACTCCTGATC	CTTACCTTTG	TGGCAGCTGC	60
TCTTGCTGCC	CCCTTTGATG	ATGATGACAA	GATCGTTGGG	GGCTACAACT	GTGAGGAGAA	120
TTCTGTCCCC	TACCAGGTGT	CCCTGAATTC	TGGCTACCAC	TTCTGTGGTG	GCTCCCTCAT	180
CAACGAACAG	TGGGTGGTAT	CAGCAGGCCA	CTGCTACAAG	TCCCGCATCC	AGGTGAGACT	240
GGGAGAGCAC	AACATCGAAG	TCCTGGAGGG	GAATGAGCAG	TTCATCAATG	CAGCCAAGAT	300
CATCCGCCAC	CCCCAATACG	ACAGGAGACT	CGAG			334

- (2) INFORMATION FOR SEQ ID NO:241:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GAATTCGGCC TT	CATGGCCT AGGGCACO	CAC TGAGTTCAGT	ACTTCAAAAT	TGCCGTGCTC	60
TACCTCTCCC CA	GTGCACAA AAACACTO	TC CACACCAAGC	TGCTGCTGCT	GGGGGATGGA	120
GGGATGGCGT CA	GCGATTCA AGACTGTT	TTT TCCTACCTGT	TCAGCACTTC	TTTCAGCGAT	180
ATGAAGTTAA AT	CCAGTCTT TCCCTGT	TC CAGGCATCAT	CGCCATCAAC	ATACAGCCAT	240
ACTCCAGGAT TG	CCCATCTT CAACATA	AAC GGACTCTCCT	GGACTCCACT	TCCCACATCA	300
GTCACAGCCA CA	ACTTCCTGA GAAAGAA	TC TACACTCTTC	ATTCACTTTC	ATTCACCCAC	360
TGCTCGAG					368

- (2) INFORMATION FOR SEQ ID NO:242:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GAATTCGGCC	TTCATGGCCT	AGAGAAAATA	AAGAGTTATA	TCAGAAATTT	ACAAACATAA	60
CTTTTTAAAT	TTTAAATTGC	AAAATATATA	TCATACGAAA	ATGAAAATTA	TAATTCTTCT	120
TGGATTCCTG	GGAGCCACAT	TGTCAGCCCC	ACTTATCCCA	CAGCGTCTCA	TGTCTGCCAG	180
CAATAGCAAT	GAGTTACTTC	TTAATCTTAA	TAATGGTCAA	CTTTTGCCAC	TACAACTTCA	240
GGGCCCACTT	AATTCATGGA	TTCCACCTTT	CTCTGGAATT	TTACAACAGC	AGCAGCAGGC	300
TCAAATTCCA	GGACTCTCCC	AGTTCTCTTT	ATCAGCTCTA	GACCAGTTTG	CTGGACTGCT	360
CCCAAATCAG	ATACCCTTAA	CAGGAGAGGC	CAGTTTTGCC	CAAGGAGCCC	AGGCAGGCCA	420
AGTTGATCCC	TTACAGCTTC	AAACACCGCC	TCAGACACAA	CCAGGCCCAC	GTCTCGAG	478
AGTTGATCCC	TIACAGCIIC	AAACACCGCC	TCAGACACAA	CCAGGCCCAC	GICICGAG	4

- (2) INFORMATION FOR SEQ ID NO:243:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 490 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GAATTCGGCC	TTCATGGCCT	ACTTACAGAA	CCTATTCACT	GGGAAGGAAG	CCCTCATTAT	60
		GTGTTTCAGG				120
TTATACACCA	CAAAAGGTGG	ATGTTCCCAA	GGCCTTGATT	ATTGTTGCAG	TTCAATGTGG	180
		TGACCCAGTC				240
ATTCAATAAG	CTGGGTCTGA	ATCAGTGCAT	GTCGGGAATT	ATCAACCATG	AAGCATACCA	300
		CCTTTACCTT				360
		CTCACACAGC				420
		GGCAGCTGGG				480
CAACCTCGAG						490

- (2) INFORMATION FOR SEQ ID NO:244:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

			AACTGTCGTG			60
TTATGTGGTA	CCTGAGAGCC	ACCCCAAATT	AGATTGACTT	TAGATCGTTT	ATACAAAAAT	120
AGCTTGAAGA	ACTGTTTTTT	CCATGGTAAA	TGCTTTTGAA	TATTAACTTA	GTTATGTTAG	180
			TTGGTTACAT			240
			TGTTTTTTGA			300
			GTGGAGTGCA			360
	TCCTCCTAAC					386
011111000						

- (2) INFORMATION FOR SEQ ID NO:245:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GAATTCGGCC TTCATGGCCT	AGCTTCAGTA	GCAAATAAGG	ACATCATCTG	CTATAACCTA	60
CAAGCAGTTG GACAGATATT					120
TATTTGTACA CAGAGCTGAG					180
GTGATAGATT ATACTTGTCG					240
CTGCTATTGA TGACACCTGT					300

AGTCAGAGCC ACAAG' CCTTCTGCCA ACACA'			CAGCCATGGC	TGAACTTCCA	360 396
(2) INFORMATION	FOR SEQ ID NO:246	5:			
(A) (B) (C)	ICE CHARACTERISTI LENGTH: 514 bas TYPE: nucleic a STRANDEDNESS: d TOPOLOGY: linea	e pairs cid ouble			
(ii) MOLEC	CULE TYPE: cDNA				
(xi) SEQUE	ENCE DESCRIPTION:	SEQ ID NO:	246:		
GAATTCGGCC TTCATCCTTATCATTT GATATCGACAATCTC ACACTCCTTTGAAGAA CCTTCCTAACCCGGGA AGAGGGACATACAC ACAGTTACTCTGTCT AAATACTAAGTTACA TATGCTGTTTTGTATT AGGTT	TTTCA TTTTATTGTG TAACC TTTTAAAAAA GAGAA AGGAGAAACA GAGAA GGCATGGAGA CTTTA GAGCAGCTGC TGTTT TTCTTATTTA TTTTT NGGGCTGCTC	TATCTCTGTN ATCTAATAGG CAGACCTCCC CAACTGATAC TTAACTCTCC ATTTCACTGT CAATAAAATT CGAG	NGGCCAAATC CCCAGTTTCC GCTTCTAGAC GGAGTCTGTG CGAAACTAAA CTTATTTAAT	AATAGATTTT TCTCAACAAT ATGCACACTG TCTTCCGCCA CTTGGTATGT TACTANTACT	60 120 180 240 300 360 420 480 514
(A) (B) (C)	NCE CHARACTERIST: LENGTH: 323 bas TYPE: nucleic a STRANDEDNESS: d TOPOLOGY: linea	e pairs cid louble			
(ii) MOLE	CULE TYPE: CDNA				
(xi) SEQU	ENCE DESCRIPTION	: SEQ ID NO	: 247 :		
AGAGTTTATT GTTCT AAGGGAAGAA AATCA GCTTTGCAAT TATGA	GCCTA GGTTTTCTGT TAGATC TTGAGCACAA ATTTCC TTCATACCAA AGACCA GTAGTAGAAA CTTTAC ACTGCTCAAC AGGCTC GAG	AGGTTGGTAT A GTAAGAGAGC A TAGCTTTAGT	ACGTTAATAA ACTTATCATC TTCCTCAATT	AAAAAATAGC GTAGGCACTG TTCCTGGAGT	60 120 180 240 300 323
(2) INFORMATION	FOR SEQ ID NO:24	18:			
(A (B (C (D	CNCE CHARACTERIST) LENGTH: 423 ba) TYPE: nucleic) STRANDEDNESS:) TOPOLOGY: line	se pairs acid double			
	ECULE TYPE: cDNA				
(xi) SEQU	JENCE DESCRIPTION	: SEQ ID NO):248:		
CTCCGTTTTT GGAG	TGGCCT AGGAACAGT CAGCGT GAGATTATT	G CAATGCTAC	A TTTCCTCCC	T CTGCGCCCTC	60 120

GTTAGTCTGT GTATAGTTCC TGGGGTGTGG CGAGTACCAG CTCTGACAGC GGAAGAGAAC 240
TATACTGTTG ATTCCCATTA TTCTCAGTAG GTGTGTTCTA TAAAATTGCT GCGAACACCA 300
AATTAGCGAA TCCTGAACCA TCGTTCCCAG AGGAATAGGG GGTTAGGGTC CTGTGATCCT 360
CAAGTTGCAA CATTGTCTTC GACTGATTAA TATGTAACCT TGTTTTATAT GTGCAATCTC 420
GAG

- (2) INFORMATION FOR SEQ ID NO:249:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

GAATTCGGCC TTCATGGCCT ACCGAAACCA AATAATTCAA GCACTGCTTA TTACAATTTT 60
ACTGGGTCTC TATTTTACCC TCCTACAAGC CTCAGAGTAC TTCGAGTCTC CCTTCACCCT 120
CGAG 124

- (2) INFORMATION FOR SEQ ID NO:250:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs(B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

GAATTCGGCC	TTCATGGCCT	ACATCTATGA	CTTTTTAAAC	ATGCGGCGTT	TTGTGAATAT	60
CATGATAATA	ACAAGAGTCA	ACAGGCTAAG	TGAGAGGAGA	GGGATGCTAC	GCCTACGCTG	120
CCCCCACCAC	GGCCAGCCGG	CTTCTGCGCC	TTTGGTGTTG	GATTTTCTTT	GTGATTTTAC	180
GGGGTTTTGT	GTTTTTTTT	TCTTGTTTTT	TGTTTTGTTA	TTTTTTCTTG	TCCACTTGAT	240
TTGCATGCAA	CACCCACAAA	AAGGAAACAC	AAAACCCCGT	CTGCTCGAG		289

- (2) INFORMATION FOR SEQ ID NO:251:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GAATTCGGCC '	TTCATGGCCT	ACACTATGAG	AGGACCGATT	GTATTGCACA	TTTGTCTGGC	60
TTTCTGTAGC	CTTCTGCTTT	TTCAGCGTTG	CCACACAATG	TCTGGCCTTC	CCCAAAATAG	120
AAAGGAGGAG	GGAGATAGCA	CATGTTCATG	CGGAAAAAGG	GCAGTCCGAT	AAGATGAACA	180
CCGATGACCT	AGAAAATAGC	TCTGTTACCT	CAAAGCAGAC	TCCCCAACTG	GTGGTCTCTG	240
AAGATCCAAT	GATGATGTCA	GCAGTACCAT	CGGCAACATC	ATTAAATAAA	GCAAAACTCG	300
AG						302

- (2) INFORMATION FOR SEQ ID NO:252:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

GAATTCGGCC AAAGAGGCCT ATTTTTTTT CTGCAAACAC TGTGTATAGT GAGACTTGTT 60
CTACTTTGGA GAACAGGTTA CCTTTTGAAA ATGAGGTTGA GTTTCTTCCT TTCTGATGCA 120
TTGATTTTTG AAGATTTTT TTTCCCCCTT CCCCTCTCCC TCGAG 165

- (2) INFORMATION FOR SEQ ID NO:253:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GAATTCGGCC AAAGAGGCCT AGCTTCTTG TATAATTAAA TCTGAGTTTT GTTTGAGCAT 60
CTTTCAACAT GTACCATATT TATGACAATT CTCTTCCATA GGATCTATCT GTTCTGCAAC 120
AAGTATTGAT CTTACAGTAA AATTTTTCAC AAATTCATTA GATTCTATGT CTCTTTTTCT 180
GGTAGGAATT TTTGTGCAGG TAGCTATCTC TTGCCCTAGA TTATTCTCCT TGTTTAGCTG 240
CTGATTCTTA AACTGGCCTC TAGATTTCCA GATTTCTTCC GGTACAGACT TTCTCTTTGC 300
AAGTTCTTCC ATCTCTAATC TTTGAGATTA ATCTTCTTTT GAAATGTCCT GCTGCTCTAC 360
TCTTGATGTT CTCGAG 376

- (2) INFORMATION FOR SEQ ID NO:254:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

TCTCCAAGGG	AAAATAAATG	CTTTTACTAT	CTAGTTTGTC	TCTTTGAGAA	TTAAAACTCT	60
TTTTTTTTT	TTTCATTCCA	GTAGCTTTTG	GGGTAGAGTT	TGGCTCTTTG	AGAATTGCAT	120
ACTAATTAAT	TTTAGGGGTG	ATTTGTACAT	CATCTCTATA	TTCCTGAAAC	ACAGTAGAAA	180
CAGCCAGCAG	TCAGGCAACC	ATCTACCATG	ACCATTAAAA	CATCCCCAAA	GTGAAACACC	240
AGATGTGATC	TGCTAGATTT	AGTGGAGGCG	GCTGGCTCGA	G		281

- (2) INFORMATION FOR SEQ ID NO:255:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 571 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GAATTCGGCC	AAAGAGGCCT	AGCTAGNCTT	GCTCAGCTTT	GTGGATACGC	GGACTTTGTT	60
GCTGCTTGCA	GTAACCTTAT	GCCTAGCAAC	ATGCCAATCT	TTACAAGAGG	AAACTGTAAG	120
AAAGGCCCA	NCCGGAGATA	GAGGACCACG	TGGAGAAAGG	GGTCCACCAG	GCCCCCAGG	180
CAGAGATGGT	GAAGATGGTC	CCACAGGCCN	TCCTGGTCCA	NNTGGTCNTC	NTGGCCCCCN	240
TGGTCTCGGT	GGGAACTTTG	CTGCTCAGTA	TGACGGAAAA	GGAGTTGGAC	TTGGCCCTGG	300
ACCAATGGGC	TTAATGGGAC	CTAGAGGCCC	ACCTGGTGCA	GCTGGAGCCC	CAGGCCCTCA	360
AGGTTTCCAA	GGACCTGCTG	GTGAGCCTGG	TGAACCTGGT	CAAACTGGTC	CTGCAGGTGC	420
TCGTGGTCCA	GCTGGCCCTC	CTGGCAAGGC	TGGTGAAGAT	GGTCACCCTG	GAAAACCCGG	480
ACGACCTGGT	GAGAGAGGAG	TTGTTGGACC	ACAGGGTGCT	CGTGGTTTCC	CTGGAACTCC	540
TGGACTTCCT	GGCTTCAAAG	GCAACCTCGA	G			571

- (2) INFORMATION FOR SEQ ID NO:256:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GAATTCGGCC	AAAGAGGCCT	ATGCGCAAGG	ATCAAGCCGA	CTACCTGTGC	TGTCTACTGG	60
GACAGCAGTC	TCCGAGCTAC	TCCGTACCTC	CCTCTGCCAG	GTCGTGGAGT	TAGGCCCCAG	120
TCCCTACTTG	TCACTGGTTC	CCACTGTGCT	CCTAACTGTG	CAGCACCTGG	GAGCTCTGGC	180
CTGGGGCTGG	AGGCCCTGGT	AGGAGCTGCA	GTTGGAGGCC	GTTCTGTGCC	CAGCAGCGGT	240
GAGCGGCTCC	CATGGGCCCT	GTGTCTGCAG	GGAGCCAGGG	CTGCGGCACA	TGTGCTGTGA	300
AACTGGCACC	CACCTGGCGT	GCTGCTGCCG	CCACTTGCTT	CCTGCAGCAC	CTCCTACCCT	360
GCTCCGTGTC	CTCCCTCTCC	CCGCGCCTGG	CTCAGGAGTG	CTGGAAAAGC	TCACGCCTCG	420
GCCTGGGAGC	CTGGCCTCTT	GATATACCTC	GAG			453

- (2) INFORMATION FOR SEQ ID NO:257:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GAATTCGGCC	AAAGAGGCCT	ATGTCATGAG	TGAACTTGGC	AATTGCCTTG	TTAAAACCAG	60
TTGGACATTA	TCTTCCACAT	TGCGAAGCTA	TACATGTCTG	ATATGTTCTG	AAAGAATAGA	120
ATTTATAGTT	AGATATACTA	TTTTTGATTA	TTTACTCAGA	AGGAGACATG	TAATTATTCT	180
TATGTTGTCA	TGAAAATCTA	TTAAATGCAT	TTATATTTCA	CATCAATGTT	ACGAAGTTCC	240
ATTATTATTA	TTTTACAGAG	GGGAAGCCAA	GATACAGGAG	TGGAAATTAC	TTGGCCTATC	300
GCTCGAG						307

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

GAATTCGGCC	AAAGAGGCCT	AAGAAGATGA	ACAAGCGCCA	GCTCTATTAC	CAGGTTTTAA	60
ACTTTCGCCA	TGATCGTGTC	TTCTGCACTC	ATGATATGGA	AAGGCTTGAT	CGTGCTCACA	120
GGCAGTGAGA	GCCCCATCGT	GGTGGTGCTG	AGTGGCAGTA	TGGAGCCGGC	CTTTCACAGA	180
GGAGACCTCC	TGTTCCTCAC	AAATTTCCGG	GAAGACCCAA	TCAGAGCTGG	TGAAATAGTT	240
GTTTTTAAAG	TTGAAGGACG	AGACATTCCA	ATAGTTCACA	GAGTAATCAA	AGTTCATGAA	300
AAAGATAATG	GAGACATCAA	ATTTCTGACT	AAAGGAGATA	ATAATGAAGT	TGCTCTCGAG	360

- (2) INFORMATION FOR SEQ ID NO:259:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

GAATTCGGCC	AAAGGGGCCT	ACCTGAAACG	GCAGTCCGGT	CCCTCCGACA	TTGTCCAGCG	60
GAAGGCCTGG	GCTTCACACT	CTGTGCCTCC	CGGCGCTACC	TGGCACGATG	CCGAGCACAC	120
AGCAGATGCT	CAATGAATGC	CCAACCAACC	CTATACCTGG	CTTGGATCTC	AAGCTCCCTG	180
GCCGGGGCCT	GATGGAAGGC	TTTGGGGGCA	CAGGAGGCTG	CCCCCTTGGG	CGCCCCGGC	240
CACCTCTTCG	CCCTCGAATC	TCAGGCAGCT	TGGTCAGGAA	CTTCTTCTCC	ACGTATTTAG	300
CGTGAATCCA	GGCCTCCTTC	TCCTGCCTGT	GGGAGGGGAG	AAGCACGCAG	TCTTCCCTCT	360
TCTGCTCCAG	GGGTCCCCCA	TTCCCCTGGG	AGGCTAAACC	CATAGCTCGA	G	411

- (2) INFORMATION FOR SEQ ID NO:260:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

GAATTCGGCC	AAAGAGGCCT	AGGGAGTGTT	TGCGTTTCTT	CTCCGTTTGG	CAGTGAAACA	60
CATCTCAGAA	AGGTGGAGCT	GATCAGAATA	ATGTTCAGCA	TCAACCCCCT	GGAGAACCTG	120
AAGGTGTACA	TCAGCAGTCG	GCCTCCCCTG	GTGGTCTTCA	TGATCAGCGT	AAGCGCCATG	180
GCCATAGCTT	TCCTGACCCT	GGGCTACTTC	TTCAAAATCA	AGGAGATTAA	ATCCCCAGAA	240
ATGGCAGAGG	ATTGGAATAC	TTTTCTGCTA	CGGTTCAATG	ATTTGGACTT	GTGTGTATCA	300
GAGAATGAAA	CCCTCAAGCT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:261:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GAATTCGGCC	AAAGAGGCCT	AGTGGGGCTG	TATTTTAATA	CAAGAAAGAC	ATTGCTCTAG	60
AACATGGCTC	GCCTTTGCTT	CAGGGCCTAG	CAGTTTATTT	TAGCCATAAG	GGTAAGGGAG	120
CAGGTCAGAA	ATGACTTTTA	GTGTAATCCT	ATCTGTAATT	AAAAATACAA	ATGCTGTCAT	180
AAGATCAAAT	GTTATCAAAA	ATCAGTATTT	TAAATTAAAA	TTACCCCCAA	ATTTCTTTCA	240
AAAAAGTTGT	AATGTTCTTT	TTCAGTGAAG	CCTTTGCACT	GCTAGAGCTG	AAGAATGTGA	300
TCAATCGGCT	TGTTGAATAA	TCCCGCACAG	TAGGTATTCC	GCTGAAGCCA	ACTCTAGCTG	360
GGGGCTCGAG						370

- (2) INFORMATION FOR SEQ ID NO:262:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

GAA	TTCGGCC	AAAGAGGCCT	AAGAAATAGG	ACTATACAAA	TTTTCAACTT	CTTTTGATAT	60
CAG	STTTTGGT	AAGATGCATT	TTTCTTCTGA	GAATTTGTTT	CATTTGAATT	TCCAAATTTA	. 120
TTA	GCATGAA	GTTGTTAATA	AAAATCTTAT	ATTTTTACTC	AAATTTTGAG	ATAGTTGTAG	180
TTA	TACATGA	AGTTGTAAAG	AATAATAGAA	AGATCCTGTG	TACCTTTTCC	CAGTTTTCCC	240
CAF	AAGTAAC	ATTTTGCATA	ACTCTAGTAC	AGTAGCACAA	CTCGAG		286

- (2) INFORMATION FOR SEQ ID NO:263:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GAATTCGGCC	AAAGAGGCCT	AGGCAAACCG	TGTACTAAGC	ATCAGTGCAG	AGATAGTGAA	60
TGAGACACAG	TATTCCCACC	TTTGAGCAGT	GCCAGTCTAG	TATTAGAATA	TTTTTGGCTA	120
TTATTAAAAA	TTGAAGCATA	AAGAAGCTTT	TGTTTGCTCT	GGTGATTTTC	ATAACATATT	180
CACATTCTTA	ATGTATTTTT	GGTTTTTCAG	AAAGTTACTT	CTGGCCTGTG	TTCTTTCAGA	240
ATATAGGTTG	CAGCTTGTGT	TAAGTGCAGG	AACTATTGAT	AGACTGAGTT	TAGAAGAAGG	300
GAAACTCGAG						310

- (2) INFORMATION FOR SEQ ID NO:264:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

- (2) INFORMATION FOR SEQ ID NO: 265:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

GAATTCGGCC TTCATGGCCT TGTGATTCTG CAAAGGAGGA ACAATAATTC ACTGTTTCCC 60 AAACTTATCT GACCATAGAA CATATNTCTC AGAGTATTTT TCAAGAGTAG TATTTTCTGT 120 AATATATGAT GAAAAATAAT CGTATCGGCC ATCTTTGTAC ATAAGGTCAA AATGTCAGCC AGCCCTGAAA TAAATGCAAG CCAAAAGGTA GAGAGATAAG TGAATAAAGC TGGCACACTG 240 TCAGTCCGGA GTACCATGCT GCATTCTGAG TCAAGCTCCA GGAAACTGAG CTAGGGTTTG 300 TCTCTAAGAA GAAAAACTGG AGCGTCCAAA GCTTCTGGAT TCCATTTAAT TAAAACCCTT TTAAATTAAA TCCTTGTAAC TGAAGAGTAT CGGTGGATGA AGAAAAAAA GTCTCACATG 420 TCTTCATTTC CATCCTTGGC TCAGTACAGC TCCAGTTCCA TTATTCTTAA ACATCTATTA 480 ACATGATTGC TAAATAATTA CACAGGCTAA CTGCCAAGCA TTTTTCACAG GAAGCAAGGC ACTGCTCGAG 550

- (2) INFORMATION FOR SEQ ID NO:266:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GAATTCGGCC	TTCATGGCCT	AGTTAAGTGG	GAAGTTAAAT	GGCAAGTACT	AGAATGCCAC	60
CTATGGCAAG	CACTAGAATG	GTCTAGGTGT	GAAATGAGGG	AGTAATGTCA	GGGAGTCAAG	120
				TGAATTTCAC		180
					AGCAGTGTTC	240
AGCTCAGTAA	AAGTAAGGGA	AAAAAAATAG	CAGTCTCTAA	AAGGAACATA	GAGCGCTCGA	300
G					0.1000010011	
J						301

- (2) INFORMATION FOR SEQ ID NO:267:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GGGGAGAGCA	TCAGGAAGAA	CAGCTAATGG	ATGCTGGGCT	TAATACCTAG	GTGATGGGAT	60
GGTCTGTGCG	GCAAACACCA	TGGCACAAGT	TTACCTATGT	AACCTGCACA	TCCTGACATG	120
TACCCCTGAA	CTTAAAATGA	AAGTTGGAGA	CCAAAAAACA	AAACACCATA	AAACTACAAA	180
ACTTCTTAAA	CAATAAACTA	GTAGAAAATT	TCTAAAATAT	ATAATTCAAG	AATTATAA	240
GAGCTCTTTT	TATATGTAAA	TATAAATTTA	AATACAAGAG	AAACATCTAA	AACAGGTTGC	300
TTCTGAGAAA	CGTGACTGGT	TATTAAGAAG	AGGTATATAG	GGGCTCACTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:268:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

CATTATTTAA	CCTTTTAAAC	AATCAAGAGA	TTGCTTTTTA	AATTGTCTCT	AAAAAGGTTT	60
GATTTTTTAC	GAAAGAGAGA	GCACTTGAAT	ATATCTTTAT	GTACCACCGT	GTCTCTTTTT	120
GTTAGATTTT	TCATCTGTGG	GTATAATATA	AAATATTCTT	AAAATGAAAG	CTTTACGCTT	180
GTGTTTGAGA	CTAAGCAACT	TGCATTGTGT	CATGACCCTT	CTAATACCAC	AAACCCTCGA	240
G						241

- (2) INFORMATION FOR SEQ ID NO:269:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GAATTCGGCT	TCATGGCCTA	CACTCAACCA	CTGAAAAAGC	TGAAAATCAA	TGTTTTTAAG	60
GTTCACAAGT	GTGCCGTGTG	TGGCTTCACC	ACCGAAAACC	TGCTGCAATT	CCACGAACAC	120
ATCCCTCAGC	ACAAATCGGA	TGGTTCTTCC	TACCAGTGCC	GGGAGTGTGG	CCTCTGCTAC	180
ACGTCTCACG	TCTCTCTGTC	CAGGCACCTC	TTCATCGTAC	ACAAGTTAAA	GGAACCTCAG	240
CCAGTGTCCA	AGCAAAATGG	GGCTGGGGAA	GATAACCAAC	AGGAGAACAA	ACCCAGCCAC	300
GAGGATGAAT	CCCCTGATGG	CCCCCTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:270:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GCGGGCACCA	TTTCCAGTAT	GTACCAAACC	AAAGCCGTCA	TCATTGCAAT	GATCATCACT	60
GCGGTGGTAT	CCATTTCAGT	CACCATCTTC	TGCTTTCAGA	CCAAGGTGGA	CTTCACCTCG	120
TGCACAGGCC	TCTTCTGTGT	CCTGGGAATT	GTGCTCCTGG	TGACTGGGAT	TGTCACTAGC	180
ATTGTGCTCT	ACTTCCAATA	CGTTTACTGG	CTCCACATGC	TCTATGCTGC	TCTGGGGGCC	240
ATTTGTTTCA	CCCTGTTCCT	GGCTTACGAC	ACACAGCTGG	TCCCGGGGAA	CCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:271:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

ACC ACAGCAAGCC 60
CAC AAAACCAGTA 120
GTC CAGACTGCCA 180
CCC ATCGTTATAA 240
TCC AAACACTCAG 300
TCC GATTCCTACA 360
407
A

- (2) INFORMATION FOR SEQ ID NO:272:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

ACTGAGCTCA	AGGACCCCTC	CAAGAAGAAG	A'I'GCAGCACA	TCTCCAACCT	GTCCATCGCT	60
GTCATGTACA	TCATGTACTT	CCTGGCTGCC	CTCTTCGGCT	ACCTCACCTT	CTACAACGGG	120
GTGGAGTCGG	AGCTGCTGCA	CACCTACAGC	AAGGTGGACC	CGTTTGACGT	CCTGATCCTG	180
TGTGTGCGCG	TGGCCGTGCT	GACAGCAGTC	ACGCTCACAG	TGCCCATCGT	TCTGTTCCCG	240
GTGCGCCGCG	CCATCCAGCA	GATGCTGTTT	CCAAACCAGG	AGCTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:273:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GAATTCGGCC	TTCATGGCCT	AGTCAAGCTA	GGTAAGCTAA	AAAGAAGAAA	ACCTGGTTAC	60
AGCCCGGTGA	ATTGATTTTT	TTCCAGCCGA	GAAATAGATA	TTTCTCTCAC	ATATATTTGG	120
AAAACTTTAG	TCATCTTCAT	AAAACTTAAA	AAGTTACCTA	AGCACACA	GCAAGTTTCT	180
CCTTTCTTCC	TTTTCCACAC	CCTTACCAGT	TCACTATGTT	TCTACCAATC	CAGTGCCCAG	240
TTGCCAATGA	TGTTGCTCTC	ACATGAATTT	ACTGCATTCC	CTTCTGGTTC	CCCAGAAGGT	300
CTTGAAGAAA	GAGGTTCAGA	CTAGTGGACC	CAAACAGAAT	TTCTTGGCTG	GTGATACTCA	360
GATTGTGTTC	AGAGCCTGGT	ATGAAGAAGG	GGCCAGGTGT	AAGAAGTAGT	TAATCAACTG	420
CACGTTGATT	TCAGGCTGAA	TATTCAACCA	TCTGCAGCCA	CCCGTCTCTA	AAAGTCTAGC	480
TGAAGCACAA	TTGATTGTGC	CATAGAATGA	GCAAACGCTT	GAAAACACAA	GCTCGAG	537

- (2) INFORMATION FOR SEQ ID NO:274:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

GCGAGCTCGT	GTTTTAAAGG	ACCAAATAGA	AGTTTACCAG	GAGAGAAGTG	ACAGAAGTGC	60
TGTCTAGATA	GAGGAAGGC	ACACACAGAT	GCAAGCATGT	GCAGAAATGA	GCAAACCACT	120
GAGACGCTGC	CTTGAGCTCT	GTGTCACACT	GCTATGTTGC	AGCCTGGGAG	GCTGTTCCCA	180
GTTGAGCCCT	TCGGAACCAG	CCATGAGATG	GCACGGGTAC	GCGGAAGGGA	GCAGTCTCCA	240
TGGCTGGGTG	GTGATGGGGG	CTTCTCGAG				269

- (2) INFORMATION FOR SEQ ID NO:275:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GATGGCTCCC CAGAGCC	TGC CTTCATCTAG	GATGGCTCCT	CTGGGCATGC	TGCTTGGGCT	60
GCTGATGGCC GCCTGCT	TCA CCTTCTGCCT	CAGTCATCAG	AACCTGAAGG	AGTTTGCCCT	120
GACCAACCCA GAGAAGA	GCA GCACCAAAGA	AACGGAGAGA	AAAGAAACCA	AAGCCGAGGA	180
GGAGCTGGAT GCCGAAG	TCC TGGAGGTGTT	CCACCCGACG	CATGAGTGGC	AGGCCCTTCA	240
GCCAGGGCAG GCTGTCC	CTG CAGGATCCCA	CGTACGGCTG	AATCTTCAGA	CTGGGGAAAG	300
AGAGGCAAAA CTCCAAT	ATG AGGACAAGTT	CCGAAATAAT	TTGAAAGGCA	AAAAGCTCGA	360
G					361

- (2) INFORMATION FOR SEQ ID NO:276:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

GCCACAATAG	CGGGATTGAT	CTCCTTAGGA	CCTATCTTTG	GCGTTGCCAG	TTCCTTTTAC	60
CTTTTGTGAG	TTTAGGTTTG	ATGTGCTTTG	GGGCTTTGAT	CGGACTTTGT	GCTTGCATTT	120
GCCGAAGCTT	ATATCCCACC	ATTGCCACGG	GCATTCTCCA	TCTCCTTGCA	GGTCTGTGTA	180
CACTGGGCTC	AGTAAGTTGT	TATGTTGCTG	GAATTGAACT	ACTCCACCAG	AAACTAGAGC	240
TCCCTGACAA	TGTATCCGGT	GAATTTGGAT	GGTCCTTCTG	CCTGGCAGAA	CTCGAG	296

- (2) INFORMATION FOR SEQ ID NO:277:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

GAATTCGGCC	TTCATGGCCT	AGGATGTAGA	ATCCTGCTTA	TCTGTGAAAT	GCAGTTGACA	60
CATCAGCTGG	ACCTATTTCC	CGAATGCAGG	GTAACCCTTC	TGTTATTTAA	AGATGTAAAA	120
AATGCGGGAG	ACTTGAGAAG	AAAGGCCATG	GAAGGCACCA	TCGATGGATC	ACTGATAAAT	180
CCTACAGTGA	TTGTTGATCC	ATTTCAGATA	CTTGTGGCAG	CAAACAAAGC	AGTTCACCTC	240
TACAAACTGG	GAACAATGAA	GACAATGAAC	TCGAG			275

- (2) INFORMATION FOR SEQ ID NO:278:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

TCGTTCCCTT	CATCTCTTCC	CTTGCCAGAG	CAGGGACTCT	CTCCATATAA	ACAAAAGGAA	60
AACCACTGGC	CAGGGTATGG	TCAATACCTC	AACATATCCA	GACATCACAG	CACCAGAACA	120
CCAGTATGTA	TATTCCACAA	GTACTCGAG				149

- (2) INFORMATION FOR SEQ ID NO:279:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GCAATCAGAT	AAAGAAAGAC	CTGGCTGACA	AGGAGACACT	GGAGAACATG	ATGCAGAGAC	60
ACGAGGAGGA	GGCCCATGAG	AAGGGCAAAA	TTCTCAGCGA	ACAGAAGGCG	ATGATCAATG	120
CTATGGATTC	CAAGATCAGA	TCCCTGGAAC	AGAGGATTGT	GGAACTGTCT	GAAGCCAATA	180
AACTTGCAGC	AAATAGCAGT	CTTTTTACCC	AAAGGAACAT	GAAGGCCCAA	GAAGAGATGA	240

TTTCTGAACT CGAG 254 (2) INFORMATION FOR SEQ ID NO:280: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 327 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:280: GACAGCCTGG AAGTTTGGAG ACCCTGACAC ACCCACCTTC TCACCTGGGC TCTGCGTATC 60 CCCCAGCCTT GAGGGAAGAT GAAGCCTAAA CTGATGTACC AGGAGCTGAA GGTGCCTGCA 120 GAGGAGCCCG CCAATGAGCT GCCCATGAAT GAGATTGAGG CGTGGAAGGC TGCGGAAAAG 180 AAAGCCCGCT GGGTCCTGCT GGTCCTCATT CTGGCGGTTG TGGGCTTCGG AGCCCTGATG 240 ACTCAGCTGT TTCTATGGGA ATACGGCGAC TTGCATCTCT TTGGGCCCAA CCAGCGCCCA 300 GCCCCTGCT ATGACCCCTG CCTCGAG 327 (2) INFORMATION FOR SEQ ID NO:281: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 357 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281: GCCTGGAACC TGATTCTCCT GACCGTCTTT ACCCTGTCCA TGGCCTACCT CACTGGGATG 60 CTGTCCAGCT ACTACAACAC CACCTCCGTG CTGCTGTGCC TGGGCATCAC GGCCCTTGTC 120 TGCCTCTCAG TCACCGTCTT CAGCTTCCAG ACCAAGTTCG ACTTCACCTC CTGCCAGGGC GTGCTCTTCG TGCTTCTCAT GACTCTTTTC TTCAGCGGAC TCATCCTGGC CATCCTCCTA 240 CCCTTCCAAT ATGTGCCCTG GCTCCATGCA GTTTATGCAG CACTGGGAGC GGGTGTATTT 300 357 ACATTGTTCC TGGCACTTGA CACCCAGTTG CTGATGGGTA ACCGACGCCC GCTCGAG (2) INFORMATION FOR SEQ ID NO:282: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 306 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282: GCGGGCTGCA GAATGATAGA CGAGCTCAAC AAAACGCTGG CCATGACCAT GCAGAGGCTG 60 GAAAGCTCTG AGCAGCGGGT CCCCTGTTCC ACTTCTTACC ACAGCTCTGG GTTGCACTCG 120 180 GGTGATGGGG TCACCAAAGC AGGACCTATG GGCCTTCCAG AAATAAGACA AGTGCCAACT GTTGTGATTG AATGTGATGA CAATAAAGAA AATGTGCCTC ATGAGTCAGA CTACGAAGAC 240 TCTTCTTGCC TGTATACAAG AGAAGAGGAG GAAGAGGAGG AGGACGAAGA CGACGACGAA 300

306

CTCGAG

- (2) INFORMATION FOR SEQ ID NO:283:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

AATCAATCAA	CTAGGCATAT	GACACAGTAG	TCCATTATAA	AAGAAGACAT	ACATCCAGCA	60
CCATCAACTA	ATTCTTAAGA	TAAGTTATCT	GGGAAAATTG	AAGAACAAAT	AAATTCAACG	120
AAATACTGTA	AAGTGAACGA	AGACATAAAA	CCAAAGAAAA	CTGAGGCCAT	TTCTGCCAAG	180
AAAGGAACAG	CAAAGAGTAA	AGATGAAAAA	TATTCTAAGA	TAATACCAGA	AAAAGATAAT	240
TCCTACATGG	ACAAAGATGA	GCATGGTTCA	TCCTCTGAAA	GTGAAGATGA	AGCGCTGGGT	300
AAATATCATG	AGGCCTTATC	CAGAACACAC	AATTCCGGAC	TACCACTCGA	G	351

- (2) INFORMATION FOR SEQ ID NO:284:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

AAGTTAAAGG	TATTAAATAA	ATGAGTTTCT	CCTTAATTTT	GTTAATGCTC	TTTTAGCTAA	60
TAAGACTTTT	TCTAGAGTTA	CATATTTTAA	TCTGTTTCAT	TTTTATTTTT	TCCTTTGGTT	120
TTATATTTT	AAAAGCCATT	ATATCCCTCC	CACTGGTAAC	ATACACATAC	ACAGACACAC	180
ATCTATTTCA	AATGAATACT	TACTACTTTA	TCATTTTCAG	TCTTAATTGT	ACT	233

- (2) INFORMATION FOR SEQ ID NO:285:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GCGGCGCCGC	AGCAGTTCCA	GGAAGGATGT	TACCTTTGAC	GATGACAGTG	TTAATCCTGC	60
TGCTGCTCCC	CACGGGTCAG	GCTGCCCCAA	AGGATGGAGT	CACAAGGCCA	GAATCTGAAG	120
TGCAGCATCA	GCTCCTGCCC	AACCCCTTCC	AGCCAGGCCA	GGAGCAGCTC	GGACTTCTGC	180
AGAGCTACCT	AAAGGGACTA	GGAAGGACAG	AAGTGCAACT	GGAGCATCTG	AGCCGGGAGC	240
AGGTTCTCCT	CTACCTCTTT	GCCCTCCATG	ACTATGACCA	GAGTGGACAG	CTGGATGGCC	300
TGGAGCTGCT	GTCCATGTTG	ACAGCTGCTC	TGGCCCCTGG	AGCTGCCAAC	TCTCCTACCA	360
CCAACCCGGT	GATCTTGATA	GTGGACAAAG	TGCTCGAG			398

- (2) INFORMATION FOR SEQ ID NO:286:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs(B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

GAATTCGGCC	TTCATGGCCT	ACACCCAGCC	AATTTTTTTG	TATTTTTAGT	AGAGACGGGG	60
TTTCACCATG	TTAGCCAGGA	TGGTCTCTAT	CTCCTGACCT	CATGATTTGC	CCGCCTCGGC	120
CTCCAAAAAA	AGAACATTTT	ATATTTGAGT	GCTATTTCTT	TTGCGGCACC	AAAACTTTAT	180
AACACACTGC	CTTCTGAATT	TTTTTTTTG	GTTTCTGCTC	AGCTCATTGT	TAATCATATT	240
GTTCCCATGT	ATGTCATGAG	TTATTTTTCT	CCTAGTCTTT	TCAAAATTTT	CTTGTCTTTG	300
ACTTTTAACA	GTTTAATTGT	AACAGTGTAT	ATCTTTAAAG	TTAAATTCAT	GCTTGTGAAT	360
TTTTATAAGA	GCCACAAAGG	CCTTCCTCTG	TGTTTTGTTT	TTGTTTTTGT	TTTTGTTTTC	420
ATTTTTGAGA	CAGGCTCTCA	CTGTCCCTCA	GTGGCTCTCG	AG		462

- (2) INFORMATION FOR SEQ ID NO:287:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

TGGACAGTCT	AGAAGATGCT	GTGGTGCCCC	GGGCTCTGTA	TGAGGAGCTG	CTGCGCAACT	60
ACCAGCAGCA	ACAGGAAGAG	ATGCGCCACC	TCCAGCAGGA	GCTGGAGCGG	ACTCGGAGGC	120
AGCTGGTACA	ACAGGCCAAG	AAGCTCAAGG	AGTACGGGGC	ACTTGTGTCT	GAAATGAAGG	180
AGCTCCGTGA	CCTTAACCGG	AGGCTCCAGG	ACGTGCTGCT	CCTGAGGCTT	GGCAGCGGTC	240
CCGCCATTGA	TCTGGAAAAA	GTAAAGTCAG	AATGTCTCGA	G		281

- (2) INFORMATION FOR SEQ ID NO:288:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

AATGGAACTG	CTGACACAAT	ACTCGTGTAA	CTGTGTGGAA	CCGCATAATC	CCAGCAATGG	60
CACATTGAAG	GAATGGAGGG	AATCCAATAT	TTCTGCCTCT	GACATAATTT	GGGAGAACCT	120
AACTGTGTCA	GAATGCAAAT	CATTGCATGG	AGAGTATGTT	GGACGGGCCT	GTGGCCATGA	180
TCACCCATAT	GTTCCAGATG	TTCTATTTTG	GTCTGTGATC	CTGTTCTTTT	CCACAGTTAC	240
TCTGTCAGCC	ACCCTGAAGC	AGTTCAAGAC	TAGCAGATAT	TTTCCAACCA	AGGTTCGATC	300
CATAGTGAGT	GACTTTGCTG	TCTTTCTTAC	AATTCTGTGT	ATGGTTTTAA	TTGACTATGC	360
CATTGGGATC	CCATCTCCAA	AACTACAAGT	ACCAAGTGTT	TTCAAGCCCA	CTAGGCTCGA	420
G						421

(2) INFORMATION FOR SEQ ID NO:289:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

AAGCCAATGG	CTGGTCGTGA	TCCTGAATGC	CAACGCACAG	AAATGATTAA	GAAAGAAGAA	60
GAACGTTTGA	GGGCTTCCAT	ACGTAGGGAA	TCTCAGCAGC	GCCGAATGAG	AGAGAAACAG	120
CACCAGCGGG	GGCTGAGCGC	CAGTTACCTG	GAACCTGATC	GATACGATGA	GGAGGAGGAA	180
GGCGAGGAGT	CCATCAGCTT	GGCTGCCATT	AAAAACCGAT	ATAAAGGGGG	CATTCGAGAG	240
GAACGAGCCA	GAATCTATTC	ATCAGACAGT	GATGAGGGAT	CAGAAGAAGA	TAAAGCTCAA	300
AGATTACTCA	AAGCAAAGAA	ACTTACCAGT	GATGAGGTAA	GACCAAATTT	ATTCAATTCT	360
AGGGGTTTAT	CCTGTACTCA	GGAGCCAACT	GCTTTGAATG	AAAAGCTCAC	ACTCGAG	417

- (2) INFORMATION FOR SEQ ID NO:290:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

CAAGCATACA	ATCAACTCCA	AGCTCGGTAT	CACCTGAGCC	CAGGAAGTGG	AGGCTGCAGT	60
GAGCTATGAT	CAGTAAAACA	CAAGACAGGT	TCACTGGCTC	CCATCCCAAC	CCGGACCAGC	120
TCCCTAGTAT	AACAACTCAC	ATGCATGTGG	ACTATACCCT	TACAGCCTTC	TTCTGTGTGT	180
TTATGTGCAT	ATATGTAGCC	ATAGGAAAAA	AAATCAAAAT	CCTTTGGTGT	TCTTTCTTAT	240
TTTTTCAAAT	ATTTCACCTG	CCCCATTCTC	TTTCCTTTCT	CCTTCTAGTA	CTCCCATTGC	300
ATGCAGTTCT	CGAG					314

- (2) INFORMATION FOR SEQ ID NO:291:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

GTGTATGTGG	GGGGTAAGTG	TGTGTGTGTG	CGTGTGCGTG	TATGTGCACG	TGTTGTGTGT	60
GTGCGCCTGC	ACACGGAGAG	CCCACTCATA	CGTAGCAGAA	AATCAAATGG	CCCCAAATCA	120
GAAACATGGC	GCATGTGAGC	ATGCCACTTC	TTGTGTGCCT	GTGACTGTTC	AGAATGTACA	180
CGGCCCTGCA	GCTCCCGAAG	GCCAGCTCTG	CTGCAACCCC	TCCTCTGTCC	AACACAGTCC	240
TCACTGGTGT	CTTTTCCTCT	TCAAATCTAC	AGCATTTCTG	ATCTCTGCAA	ACAATTTAAC	300
CCAAAACCAA	GTTCTGGCTG	ACAAGGCTAC	ATCTTGTTTC	TTGTGCGTGA	TTAGCCTCGA	360
G						361

(2) INFORMATION FOR SEQ ID NO:292:

	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 237 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:	
AAGTCT CACTTT	TGAAT TCTAGACCTG CCTCGAGTCG ATGCACCGAA AAGGGTGAAG TAGAGAAATA ICCCC GCTGAACTAC TATGAGGTCA GAAGCCTTGC TGCTATATTT CACACTGCTA IGCTG GGGCTGGTTT CCCAGAAGAT TCTGAGCCAA TCAGTATTTC GCATGGCAAC AAAAC AGTATCCGGT GTTTGTGGGC CACAAGCCAG GACGGAACAC ACTCGAG	60 120 180 237
(2) II	NFORMATION FOR SEQ ID NO:293:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:	
GAGTC' AGCCC CTTNA	CGGCC TTCATGGCCT ACTTTATTT TTTAATTATT ATTAGTATTA TTTTGAGACT TTGCT CTATCACCCA GGCTGGAGTG CAGTGAGCTG AGACTATGCC ACCGCACTCC GGGCG ACAGAACGAG ACTCCATCTC NAAAAAAAAAA AAAAAAATCT ATGTTCATGC CACCT GTTTCTGCAC ATAGCTGTGC AGTATATTCT TCTTCTAAGC AACGACCCAG ATCCA AACAAAAGTT CACAAATATG TAGTTATCCA AGGCACCTCG AG	60 120 180 240 292
(2) I	NFORMATION FOR SEQ ID NO:294:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 136 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:	
TCGGG	CGGCC TTCATGGCCT ACAATCTTTT AACTTTGGGG GTCACAGTTT TAGCCACCTT GGGGTG ACTGGAGCAG TAGGAGGTGT GGGGTCATTT TATGAATATA ATAAAATGGA	60 120 130
(2) I	INFORMATION FOR SEQ ID NO:295:	
	(i) SEQUENCE CHARACTERISTICS:	

(ii) MOLECULE TYPE: cDNA

(A) LENGTH: 264 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GAATTCGGCN TTCATGGCCT AAAATAACAC ACAATTAGTA TAGAAAAATT GCAAACACAG
ATAAAAGTCC TTTCCCTGTG AATTTCTGAA TGCACCTTTG AATATTCACA TCTTACTGCC
AAAATGAGAT TGTCTTGTGT GCCGTTCTGG AATTTGCTTT TTTCCAGCTT ACATGTTCTA
180
GGTCCTTCCA GATCAATAGC TGCACTCCCT CCTTCCTCTG CTGGTTTCTC AGCTCGATGG
240
GCTGTAAGTG GCATTACTCT CGAG
264

- (2) INFORMATION FOR SEQ ID NO:296:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GAATTCGGCC TTCATGGCCT ACAACCTCAT AAATCTCATT CTTAATTTCA CTCTAGGACA
GAATTATTGT AGCACCTGTG TTCTGTTATT TTAGATTCAT TTTAACTTAC CTAGACACGG
120
GTACTGTGGT AGTTGTAGAG GTACAGATGT TGAGTTCCCA TCCTCCTGGC TTAATGTCAC
TGGGGTTATT AATACACTTC ATAAGCATTT TAGGGACACC TGCTGTCTGC TCAACCCCCA
240
GCAAACTCGA G
251

- (2) INFORMATION FOR SEQ ID NO:297:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GAATTCGGCC TTCATGGCCT ACATCTGGTA AATTTTTCTT TCTGCCTGAG GAACACCCTT
TAGCATTTAT TTAGTCTGCT GGTGACCAAT TCTCATATTT TGTTTGTCTG AAAAATACCT
TTATTTTGTT TTAATTCTTG AAAGATATTT GCACTGGTGT GATTGGATTC ATGATTGCTT
ATTATTTTCT TTTTCTTTTT TCTTTTTTTGA GACAGAGTCT CGCTGTCGCC CAGGCAGGAG
TGCAGTGGCC CGTACTCGAG
260

- (2) INFORMATION FOR SEQ ID NO:298:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

GCTCTGAATC TATTTTCTAG GACATTTTT TCCCATTTAG ATTAAGCCAG AGAGAGCCCT
TTCTTGCCTC CCAAGAGTTT TTCTTTGTGT GACTGTTGGT ATTCTGAACC TCTTGGATTT
120

GATGCCTGGA ATTGTCCTAG AGACTCTCCT GATTTCTGTC TCATTCTTTG ATTTCACCCT GGGGAGCTGG GGAAGAGATA CCTTCCCATG GCATCACTTG TTAAGAGTGG ATCCCCCTTC CCCCTTTCCT TCTGTCCCCC TCGAG	180 240 265
(2) INFORMATION FOR SEQ ID NO:299:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 311 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:	
GAATTCGGCC TTCATGGCCT ACCAAAACAA AAGAAGAAAT CATTTCACTC ATGCTTAGAA AGATGTCAAG AGGATGGAGG ACTCACATTC TGTTAACTCT TCTGCCTGTA ATATATGCTT TAAACACTAA AAATGATGAG CATGAATCTG CAATTCAAGC CCTCAAAGAT GCTCATGAAG AAGAAATTCA ACAAATTCTT GCTGAAACAA GAGAAAAAAT ATTGCAGTAT AAAAGCAAAG TAACAGAGGA GCTAGACCTT AGAAGAAAGA TTCAAGTTTT AGAATCATCA TTAGAAGATC ACAATCTCGA G	60 120 180 240 300 311
(2) INFORMATION FOR SEQ ID NO:300:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 255 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:	
GCGATTGAAT TCTAGACCTG CCTCGAACTC GTGGCCTCAA GTGATCCACC TGCCTCACCC TCATCACCTG CCAAGTCCTA CCCATTCTAA CCCTGATAGC TCTTAAATCA GGTCTTTCCA CCTCAACCTC ATTATCACTG CTCTAGAGCT CAAGCCTTCA GTGTCCTTTC ACTTCCTGAA TTTACTGTCT TAGTGCTCTT GCTCACATTG TATTCTNTGC CCAAAATGCT CTTACCACTC CCNTTCTTTC TCGAG	60 120 180 240 255
(2) INFORMATION FOR SEQ ID NO:301:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 345 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:	
GAATTCGGCC TTCATGNCCT ACTTGGATTT ATCACAGTAG CATTTGTCTT CAATCTGTGT GTTAACTAGA AATCAAGGAA AGACATGAGG AGATTTGTCT ACTGCAAGGT GGTTCTAGCC ACTTCGCTGA TGTGGGTTCT TGTTGATGTC TTCTTACTGC TGTACTTCAG TGAATGTAAC AAATGTGATG ACAAGAAGGA GAGATCTCTG CTGCCTGCAT TGAGGGAGAT CCGCACGCAG CTGGTGGAGC AGTTCAAATG TCTGGAGCAG CAATCAGAGT CGCGACTGCA GCTGCTTCAA	60 120 180 240 300

345

GACCTCCAGG AGTTTTTCCG CCGGAAAGCT GAGATTGAGC TCGAG

- (2) INFORMATION FOR SEQ ID NO:302:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

GAATTCGGCC	TTCATGGCCT	AATCCTCCAG	ATTATTATGG	ATATGAAGAT	TATTATGATT	60
ATTATGGTTA	TGATTACCAT	AACTATCGTG	GTGGATATGA	AGATCCATAC	TATGGTTATG	120
AAGATTTTCA	AGTTGGAGCT	AGAGGAAGGG	GTGGTAGAGG	AGCAAGGGGT	GCTGCTCCAT	180
CCAGAGGTCG	TGGGGCTGCT	CCTCCCCGCG	GTAGAGCCGG	TTATTCACAG	AGAGGAGGTC	240
CTGGATCAGC	AAGAGGCGTT	CGAGGTGCGA	GAGGAGGTGC	CCAACAACAA	TGATCTCGAG	300

- (2) INFORMATION FOR SEQ ID NO:303:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

GAATTCGGCC	TTCATGGCCT	AAAAAAAAGA	AGTTTATTTA	AAGAAACTCT	ATAAGAGCAG	60
CTTGGATTTT	ATATCTTTAG	ATCCAGAGTT	TTTACTTTTC	TGGAATTAAA	TATAATTGTT	120
TGGAATTTAC	TCTTTATTGT	TGAATTTTAA	AGCGTGACTA	AAGTAGTGCT	TCTTAAGATA	180
ATTGTCATGT	GTTTTTGTTT	TGTTTTGTTT	TGTTTTTTGG	TGCTGAGTGT	TGCTCTGTCG	240
CTCAGACTGG	AGCTCGAG					258

- (2) INFORMATION FOR SEQ ID NO:304:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GAATTCGGCC	TTCATGGCCT	ACAATTCCGA	TAAAGTTTAA	GGTCAGCTGA	TGAAGAACAC	60
TCAAACCAAA	GTCGCCCATT	GGAGGAGCGC	CCTACCTCAC	AGGAATAGGC	CTGCATTATT	120
AGTATACCTT	CTTCATTCAG	TTATTGTTAT	TCTTATGGAA	ACAACCCATG	GGAAATGTAG	180
CCTTGGCATG	ACTGTATCAA	TGGATTCAGA	GAGCAGTAGC	GGGGACCCCC	CCAGTCAATT	240
ACGTTCCACA	GCAAGTCTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:305:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

GAATTCGGCC TTTCAT	GGCC TAAATCTCAT A	AAATAGAAAG	NAAAATAATC	TAGAAATTTT	60
TCAAAGCTAG TACTCT	TTCT CCTTATAAAT G	GTACACAATT '	TTAATCTTTT	TACAAATTTA	120
TTTAACTGTA CCTACT	GTAC TTATTGTAGA T	TTCAATGACG	CAGTTAAGTC	ATCACCCAAG	180
GATTTATGAA TTTGAG	ATTA CTGACCTGTT T	TTCTTCATAT '	TGCATTCACA	TCAATATTTG	240
TGAATTTGTT GTTCAG	CTTT TCATTCAAAC A	TTATAAAAA	CCCCCAAGAA	AACTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:306:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GCGATTGAGT	TCTCCCTGCT	GGTTCTTTTG	AATCACACCA	AATGAATGGC	TTGCTACTGT	60
TCCCTCACAC	CTTCATATTG	TCCATGGTTT	TTCCCACCTC	CTTAGCTATA	CAGCTGCTGT	120
TCCTCCTGCC	TAAAATGTCT	GAACATTCCC	TCAGTGTTCA	GCTCAGCCCA	CATCTTACAT	180
CTTCCCTAAG	GATGTTTTTC	TGCTGCTATC	ATTCATTTTC	TTCCTATGAG	TTCCTCTGTT	240
ATATTGCGCC	ACCAGAACTC	GAG				263

- (2) INFORMATION FOR SEQ ID NO:307:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GAATTCGGCC	TTCATGGCCT	AGCCCCGACT	AGCTTTGCCC	TAACTCCTTC	ATCAAAAGAC	60
CCCCCGCCAG	CTTCCCACAC	CTCATACGCA	GCCACATCTG	CCCTATTCTC	CATGCTTTCC	120
AGCTTGCCTG	CCCTTCCTCA	TCTCTCCCTG	CCTGTGCAGA	CCTCCACCCT	TCTTTCCTCC	180
ACCCCTCCAT	CCCCCAATGC	TTGTAGACCT	TCCATTCATT	CCGTCTCATC	GTGCGTGGTC	240
TCTGATCGTC	CATCACCTGA	CCTCGAG				267

- (2) INFORMATION FOR SEQ ID NO:308:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GAATTCGGCC	TTCATGGCCT	AGCCAAAATC	ACAAGAAAAA	TAACTTTGAC	TTTGAAAACA	60
AATAAGTTAG	AAATGCAGTG	TTTGCACTTC	GTGGTTTATG	TTTGCTTTGG	TGGCCTCTCA	120
TTCCCACTTA	GCCTCAGTCT	CCAGGGCCTG	GGCTCCACCA	AGGAAGACTC	CATCTGCTCT	180
CTCTATTTGC	ACACTGGGAA	CTTTTTTCCC	CAAGGTACAG	GATATGATTC	AGGGTTTATG	240
GATGACCTCC	CACCCTCGA	G				261

- (2) INFORMATION FOR SEQ ID NO:309:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

GAATTCGGCT	TCATGGCCTA	CCTATTCCCA	AACTTTAAAT	GTTGTCTACC	AAATACTGAC	60
AATTATGAAA	ATTCTACCAG	TAGAACACAC	CTCCCCTTTG	AGCTCCAGAG	CACATGCTTG	120
ACATCTCATA	TTAGAAAGAA	TCTTGATTTC	CCCTCCAGTC	TAGTCTTTCA	TGTTTTGTTT	180
TTCTTTGTGA	GAGTCTCCCT	CAGCCTGCAA	TGGCGTGATC	TCGGCTCACT	TCAACCTCCC	240
GTGCTCGAG						249

- (2) INFORMATION FOR SEQ ID NO:310:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GAATTT	STTT	NAAAAAAAA	AAAAAAAAA	AGGGCNGGGG	GGAAAAAAAA	AAAAAAGAAC	60
TCCTGG	AGAG	GGAAATAGCA	AATGTGTCTT	GCCTTTTGTT	GCTCTCTCTC	TCTTTTTTT	120
TCTCTC	GCTC	TCTTTCTTTC	TCTTCTTCTC	TCTGTTTTTA	AGTCAAGCAT	TGGTCTCGAG	180

- (2) INFORMATION FOR SEQ ID NO:311:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 742 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

NNNANNNNN	NNNNNNNNN	NNANNNANN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	60
ANNNNNNNN	NNNNNNNNN	NANNNNNNN	ANNNNNNNA	NNNANNNAN	NNNNNNNNN	120
NNNNNNNNN	NNNNNANNNA	NNNNNNNNN	NNNNNNNANN	NNNNNNNNA	NNNNNNNNN	180
NNNNNNNNN	NNNNANNNN	CNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NANNNNNNN	240

ANNNNNNNN	NNNNNNNAN	NNNNNNANNN	NNNNNANAN	GNANNNNNN	NNNNNNNNN	300
NNANANANN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNC	CCCCTTTGTC	360
ATNGTTNTCG	TTCCCNTTCT	TCCTTGTTTC	TTTTTCGGCA	CAATATTTCA	AGNTATACCA	420
AGCATACAAT	CAACTCCAAG	NTCGGAATTT	TAATTACTTC	ATGGCCTACT	TGATGCAGGC	480
TGGAATGTTA	TCCCTGGGGT	GTGCTTGGAC	CCCACCTGCT	TTCTTTCTCT	CCTGCCCCTC	540
CCCTACTCTC	ACTGTAATTT	ATGGACCCTG	CCCGCCTGCG	TGTTGTGTGT	ATGTCCTGTG	600
CCTTTTCTCA	CTATTGTTTG	GGTGTGGGAG	GGGGTGGTTT	TTCACTGAAA	AGGGGGTAC	660
ACCTATAGCT	TTCTTGATGT	TCAATCAATC	AGTCACTGTG	TCCCAGACAT	ATTCAATAAA	720
CACAGATTGG	TACCATCTCG	AG				742

- (2) INFORMATION FOR SEQ ID NO:312:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

GCGATTGAAT	TCTAGACCCG	CCCCAGGAGC	CTCCAGCTGC	CTAACCAGTG	CCATTCTTTC	60
ACAACACGAT	TTTCTACAAA	TCTACAGCAC	AACCGAGTTT	GTAACCCGTG	GGTTAGTATG	120
AGGACCGGGT	TCGTGTACTC	TCTGTATCTC	CTCTTAAGCT	TCGTCCAGGG	TTCTTTATTT	180
TTGTCTGCTG	CCAATGTCGT	CTCGCATGCC	TGCACCCTCG	CATGCACGCT	GCCCGCATGC	240
CACGTGCCAC	GCTGTAGCCA	CATCCTCGAG				270

- (2) INFORMATION FOR SEQ ID NO:313:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

GAATTCGGCC	TTCATGGCCT	AGTTGATGTC	CTCTCATATT	TTGTTGTTTA	AATACGCAGT	60
GTGGTGGTTG	TTATTTAGGA	CTGCCTCTGC	TCTGACAGAT	GTGTCTACTC	TACAGAGAGA	120
					ATGACCTTTC	180
TGCACTCTGC	CTGGCTATTG	GTTACAGTTT	ACATTCTACC	TTCTCCCAAG	GTATTGAGGG	240
	GCAATTCTCG					262

- (2) INFORMATION FOR SEQ ID NO:314:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

GAATTCTAGA CCTGCCTCTC CTGACACGGG CCACCAAACC CCTTACCTGG TTCCTTGCTG 60

TAAAACTTCA CCAAATGAAG CCAGAGTTGA TCATGACCCT CTCGTGCTCG AATCCCTTCT GGGCTCCCCT CTGCCCCCTG CAAAGCCCAC ATGATACCAC AGAGAAGACC TGTCCCCTGC AGGCCAGCTG CTTCAGCCTC TTCCCTCACA CACATCGTCC CGCACACGGC AGCCACCATG GACTCAACAT CCCCGACACA CGGTGCTGCC CTCTGCATGC ACCGACCCCC TGCCCCTCCC ACCAGCTCGA G	120 180 240 300 311
(2) INFORMATION FOR SEQ ID NO:315:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 232 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:	
GAATTCGGCC TTCATGGCCT ACCTAGGTGC TTTTTAAAAT ATTCAGACAA ATATCTATCT TACATTGATT AAACCCGTGT AAATTCATTT GCAGTATCTA CATCGAATGT CAAAAAAGTA TACTTATTTT TGTTCCATAC TTATGTACAA TTTTTTCCCT CTTCAGGCTT TTTCATTTAC CTTTTTGAAA AAGCACTTAC TCTCCCCTTC CCTATCACCC CATCCCCTCG AG	60 120 180 232
(2) INFORMATION FOR SEQ ID NO:316:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 205 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:	
GAATTCGGCC TTCATGGCCT ACAGTTGTTC ATACTTCCTT TACAAATATA AAGATAGCTG TTTAGGATAT TTTGTTACAT TTTTGTAAAT TTTTGAAATG CTAGTAATGT GTTTCACCA GCAAGTATTT GTTGCAAACT TAATGTCATT TTCCTTAAGA TGGTTACAGC TATGTAACCT GTATTATTCT GGACGGACAC TCGAG	60 120 180 205
(2) INFORMATION FOR SEQ ID NO:317:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 299 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:	
GAATTCGGCC TTCATGGCCT AGGGCTTGTC TTTTTCATTG TTGAGTTGCA GGAGTTCTTT ACATATTCTG GATACTAGAC CCTCATCAGA TATGGTTTTA AAATACTTTC TCTCATTCTT TTCACTTTCA AGTATCCCTT TGATGCACAC ACCCAAAAAA GCAAATAGTG TCCAATTGCA TTCTTTGATG AAGAAGAATA CAAGCAGTAA GTCAATTACA GCCTATTTTT TTCTTTTCTT	60 120 180 240 299

(2) INFORMATION FOR SEQ ID NO:318:

(A) LENGTH: 95 base pairs

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:	
GAATTCTAGA CCTGCCTCGA GCTCCAGCTG CCAACACCCT TGGACACAAT ATTCCAGTCT CCACTGCCCA TCTCATGTGG TTCAGGTTCC TCGAG	60 95
(2) INFORMATION FOR SEQ ID NO:319:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:	
GATGCTTGGC TCACTCCCG CTACTGGCCC CCAGACTTTT CCACCCCAGG AAATGTCTCC CCTGCCTGCA GCTTCAGCGA AAGCCCAGGA GGCAGGCCAA TCACTTGAG	60 109
(2) INFORMATION FOR SEQ ID NO:320:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 253 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:	
GAATTCGGCC TTCATGGCCT ACACATTTCT GTACCTGGAA AAAAAATGTA TCTTATTTTT GATAATGGCT CTTAAATCTT TAAACACACA CACAAAATCG TTCTTTACTT TCATTTTGAT TCTTTTTAAAT CTGTCTAGTT GTAAGTCTAA TATGATGCAT TTTAAGATGG AGTCCCTCCC TCCCTACTTCC CTCCCCACTC GAG	60 120 180 240 253
(2) INFORMATION FOR SEQ ID NO:321:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 334 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:	

GAATTCGGCC	TTCATGGCCT	AGGTTGTAAG	TGATTTTATT	TTTTCTTTTC	TATTTTCCAG	60
TGTTTCTGTA	ATGCTTTCAT	ATTTCTTTTG	GTAGTTAGAA	AATAAAGGCT	AATTTTTAAA	120
AAGAATATCA	TAGTCTAAAA	AATTAAAGGA	TGCATAGAGT	TCCCTCTTGA	CTATGTGACA	180
TCTAAACTGA	ATGAACTGTC	TGCGTGGCAC	AGTGGAACAG	CGCAGTCTCA	GGATTCTGAC	240
AGATTTTTGG	ATCCCAGCTC	TACCACTAAC	CTTGGGCAGG	ATTTTAGTCC	CTCTGAGACC	300
TGCTTTCTCG	ATTGAATTCT	AGACCTGCCT	CGAG			334

- (2) INFORMATION FOR SEQ ID NO:322:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 226 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

GAATTCGGCC	TTCACCTAAA	TACTCCTCCT	TTTGTATCAT	TCAGCCTTTT	GTTTTAGTTT	60
GGTAAGTTTT	AAGAAATTTC	AGCAGCAAAG	TTGTTATTCA	GTGGGCACGA	TGGACTCCAA	120
ATGCCTCAAG	TTATGTATAC	CTGTGGAGGT	CACGTACTTC	CAAATTGTTC	TCTTCCTCAT	180
CTTCTCCCTT	TACCTGCACG	CCCAGGTGCG	CCAGCCGGGC	CTCGAG		226

- (2) INFORMATION FOR SEQ ID NO:323:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 164 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

GAATTAAAAT	AAACAAAAGG	CAGCCAAGGA	TGAAAGGATT	TAGTTCTAAG	ATGTTTCACA	60
GTTGTGATTT	GTTTATTTTA	ATCCTTAGTA	GTAAATTAGT	ACTAGAAGGA	TCAGGTATAT	120
CTTCCTTAAT	TCTTCCCAGG	GGAGAGAAAG	TCCCATTTCT	CGAG		164

- (2) INFORMATION FOR SEQ ID NO:324:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324.

GAATTCGGCC	TTCATGGCCT	AAGCCTATGT	TGATCTTGAA	CTCCTGGGCT	CAANCCNTCC	60
TCCTGTCTCG	GCCTCCCAAA	TTGCTGGAAT	TATAAGCACA	TTACACAGTG	CCCAGTCTAC	120
CTACATTTTG	ACAGACATAT	AATATTCCAT	GGCATGGTTA	CATTATTCAG	TTAAGAATGT	180
TCCCGGTTTT	CTCTAAGATA	ATGCTGCCCA	TCTGTGTCTC	ACTCTGGACA	TGTAGAGTAC	240
CTGCAAAGAC	TTGGACTGCT	TGAGCAGAGG	GCCTGCTTTT	GTTTTTTGTT	CTTCCTGCCT	300
GTTGTAACTT	GATGCTGCCA	AATGATCCTC	TTAAATGATT	GTACCACCTT	CCCTGCCACC	360
ACCAGATTTT	AAGGATTCTC	TGTACCTCCC	AACACATGAT	GACATCATAC	ATGAAAAGTT	420

•	
TTGCCTGCCT GATGGAATAA TTGAGTCAAG AAATAGGATG CTAATGGCAT CTTCGCTTAC CCGGTCTCCT CGAG	480 494
(2) INFORMATION FOR SEQ ID NO:325:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 295 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:	
GAATTCGGCC TTCATGGCCT AGTTGGGTGT TGAGCTTGAA CGCTTTCTTA ATTGGTGGCT GCTTTTAGGC CTACTATGGG TGTTAAATTT TTTACTCTCT CTACAAGGTT TTTTCCTAGT GTCCAAAGAG CTGTTCCTCT TTGGACTAAC AGTTGTCCTG ATGAATAATT TCATTTTCCT CAAGTTTATG ACACTCGGAA CGTCAAGAAC TGGAGGTTTG TGCAATTTGA GACCGGTCGG CACTGTGCAG AGATCAGAGT ACTAAGAGAC AGAGATTAAA ATGGCTATCC TCGAG	60 120 180 240 295
(2) INFORMATION FOR SEQ ID NO:326:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 418 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:	
GAATTCGGCC TTCATGGCCT ACAAGGATAG AATTCATTCC ACCTATATGT ACTTAGCAGG GAGTATTGGT TTAACAGCTT TGTCTGCCAT AGCAATCAGC AGAACGCCTG TTCTCATGAA CTTCATGATG AGAGGCTCTT GGGTGACAAT TGGTGTGACC TTTGCAGCCA TGGTTGGAGC TGGAATGCTG GTACGATCAA TACCATATGA CCAGAGCCCA GGCCCAAAGC ATCTTGCTTG GTTGCTACAT TCTGGTGTGA TGGGTGCAGT GGTGGCTCCT CTGACAATAT TAGGGGGTCC TCTTCTCATC AGAGCTGCAT GGTACACAGC TGGCATTGTG GGAGGCCTCT CCACTGTGGC CATGTGTGCG CCCAGTGAAA AGTTTCTGAA CATGGGTGCA CCCCAGGGAG TGCTCGAG	60 120 180 240 300 360 418
(2) INFORMATION FOR SEQ ID NO:327:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 588 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:	
GAATTCGGCC TTCATGGCCT ACAGACATCT AATCGGAATC TTGCTCTTGT TGCCCAGGCT GGAGTGTAAT GGCACAATCT CGGCTTACTG CAACCTCTGC CTCCTGGATT CAAGTGATTC TCCTGCCTCA GCCTCCCAAG TANCTGGGAT TACAGCCCTG AAAACCACTC GCTTGCAGAG CGCTGGATCA GCAATGCCTA CTAGTTCTTC ATTCAAACAC CGGATTAAAG AGCAGGAAGA CTACATCCGA GATTGGACTG CTCATCGAGA AGAGATAGCC AGGATCAGCC AAGATCTTGC	60 120 180 240 300
TCTCATTGCT CGGGAGATCA ACGATGTAGC AGGAGAGATA GATTCAGTGA CTTCATCAGG	360

CACTGCCCCT	AGTACCACAG	TAAGCACTGC	TGCCACCACC	CCTGGCTCTG	CCATAGACAC	420
TAGAGAAGAG	TTGGTTGATC	GTGTTTTTGA	TGAAAGCTCA	ACTTCCAAAA	GATTCCTCCA	480
TTAGTTCATT	CCAAAACACC	AGAAGGAAAC	AACGGTCGAT	CTGGTGATCC	AAGACCTCAA	540
GCAGCAGAGC	CTCCCGATCA	CTTAACAATT	ACAATGCGGG	AACTCGAG		588

- (2) INFORMATION FOR SEQ ID NO:328:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

GAATTCGGCC	TTCATGGCCT	ACGACTGGGG	GAAATGTCTA	TTCTCCTGTG	TATCTCTGGG	60
CTTTTCTTGT	TTTTGGCTGC	CTCCTGCTCA	GTTCCTCTCT	TTAGGTATTT	AGTAAAGCGT	120
TCATGTAATG	TCATTCCTGA	GGACCCAAAG	TGATGCTCTT	TAACATGGTG	AACAATGGTC	180
ACTATATGTT	GGGCAAACAG	TTCTGAGGGG	CTACGCTGAG	ACTGAGCTGA	TTGTATGTGC	240
TGGAAAATGG	AACGAAACTC	CTGTTCCTTT	TTGTTGCTAT	GGACTAGATC	TCGGCAAAGC	300
TTGCGTTCCT	GAGCCAATAA	GCCACTGGGT	CGTGCGAGGT	CCTCATCAAA	AGAGTCCATC	360
CGGACATTGA	CCTGTGCCTC	TCGAG				385

- (2) INFORMATION FOR SEQ ID NO:329:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GAATTCGGCC	TTCATGGCCT	AGCAGTTCAC	CACTGCAAAA	CCACGGGGCT	GCGTGGAGGT	60
ATTCATGGGA	CACCGAGTGG	TATCACTAGC	AGCGGACTCT	GCATGCTTAC	TTAGAGCATA	120
AAAGGATAGC	ACCCTTGGCC	ATTGCCTGAC	ATGAACTCAG	TTTGGAAATT	GCAGAGGTGT	180
GGAGAGCCAT	GGATGGGTTT	TATAATTTAT	TCTAATGTAA	TCTCTGTGCT	AAAGGCTGTT	240
TGAAAAAAAT	AATGAAGTTG	ATGTTGCTTA	AGTTATATGC	AAATGTAAAC	TGGTCTTCCT	300
TCAAGATGTT	TGGAATGGAA	TGAATGCCCT	TCCCCTGGGT	ACCTCCCAAT	ACCTACCCTC	360
AAAAGAGCTC	CAGTAAGGCT	TCCTTATCTT	TCCTTGCCCT	GCTTCCTACA	CTGCTGCTGC	420
AGGTGTCTCT	GGGTGATTGT	GGGGGAAACC	ACTGTGGTTA	AGCACCAACA	CCAAGACTCG	480
AG						482

- (2) INFORMATION FOR SEQ ID NO:330:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 532 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

GAATTCGGCC	TTCATGGCCT	AAGGCCTTGG	TGCCCTGTGG	GTGGACTCTG	GGGAGGCCAG	60
GGGCCCAAGG	CCACCTTCTA	GGGCCTGAGG	AGCCCTCTGA	GACCTGCACA	CCCACCCCAG	120
GGAGCGCCCC	TCCCTCCACC	TCTGTGCCCC	CCCAGTGACT	CTCGAACCTC	TGTCTGTTTT	180
GCAGATTCAT	CCGGAAGGGC	CGCCAGCCAG	TGGATTTCCC	GGGCCCTCAG	CCCTCTGGAG	240
TGTACGAGTT	TTGGAGAAAC	CTCTTCCTCT	GTATATGCTT	TTGACTTTCC	TGGACTGATG	300
TAAAAATACT	CTTTTCTTTG	ACCTGTTTAT	TTTTAAGACA	CGACGTGATT	GTGTCAGCTT	360
TTATTTATT	GCTGAAGTAA	ATTTTCAAAT	GTTTTATTAG	TTTTTTTGGA	TCTTTGTCTG	420
CTCATTTTGG	AGTTTTTGTA	ATTTTGATAG	GTGTTCTTTT	ATGCTTTGTA	TTGTTTTCTT	480
AATGACTTTT	ACCTTAGTTT	TTAACAAACC	CATAGTACAG	TGTACCCTCG	AG	532

- (2) INFORMATION FOR SEQ ID NO:331:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

GAATTCGGCC	TTCATGGCCT	ACATTTTTGG	АААААААА	ATCTACTTTG	TGTATGTGTG	60
GGGTGTGGGG	TGTGAGAGAT	ACATTCCTTT	TTNGTGTCTA	AATCTCACAG	TCCACATATG	120
ACTTTCCCCA	CTTGAGAATT	CTCTCTCATC	TGTGTGGCTC	CCTGCATTCT	TATAAAAATAT	180
AATAAATAA	AATTTTAAAA	AGTATAAAGC	CGGTGCCATG	AGACCCTTGG	GTTGGGCAAA	240
GCCTGTGAAG	TTTGAACCGG	TTAACGCACG	AATACAAGGG	AGTGATTATT	ACAAGGCCAT	300
CCCGCTTAGC	ATCGGGGAAT	CATTTGGGGA	GAGAGATTCA	ATTTCATAAA	GATGATTTTC	360
AAGGGCTGTC	TCGAG					375

- (2) INFORMATION FOR SEQ ID NO:332:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

CAATTCCCCC	TTCATCCCCT	N CN CCCCCTC	N N CTCTCCNC	CCCTCATCAT	AAACATGCCT	60
						• •
CTTCTCCTAT	TGTCCTTCTC	CTCTCTAAAG	CAAGGTCATT	TCTGTGCTCG	TCAGGCAGTG	120
GCAGGGGTTG	GGAGGAGGAG	AGAGGGAAAC	ACTGTGGTCA	GGCTCTGGGG	AGAGTTGACT	180
ACAGTGTAGC	TCTTGGATTA	TTTATGAATA	TTGCCCTCAG	ATTTATTTTC	ACTCTGCTCC	240
TTCCATTCAT	ATTCCCAGAG	ACAACCAAGA	GCCGACTGTA	GAAAAAGACT	TCCAGACACC	300
TAGAATATAT	ATCAATAGAC	ACTGTTTAAA	AGGGGAGACT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:333:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

TGGCCTAAAG	GGGGTGGGTA	CTCCGGTGGG	GTAAGGTCAG	AAGGTCCCTG	TGCAGGGAGG	60
GACTGGTCCC	TTGAGAAGGA	ACAGAGGGCA	AATCCTGAAG	AGTCCTGGAG	GCCCAATGTA	120
GACAGCAGAA	GCTGGGAGCT	GACCTAGGAG	TGATCGGGGG	CCTGATCCAG	ACAGGACAGA	180
CACAGGCTGA	CACCGGAGAG	TCCCAGGTGC	CAACATGAAC	AGT/TAAGGCA	GGGGCTGACC	240
CCAAAGAAAT	CAGGGGCCCG	CAGCTGACCC	CGGAGGGTCC	CAGGTGCCGA	CCTAGACAGC	300
AAAGGCAGGG	CTGACCCCAG	AGGGTCCCGA	GCCGACCCAG	ACGACACAGG	CAGGGCTGAT	360
CCCGGAGGGC	CCCGCCCCGA	CCCGGACAGG	CAGTGAAGGC	ACAGGCAGGG	CTGACACTCG	420
AG						422

- (2) INFORMATION FOR SEQ ID NO:334:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GGGAACGAAA	GATGGCGGCG	GAAACGCTGC	TGTCCAGTTT	GTTAGGACTG	CTGCTTCTGG	60
GACTCCTGTT	ACCCGCAAGT	CTGACCGGCG	GTGTCGGGAG	CCTGAACCTG	GAGGAGCTGA	120
GTGAGATGCG	TTATGGGATC	GAGATCCTGC	CGTTGCCTGT	CATGGGAGGG	CAGAGCCAAT	180
CTTCGGACGT	GGTGATTGTC	TCCTCTAAGT	ACAAACAGCG	CTATGAGTGT	CGCCTGCCAG	240
CTGGAGCTAT	TCACTTCCAG	CGTGAAAGGG	AGGAGGAAAC	ACCTGCTTAC	CAAGGGCCTG	300
GGATCCCTGA	GTTGTTGAGC	CACCTCGAG				329

- (2) INFORMATION FOR SEQ ID NO:335:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GAATTCGGCC	TTCATGGCCT	AAAACAGATA	ACGCTATAGA	GAAAACACTG	TTTACTGAAC	60
AGTGCTTTGA	AACCACGAGG	GTGATCAGAG	CCCCATTTCG	CCTTCTAGAG	ATAAACCTGT	120
CTCCCTTCCT	GCAGAGCTAG	CTCCTCCTAT	TGCTTCTGGT	TGTCGTTTGT	CTTCAGTCTG	180
CTTCCTGCCA	GTGCAGCAGC	TCCTGCTAGA	TCTTGACATC	CTAGTGGCCA	GATCCCAGGG	240
GCGGTGCTGG	TCCTATCCGA	GCTCTCTGCC	TCATCTCCCA	TTCCTTTTTT	CCACACTCAG	300
TGTGTATTCT	CTTGGATTTC	CATACCCTGT	TCCTCCTACC	ATCCACCTCT	CTACCTCATC	360
TCCCGACCTG	CCTCGAG					377

- (2) INFORMATION FOR SEQ ID NO:336:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GAATTCGGCC	TTCATGGCCT	AGCAGGTCAG	GAGCCCGGGG	AAGGCCCAGA	GGTACTCCAA	60
AGGGGGCCGG	CTGGTATCTG	AAGGCCCCTT	GCAGTTAGTG	TGTTGTTGAG	CTGTGGGCAT	120
GAACATGCCA	CAGGCAGACA	CTGTTTAGCC	AGGGTTTTAA	GAAACACGGA	GGGTCCTGTG	180
GATCTGGAGT	TCATTTGTCA	GGACAGGGAT	GGGGACCCCT	CTGAAGTATT	CACTGTGGGC	240
TGAGGGGTGC	TGGCCACACA	ACCTCTGTGG	GAGGCATCTC	TTGCAGTGAA	GCTGTTGGTC	300
CTCAGTTCAG	TGCCCACTGA	GGGTAACCAG	GCCCCAGCTC	TGCACCCCCA	CTCGAG	356

- (2) INFORMATION FOR SEQ ID NO:337:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GAATTCTAGA	CCTGCCGCAG	CACAATCCCG	TGGACAGAGC	TTACTCCATC	TAACTCGTTT	60
TCAAGTGCAT	GATTTTCACT	TTCACTTTTC	CTTTTTCCTT	ATTATGTTGC	TTAACTTGTA	120
CAGTGGCAAC	TGAAATGCAT	TTCAGAAATA	GGAGGTTTCG	TCCAGCACCC	TCTGCAGCCT	180
TGGTGCCTGT	AGCTCTGGAC	TTCCCTGGGC	CTTTCCCTGT	GGGAGGGCCC	TGTAGACCAC	240
ATCAGGGTGG	GGTGGGGGTC	ACTTGGCAAA	AAGGGCCGAG	GTCTGGTGAT	GTGGTTCCCA	300
GGATCTGGAA	CCTCTCCCAC	CCCTCCTGCA	GTTGGACTGA	ATTCTTCCCT	TTCATCCGAA	360
GAAACCCACT	TGCTGTTTCC	AGCCAACTCG	AG			392

- (2) INFORMATION FOR SEQ ID NO:338:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GCAAGATGGC	GACCGAGACG	GTGGAGCTCC	ATAAGCTAAA	GCTTGCCGAA	CTAAAGCAAG	60
AATGTCTTGC	TCGTGGTTTG	GAGACCAAGG	GAATAAAGCA	AGATCTTATC	CACAGACTCC	120
AGGCATATCT	TGAAGAACAT	GCTGAAGAGG	AGGCAAATGA	AGAAGATGTA	CTGGGAGATG	180
AAACAGAGGA	AGAAGAAACA	AAGCCCATTG	AGCTCCCTGT	CAAAGAGGAA	GAACCCCCTG	240
AAAAAACTGT	TGATGTGGCT	CTCGAG				266

- (2) INFORMATION FOR SEQ ID NO:339:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GAATTCGGCC TTCATGGCCT AAACAATGAA TAAAGCCAAG CCAGTTCCTG CCCCCGTGGA 60

TGCAAGCTGC TAATGTCCAC	AAGACATTGA ACAAGTGATC AGAAAGATGT TGACTGCTGC AGCAGAGGGT TCATGAGTAT ATAACAAGTA GCCCTAACCA AAGCATTCTC TCCCTTGGTT CCATTGAGGT GACTGCTAAA TACTAATCCA TGACTCTATC CCTTGGCATT CATCCACTTA CCTGCCTCTC CAACCTCCCT GCCTCGAG	120 180 240 288
(2) INFORMA	ATION FOR SEQ ID NO:340:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 313 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:340:	
TTCACACTTT CCTCTGCCAC CCTCAATTCT	TTCATGGCCT AGTCTCTGCC ATGTTCTAAA CTGAAAACCT CCTAGTCAAC ATTCCCTGAT CCTCAATTGG TTCCCATGTC CCGTTAGTGT TTCTTGTAAG CACCGCAGAT CGAACTCTAA TCACATCTCA CCTGAATTAT GGAAAAGTCA CTCACCCATC CCAGCCTCCA CTATGGATTA ATATGCCTAA AGCAGAGCTG TGAGAAGAAT CTGAGAGGGA AGCAGCAGCA AACACAAGAG TCACTGGACA GAG	60 120 180 240 300 313
(2) INFORM	ATION FOR SEQ ID NO:341:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 284 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:341:	
AGTAGCTTAA CCAGTTCTCT CTCTGCTTGT	TTCATGGCCT AAGAAAAAAG GATAGACAAA TAGTATTTTT GTGATTTTAC AACTATAGGA TTTTTTTCC CCATTACTTT GCAACAACTG ATACTTTTGA TTCCTAAGCA TTTCTCCT TGAGCTATTA CCCAAATTGT CCTAGTTCTT CCCTCAGCTA TACACAGTCA CTGAGGCTCT GTGCTTGGCT TCTGTTCCTC GGGATTCCTC ATGTTGGAGT TCATCAAGCT CGAG	60 120 180 240 284
(2) INFORM	ATION FOR SEQ ID NO:342:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:342:	
TGGATGAGGG GTGCTTATTT CTGCCCATTG	TTCATGGCCT ACCACGATAG ACCAGCTGTA GCTCATTCCA GCCTGTACCT GTAGCCTCCC ACTGCATCC ATCCTGAATA TCCTTTGCAA CTCCCCAAGA AAGTGTTAAT ACTTTTAAGA GAACTGCGAC GATTAATTGT GGATCTCCCC CCTGCTTGAG GGGCACCACT ACTCCAGCCC AGAAGGAAAG GGGGCAGCT AAGAGGGAGC TGATATCATG AGGATAACAT TGGCGGAGG GGAGTTAACT	60 120 180 240

GGCAGGGCAC TCGAG 315

- (2) INFORMATION FOR SEQ ID NO:343:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GAATTCGGCC	TTCATGGCCT	AAAGATGTTA	GATATTACAA	TTTGACTGAA	GAACAGAAGG	60
CGATCAAGGC	CAAGTATCCG	CCAGTCAATA	GGAAGTACGA	GTGTGAGAGA	TGACTTACAG	120
TCTCTTCTGT	TTCACTTTTT	GGATGAATGG	CTTTATAAGT	TCAGTGCTGA	TGAATTCTTC	180
ATACCCCGGG	TGGGGAGAAG	AATTTTCATT	GTCCAAGCAC	CCTCAGGGAA	CAGAAGTCAA	240
AGCAATAACA	TATTCAGCAA	TGCAGGTCTA	TAATGAAGAG	AACCCG		286

- (2) INFORMATION FOR SEQ ID NO:344:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 545 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GAATTCGGCC	TTCATGGCCT	ACCTCTGTGA	TTAATTTAAA	TTTTATATCC	TGATTAATAT	60
ATTGTGACTT	TAGGCCCATT	TTTCATGTGC	TTCACTTTGA	TAGAGTTAAT	CCATAAAATT	120
GCTCTTTACT	TTAGCTTATC	AAATGAAGTA	TTATTTTGTG	GACTGGAGGC	CAAAAAGTCA	180
ATGTGAGCTT	CTCACAGGTT	TTTAAAGCTC	CACTAAAAAT	AATTATCCAC	TTGTCTTTAC	240
TTTTGTTGAC	CAGAATAGTT	GGTAACTCTG	CCAGAGCCTG	TACTTACCTG	CCAAAAACAA	300
TTAAATCTGG	TTAATGCCTG	AAACCAAATC	TCTCAGTCTC	AAGTGTTATA	CTATCCAAGT	360
TTTAAATGGA	AAGGTAAACT	GTGGAGTAAT	GAAATTTTGG	TTTTACTGTA	CCTTTTGCTA	420
TCAAGATAAT	ATTCATGTTT	GAAATCTTGT	CTTTATTTGG	AATTTAGTTA	CTGTCTGCTT	480
TTAACCTTTG	CTTTCCTAAA	GAAAGTTTGA	GATCCAGAGA	GTTCAAGGGA	TCGGGGAGTC	540
TCGAG						545

- (2) INFORMATION FOR SEQ ID NO:345:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

GAATTCGGCC	TTCATGGCCT	ACAATAAGTG	TGTTATACTT	GCTTTGGTGA	TTGCAATCAG	60
CATGGGATTT	GGCCATTTCT	ATGGCACAAT	TCAGATTCAG	AAGCGTCAAC	AGTTAGTCAG	120
AAAGATACAT	GAAGATGAAT	TGAATGATAT	GAAGGATTAT	CTTTCCCAGT	GTCAACAGGA	180
ACAAGAATCT	TTTATAGATT	ATAAGTCATT	GAAAGAAAAT	CTTGCAAGGT	GTTGGACACT	240

TACTGAAGCA GAGAAGATGT CCTTTGAAAC TCAGAAAACG AACCTTGCTA CAGAACTCGA

300 301

	(2) INFORMATION FOR SEQ ID NO:346:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 447 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:	
-	GAATTCGGCC TTCATGGCCT ACACATTTG ACAGCTTCCT TTCAGGTTTC TTGAGCTCTC AGAAAAATTA GAAGGAAGTG GGCTGGGGAT ATAGAGAGAG TCCAAACTAC CAACTAATGA ATGAATCTGA AGGAGACACA GAAGGGCAAG TAGAGTTTAG AGTTTGAGAG TGCAGGAAAG TTTTGAAATG GTCAGAACTG CCAGAGTAAT TTCTGAGATC TTACTAAGCA CTCTCCCACC GTTTGCCTTA AAGATACCCC TTCCCCCAA TTGAAACATC ACAAATCTGC AGAGCTCTTT AATCAGGTGT GTTATACACA ATGAATTTAA TTCTCTTATT GCCCTGGAAG AAAGATAAAC CAGATGTGGC CCTTGCCCCT TTTCAGTAAG TATTTGTTAG ATCTTCATTA CATTTTAGGC CTCCTAGGCC ATGAAGGCCG GCCTTCA	60 120 180 240 300 360 420 447
	(2) INFORMATION FOR SEQ ID NO:347:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:	
	GAATTCGGCC TTCATGGCCT AAAATTCGGC TGATTTCCCC CTTGGCTAGC CCAGCTGACG GAGTCAAGAG CAAACCAAGA AAAACTACAG AAGTGACAGG AACAGGTCTT GGAAGGAACA GAAAGAAACT GTCTTCCTAT CCAAAGCAAA TTTTACGCAG AAAAATGCTG TAATTTCTTG GGAAGATTTT AATGTACACC TATTTGTAAA GTCATCAGAA TAGTGTGGAT TATTAAATAT CTAGTTTGGA AGAAAATAAT TTATATAAAT TATTGTAAAT TTTTATGTAA ACTCGAG	60 120 180 240 297
	(2) INFORMATION FOR SEQ ID NO:348:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 241 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:	
	GAATTCGGCC TTCATGGCCT AGAATAAAAC AAAGCCTTTT CTGCCTTTTA CATTCAGTTC AGTAACCGTC AACACCCCAC CCATATACTC CCATACCATG AGGTGTAATT TTCAAACTCC TCGCATACTT TTAATTACTA GTTTAATTAT TTGCCTTCTC ACTGAAGTCTA TAATCTCACT TAGGGTAAGA ACAGAACTCA ATTACAGATG CTCAGTAAAC ACTGGAAGGC CGCGGCTCGA G	60 120 180 240 241

121	INFORMATION	FOR	SEO	TD	NO - 349 -
12.1	INFORMATION	ruk	350	10	110.349

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GAATTCGGCC	TTCATGGCCT	AGGGCTGCCC	AAGATTGTGA	AAGGTAAGTA	GTATCTTTAT	60
TTGGGGGTAA	CTTAATTATA	GATAAAAGAT	GGTCCAATAC	TGGAAACTGT	TCGTTTCTTC	120
CCTTGGATCT	AGTCTTCTTC	TGCTTTATAT	AGAATCCCAC	CATCATCTCG	AG	172

- (2) INFORMATION FOR SEQ ID NO:350:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

GAATTCGGCC	TTCATGGCCT	ACACGTGACA	GCCTTTCACT	TTTCAGATCA	CCTTCCTCAC	60
ACTGATGGTC	TCATACAACA	TCATTTTGAA	TGTCCTCAGC	TCTCTGCACC	ACCCACCCAA	120
CTCCACTCTG	GGCCACCGCT	GGTGTATCCA	AGATCAGGAC	ACCAGTCCCT	GGGCACCAGG	180
GAGTATGCTG	GCCACTGAAG	CAGCTTCGTT	TTTCCGGCAC	CCATGTTGTA	AAATCGACTC	240
CCCCAAACTC	GAG					253

- (2) INFORMATION FOR SEQ ID NO:351:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

GAATTCGGCC	TTCATGGCCT	AGAAAGTTTA	AAGATTAGCG	TACTGATTAT	GATGGGATTT	60
TTACTGAAAA	TTAGTTTTGT	CAGGCTGCTT	GCTTGTCTGT	GTATTTTCTA	TTCTAATTTA	120
GTTTTTATTT	TTATCAAAGC	TGTATTTACT	TATAATGTAA	AAAGTCAATT	AGTTTTCCAA	180
GGCTTATTAT	GGAAAACAGT	AGTTCCCCAG	GCTCCCATCC	CTATGTCCAA	CAAACTCGAG	240

- (2) INFORMATION FOR SEQ ID NO:352:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:352:	
War, bagoanca babanii 120M. Bag 15 No.332.	
GAATTCGGCC TTCATGGCCT AGACCTGCCT CTAAGCCTTT GATTATTCAG CTGCCACTGC	60
CTACAGGCCT TCTCCCATAT TCCTTCCTTC TTGCTAAGTC TGACTTAAAC TAGGCTTAGG	120
CACCAACTCC TATAGGAAGC CTTCCTTGAA CCTGGCCCTC TACTTTTCAC TCACTGACTA	180
CCACTCAATT AACTGAACGG TGAAAAGTAA CCCACAGCTA CGCATTCATG CAGACAACAG	240
AATTTTACTA CTTCTTCTCA CTACTGGTTC ATATTTCTGC AACCAGAAAA TATCATTTCA	300
TCCCTAGTAA CTATGGCTTC CATCTGTTAC TTCC	334
(2) INFORMATION FOR SEQ ID NO:353:	
(i) SEOUENCE CHARACTERISTICS:	
(A) LENGTH: 92 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(II) NOBECORD FILE. COMA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:	
GAATTCGGCC TTCATGGCCT AATAATGACT TGTTGGTTGA TTGTAGATAT TGGGCTGTTA	60
ATTGTCAGTT CAGTAGGCCA TGAAGGCCGA AG	92
(2) INFORMATION FOR SEQ ID NO:354:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 280 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO:354:	
GAATTCAGTT CCTTATATAT TCTAGTTATT AATCCCTTAT CAGGTGGATA GTTTGCAGAT	
ATCTTCTCCC ATTCTTTAGG TTGTCTCTTC ACTCTGTTGA TCGTTTCCTT TGCTCTGCAA	120
AAGCTTTGTA GCTTGAGATA ATCCCATTTG TCTGTTTTTG CTTTTGTTGC CTATGCTTTT	120 180
GAGGTCTTAC TCAAAAAATT TTTGCCCAGA CCAGTACCCT TGAAGCATTG CCCCAATGGT	240
TTTTTTTTT AGTCATTCA TAGTTCAGGT CTTACTCGAG	280
(2) INFORMATION FOR SEQ ID NO:355:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 398 base pairs	
(D) MVDE, must six and	

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:
- GAATTCGGCC TCCATGGCCT ACATAGATGG GCACACTCAC ACACAGAAGT GTGCTTGTAC
 AATCACCACA CACGCACAAA CACACACAC CACTAAAAAT ATAAAACACA TGCGTCACAT
 120

GGGCATTTCA	GATGATCAGC	TCTGTATCTG	GTTAAGTCGG	TTGCTGGGAT	GCACCCTGCA	180
CTAGAGCTGA	AAGGAAATTG	GACCTCCATG	CAGCCCTGAC	AGGTTGTGGG	CCCGGGCCCT	240
CCCTTTGTGC	TTTGTATCTG	CAGCTCTTGC	GCCTTTTATA	AGTCCATCCT	AGTCCCTGCT	300
GGATGGCAGG	GGGCTGGATG	GGGGGCAGGA	CTAATACTGA	GTGATTGCAG	AGTGCTTTAT	360
GAATTCACCT	TATTTTATCG	AAACCCATTG	GACTCGAG			398

- (2) INFORMATION FOR SEQ ID NO:356:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GTGTCAGAGC	AGGCATTTCC	CAACCTAAGG	AAATCTTTGT	TTTCAAATAT	TAGGGTTTTT	60
TTTTAATTGT	GGTTAAAGGA	TTTTGGACAT	GCTTTGTAAA	TTGTTAGTAA	AAGGACCTAT	120
TTTCCACCTG	TATTCTAAGT	TATTTTTTC	CCTCTTTTTG	AATTTTTCAG	GTCAGCCCTT	180
CATAAACCCA	GATGGGAGTC	CAGTTGTGTA	TAATCCTCCT	ATGACTCAAC	AACCAGTTAG	240
ATCCCAAGTG	CCTGGACCTC	CACAGCCACC	TCTGCCAGCC	CCACCTCAAC	AACCAGCAGC	300
TAATCACATT	TTCTCACAGG	CGCATCTCGA	G			331

- (2) INFORMATION FOR SEQ ID NO:357:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

GCTGCCTCGA	GGTCTCCAAG	ACTTTTTCAT	CTCGTATCGT	TTCGGGATCC	GTATCCATAC	60
TTTTATTTTC	ACTTTCTTCC	TCTTCCTCCT	CGAACTCCTC	GTCGCCATCC	TGTCTGCCCA	120
GCTTCCCGTA	GCCATCCTCG	CCTTCTTTCT	CGTGCTCCTT	CTCGCTCTCG	CCATCCCTCG	180
GCATACTCTC	CCTCTTCCTC	TCGAG				205

- (2) INFORMATION FOR SEQ ID NO:358:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 584 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

CAAAAGAGAT	GGTACCAGCA	AGAGATTAAT	ACTAAAGAAA	TGCAGTCAGA	TTTTAAAGAA	60
ACTGGAAGAA	GAGCCATTTC	TCCCAGGGAG	AAGATTCTAG	ATGTGATTGA	TGACACCATA	120
GAAATGGAGA	CAGGTCTGAA	AGCAATGGGA	AGAGAGATTT	GTCTAAGGGA	GAAGACGCCA	180
GAGGTGATTG	ATGCCACTGA	GGAAATAGAC	AAAGATTTGG	AAGAAGCTGG	AAGAAGAGAA	240
ATATCCCCAC	AGAAAAATGG	CCCAGAGGAG	CTTAACCCTC	TAGGTGAAGT	GGAGACAGAT	300

	-35-
TTGAAAGCAA CTGGATATGA GAGTTCCCCA AGGGAGAAGA CACCAGAGGT GACTGATGCC ACTGAGGAAA TAGACAAAAA TTTGGAAGAA ACTGGAAGAA GAAAAATATC CCCAAGGGAA AATGGCCCAG AGGAGGTCAA GCCTGTAGAT GAAATGGAGA CAGATTTGAA CGCAACTGGA AGAGAGAGTT CTCCAAGGGA GAAGACACCA GAGGTGATTG ATGCTACTGA GGAAATAGAT TTGGAAGAAA CTGAAAGAGA AGTATCCCCA CAGGAAAACT CGAG	360 420 480 540 584
(2) INFORMATION FOR SEQ ID NO:359:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 344 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:	
GAATTCGGCC TTCATGGCCT ATGCTTTCTG AATTGGCAAG ATATTCCAGG CTTATTTGGC ATTCATCTTA CTCTAGACCT ATTATCAACC ATGTCTCCAA GGATAAGTAG ATCCTTTTAA GGGAAAATGG TATTTTGAAA GCATAGTGTG GGATCTTAGAG ATACCTATTC CTGTCAGGTT GGTTATTGTT TGTTTTCAGT GAGTAGATCT TGGACTTTAT TAATTTTATT TATTTATTTT AAGAAAAGTA CATCATGAGT TATAAGTAAT AATTCCAACT CAAATTTTAA TATTGCTTAA CTTCTTTGAT TTTATATTTA TCTTTTACAC TGAAAAGTCT CGAG	60 120 180 240 300 344
(2) INFORMATION FOR SEQ ID NO:360:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 362 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:	
GCGGGTGGAC AAAAATGAAG CCAATGAAGA AGGCATGCAC TGGCCTTTCA GGTCCTGGCA GTGGCAGCAA GTCCCCCCA GCCACCAGGG CCAAGGCTCT GAGGCGGCGA GGGGCTGGGG AGGGTGACAA GCCAGAGGAG GAGGATGACG AGGCACAGCA CAGTCCGGGC CCGAAGAGGC TGAGGAAGGG GAGGAGGAGG AGGCTGAGCG GGCCCTGGG GCTGAAGGTC CTCCACTGGA GCTGCACCCT GGCGACCCGG CTCCAGGCCC AGCAGAGGAC CCCAAAGGGG ATGGGGAGGC AGGCCGCTGG GAGCCCTCAC TCAGCCGCAA GACAGCCCCG TTCAGTCTCG AG	60 120 180 240 300 360 362
(2) INFORMATION FOR SEQ ID NO:361:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 378 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:	
GCACCACCTC TTGCACTGTG AGGAGTTTAT TGATGAATTC AATGGGCTGC ACATGTCCAA GGACAAGAGG ATCAAGTCAG GGAAGCAGTC CAGTACCTCC AAGCTGCTGC GTGACAGTCG	60 120

AGGCCCGTCG	GTTGAGAAAC	TGTCCCACAG	ACCTTCAGAT	CCTGGAAAGA	GCAAGGGGAC	180
					GGTATTCAGG	240
					CTACCCCCAG	300
TGGTTTGCAA	ATAATGCCCC	TGAAAAAGTC	TCAGAACGGG	ATGGAAAATG	GGGACGCCGG	360
CTCTGTAAGG	ACCTCGAG					378

- (2) INFORMATION FOR SEQ ID NO:362:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

GATTGTATTG	AAAGTCAGAC	ATAGGTGTGG	AACCAGTTAT	GGGAGTGAGG	ATAAGTCTAG	60
ATTTGGGAAT	CAGTCGCAGA	GAGGTGGACG	ATGAAAGTCT	GAGAAGAAAG	GATCTTGCTA	120
ATGGAGTGAA	CTCAGAGCTT	GATAAAGGGA	GGATGAGTGG	AAATGGAGCT	CAACGCTGTG	180
CCTTGGGAAA	TACCTCTGTG	GATTGGTGGG	AGCACAGTGA	GAAATTCAAG	AAAGACACAG	240
	AACCAGAGAA					266

- (2) INFORMATION FOR SEQ ID NO:363:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

GAATTCTAGA CCTGCCTCGA	GCATTGCCCC	CGGCCTAAGA	AGCTCTCTTA	TCTTGCATCT	60
TGGGCTGGAC TCCTACAACA					120
CCCATCTCCT GTCGTTTTCG					180
CCTGTCGTTC CTCAAAATCC					240
TCTGCCTTAG ATGCTCTGGG					300
TCTGGCCATA ATGGTCTTCT	CTGCTGTTCC	TTGAACATTC	CAGGAACATT	CCCCCATAC	360
CCTCGAG					367

- (2) INFORMATION FOR SEQ ID NO:364:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

GAATTCGGCC	TTCATGGCCT	ACTGGGTTCT	GAGAAGCAGT	GGCCCGAGCT	GAAGCATCCA	60
GACAATGAGT	GTTCAGAAGC	TGCCAGATTC	TCACCTAGCC	TTAGAAGTAA	CACAGCCACA	120
					GGCAATTAGA	

TTTGACCCCT	TGATGAAGGA	GGGCAAGGTT	ACACTGAAAA	ACAGCATAGG	GACTGGGAGA	240
TATTATGATG	TCCATTTTTG	GAAAATCTGC	CACAGACACA	GTGAAGACAG	AGAGCCCTTC	300
			CTGAGTCACT	CAGGTATGCT	GGACCATTCA	360
CACTCACCCC	GGAAAAGCTC	GAG				383

- (2) INFORMATION FOR SEQ ID NO:365:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GAGGTTCACA	GGTTTAAGCA	TTTGTTTTTA	CAAAAAGGAA	TGGGATATGG	GGGTGGTCAA	60
GTTTTACGGG	TAATAACAAC	ATTCTCTCTA	GATGGCAGGG	GGTAAGTCTG	CCTGTCCTCC	120
ATTGCTGGTA	CCACATAAGG	GATACATTAG	TAAAGTAGGG	AAAGGGTCAT	ATGTGTGGTT	180
GACCTGTTCT	TCAGAGAGGA	ACGTGGGATG	GTATCTGCTG	TGTACCTGTC	TCAGACCAAA	240
CCTGGGGGTG	GACCAGTGCC	CCTTTCTTCT	CAGCCTTCTT	CCACAGCCTG	ACTGTACTGC	300
CACCCGCACC	CATGAGAAGG	AGGTNNTGAA	GGAAGCTTGA	GGACATCCAC	CTCGAG	356

- (2) INFORMATION FOR SEQ ID NO:366:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

					ACGAAAGTTC	60
CCCTTAATCA	CAAAGAACCA	CAGTTGACAG	GGTTGATAGA	TGTTTTTCA	GATTTTTTTT	120
TTCATATGTC	TGCTATCTTT	CCCCACAGGA	ACTGGGTTTT	ATTTTAGGTG	TTGTTTTGCA	180
					ACAGGCCCAT	240
CTCGAG						246

- (2) INFORMATION FOR SEQ ID NO:367:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

GAATTCGGCC	TTCATGGCCT	ACAAAAAAAC	AACTTTCCAG	TGGCTTCTCA	CTGCTCTGAG	60
AATAAACTCC	AGGCTCTTCC	ATTGCAACCA	ACAGGATCTG	GTGATTCGAC	CCCAGCCCCT	120
				CCTGCTCCAG		180
TGCCTTCCTA	TTCCTCCAGC	ATACCAAGAT	TGTTTCTGCC	ACAGGGCCGC	CACTCGAG	238

- (2) INFORMATION FOR SEQ ID NO:368:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GAATTCGGCC	TTCATGGCCT	AGTTTTTTCT	ACTCCTACAA	GTGTAAATTG	AAAAATCTTT	60
AAAAATTATA	AGTAAACTGT	TATGAAGCTG	CTATGTACTA	ATAATACTTT	GCTTGCCAAA	120
GTGTTTGGGT	TTTGTTGTTG	TTTGTTTGTT	TGTTTGTTTT	TGGTTCATGA	ACAACAGTGT	180
CTAGAAACCC	ATTTTGAAAG	TGGAAAATTA	TTAAGTCACC	TATCACTCGA	G	231

- (2) INFORMATION FOR SEQ ID NO:369:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GAATTCGGCC	TTCATGGCCT	ACTTGGTCTT	CTGCACTTTT	GTCTCTGACG	TACTTCCTTT	60
CTTCACAAGT	GCCATTTACA	GAAAGCTGGG	CTTAAACCAT	TCCCAGCTAT	TCCTCCTACA	120
GCTTTCCTGA	ATTATTTCAG	AATACAAAAT	TCTGTATCTC	CAAGAAACTA	TTACAGATTT	180
AGATTTAAAA	ATATGCACTA	TTTTCTACCT	TGTATGTTTT	GCTTACTATT	TTTTTTTTGC	240
AGAGGATATG	TCTTAAAAAT	TGAAATGCAT	CAAAAAT			277

- (2) INFORMATION FOR SEQ ID NO:370:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

GAATTCGGCC	TTCATGGCCT	ACCAAGTCAA	AAAATAGAAC	AGTTCCGGCA	CCCCAGAAGC	60
CCTTTGCCAC	GTGGTCACAA	CCCTCCCTGT	TTCCACCAAC	AGTAACATTC	TAGTTTTTAC	120
AGTAATTTCT	TCCTTGCTTT	TCTTTGTAAT	TTTACTGCCC	TGTGTTTCTT	AATATGATTT	180
AGTTTTGCCT	GGTTTTGCCT	TCATATAAAT	GAAATCATAC	TGAATATATT	ATTTCATATT	240
TTGCCCAATA	TTTTGTTTGT	AAGATTCATC	CATCTTGTAG	CTCCAATGTA	TTTATTTTCA	300
TTTTTGTATA	ATTATATGAT	TATGCCACAG	TTTGTCAGTT	CACTCGAG		348

- (2) INFORMATION FOR SEQ ID NO:371:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GAATTCGGCC	TTCATGGCCT	AGAATTATTA	GGAAACAAAT	GGTTTTGCTG	TCTTTTGGTC	60
ATTAGCTTGG	CCCCATGTTT	AAGCATTCGG	TAACAACTGT	GAAGAGCCTG	CTACAAATAA	120
AGTGGTAGGT	GCTCTGAAGA	AAAATAAAGC	TGTTAAAGGG	AATAGAAAGT	GATGAAGGCA	180
GGGGCTGTTA	GACAGGCTGG	TCAGTGTCTG	AGGAAGTAGC	CCTGCACTGA	GACCTGAAAA	240
GTAAAGAAGC	AAGCCATGGG	GAGTTGGGGA	GGAGCATTCC	AGACAGAGGC	TTGATGTGTT	300
GAACCATCTT	TTCCAAGCTC	TTCCTCTGTT	ACCTTCTCTT	TAGTCACTAT	GTCCCCTTTC	360
TATCCCAGAC	CATAATTCCA	CCATTTATCT	TAAGGCTGAG			400

- (2) INFORMATION FOR SEQ ID NO:372:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GAACGATTGA ATTCTAGAC	TGCCTCGAGA	TCAGCACTAA	CCCCCCAAC	TCCCAGCCTT	60
TAGTTTGCTG TAGGCTGTC	AACCAGATAA	CCAAACTTGT	TAAATTGAGA	ATCAATAGGC	120
TGTACATAGG GACTACAACA	GAATGACGCT	CATTATTGAC	AGAATCAAGT	TCAAACTCCT	180
TGTCCTGGCG TCTGTTGGCC					240
TTGCTGCAAC CCTCCCACC					268

- (2) INFORMATION FOR SEQ ID NO:373:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

GTGAGGTTTT	AACTGAGCTC	GAAGAATTGG	AATCAAAAGA	GATAGGTTTG	TCTCAGTCCA	60
GACAGTGGAT	AGCATAAGGA	AAGTACAACT	GCAGAAAAGA	GGGGGACAGC	GAAGAGACTG	120
GATTGATGCG	TTATCTAGGC	GGTACCTGTC	TCCATTCTTT	TCTAGCCAGC	CTTTGAGCAT	180
TTCATCAAGA	ATAGAGGAAT	TCAAAGTACT	GCAGTCTGCT	TGAACCAGTG	CTTGTGAGTG	240
GCTCTAAAAA	AAATACTTGA	ATTTGAACTT	GAAAGAACAC	TCAAATAAGG	TTTGGGGCTT	300
CTCTTTGTTT	AATACTTTAA	GCGTCTTATT	TCTAACATAA	ATATACTGAT	TGCACAGAAT	360
TTGATTGTTC	ATAGCAGCAG	TTGCCTGTAC	TTTAGAATTC	TCAGATATTA	GAGCTGAAAG	420
ATCATCTGAG	TTACTTTATA	AATGGGGAAA	TCTCGATCTC	GAG		463

- (2) INFORMATION FOR SEQ ID NO:374:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 451 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

GAACGGCAGC	CATTGAAGCA	TATTGGAAAA	GGAACTGGGG	AATTTATTAA	AGCACTCATG	60
AAGGAAATTC	CAGCGCTGCT	TCATCTTCCA	GTGCTGATAA	TTATGGCATT	AGCCATCCTG	120
AGTTTCTGCT .	ATGGTGCTGG	AAAATCAGTT	CATGTGCTGA	GACATATAGG	CGGTCCTTGA	180
GAGAGAACCT	CCCCAGGCAC	TTCGGCCACG	GGATAGAAGA	CGGCAGGAGG	AAATTGATTA	240
TAGACCTGAT	GGTGGAGCAG	GTGATGCCGA	TTTCCATTAT	AGGGGCCAAA	TGGGCCCCAC	300
TGAGCAAGGC	CCTTATGCCA	AAACGTATGA	GGGTAGAAGA	GAGATTTTGA	GAGAGAGA	360
TGTTGACTTG	AGATTTCAGA	CTGGCAACAA	GAGCCCTGAA	GTGCTCCGGG	CATTTGATGT	420
ACCAGACGCA	GAGGCACGAG	AGCCCCTCGA	G			451

- (2) INFORMATION FOR SEQ ID NO:375:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

GAATTCGGCT	TCATGGCCTA	CTCAGATCTT	AAAATTCAGG	CTGTCAAAGA	GATTTGCTAT	60
GAGGTTGCTC	TCAATGACTT	CAGGCACAGT	CGGCAGGAGA	TTGAAGCCCT	GGCCATTGTC	120
AANATGAAGG	AGCTTTGTGC	CATGTNTGGC	AAGAAAGACC	CCAATGAGCG	GGACTCCTGG	180
AGGGCAGTGG	CCAGGGACGT	CTGGGATACC	GTCGGTGTTG	GGGATGAGAA	GATCGAAGAC	240
GTCATGGCCA	CTGGGAAAGG	CAGCACTGAT	GTAGATGACC	TCAAGGTTCA	TATAGACAAG	300
CTGGAAGATA	TTTTGCAAGA	AGTCAAAAAG	CAAAATAACA	TGAAAGACGA	GGAGATAAAA	360
GTCTTAAGAA	ATAAAATGCT	CAAAATGGAA	AAAGTCTTGC	CACTGATCGG	ATCTCAGGAA	420
CAGAAAAGCC	CAGGAAGCCA	CAAAGCAAAG	GAGCCTGTTG	GTGCTGGTGT	TAGTAGCACC	480
TCTGAGAATA	ATGTAAGTAA	AGGAGACCTC	GAG			513

- (2) INFORMATION FOR SEQ ID NO:376:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

CAGAATGGGA '	TCGAAGCCTG	CCTCCTTAGG	NTCTTTGCCN	TCATCCTCTC	TGGCAAATGC	60
AGTTACAGCC	CGGAGCCCGA	CCAGCGGAGG	ACGCTGCCCC	CAGGCTGGGT	GTCCCTGGGC	120
CGTGCGGACC	CTGAGGAAGA	GCTGAGTCTC	ACCTTTGCCC	TGAGACAGCA	GAATGTGGAA	180
AGACTCTCGG	AGCTGGTGCA	GGCTGTGTCG	GATCCCAGCT	CTCCTCAATA	CGGAAAATAC	240
CTGACCCTAG	AGAATGTGGC	TGATCTGGTG	AGGCCATCCC	CACTGACCCT	CCACACGCTC	300
GAG						303

(2) INFORMATION FOR SEQ ID NO:377:

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 334 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:	
GAATTCGGCC TTCATGGCCT ACTTCATTGT AAGGTACTTC TTTGCGGCGC TGACAGTGCT CACGCTCCTG GGCCTCCTCC ATGGACTCGT GCTGCTGCCT GTGCTGCTGT CCATCCTGGG CCCGCCGCCA GAGGTGATAC AGATGTACAA GGAAAGCCCA GAGATCCTGA GTCCACCAGC TCCACAGGGA GGCGGGCTTA GGTGGGGGGC ATCCTCCTCC CTGCCCCAGA GCTTTGCCAG AGTGACTACC TCCATGACCG TGGCCATCCA CCCACCCCC CTGCCTGGTG CCTACATCCA TCCAGCCCCT GATGAGCCCC CCAGGTCCCT CGAG	60 120 180 240 300 334
(2) INFORMATION FOR SEQ ID NO:378:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 305 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:	
GGATTTTAAG GATCACATTC CAAGGGAAAC TGATATGAAG GTTGCAATGA ATGTGTATGA GTTATCATCA GCTGCCGGAT TACCTTGTGA GATTGATCCT GCATTGGTCG TAGCTCTTTC TTCACAAAAA TCGGAAAACA TTAGTCCAGA AGAAGAGTAT AAAATTGCCT GCCTTCTCAT GGTGTTTGTG GCAGTTTCTT TGCCAACACT GGCCAGTAAT GTGATGTCTC AGTACAGCCC TGCTATAGAA GGGCATTGCA ACAACATACA TTGCTTGGCC AAAGCCATCA ACCAGATTGC TCGAG	60 120 180 240 300 305
(2) INFORMATION FOR SEQ ID NO:379:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:	
GAATTCGGCC TTCATGGCCT ACCCAAACAT TATCCCTCTA CACTGTCCCC ACTATGCTAT ACCCCTGCAC TATACCCCTA TGCTGTCTCC CTTACGCTAT CCCCCTATGC TATGTCCCCT ACACTATCCC CCTTTGTTGT CCCTCCATGC TACTCCCTAC GCTATCCCAC TACTCTATCC CCCTGACGCT GTCCCCCTAC GCTATCCCGC TACACTGTTC CCCCTACACT ATCTCCATAC	60 120 180 240
ACTGTCCCCC TACACTCTCC CCCTACTCAA TTCCCCCTAC ACTCTCCGCG TACACTATCC	300

(2) INFORMATION FOR SEQ ID NO:380:

CCGCTACACT ATCCCCCGAC GCTCTCGAG

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs

329

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

GTTCGAATGC TCTT	TTACTTC CTTTGTGGA	G CCTCCCTGCA	CAAGCAGCAC	TTTCTTTTGC	60
CATAGCAACA TGTO	GCATCAA TAATTCTTT	A GTCTGTAATG	GTGTCCAAAA	TTGTGCATAC	120
CCTTGGGATG AAA	ATCATTG TAAAGAAAA	G AAAAAAGCAG	GAGTATTTGA	ACAAATCACT	180
	CAATTAT TGGCATTAC				240
	AAGTGAA ACAGCATCT				273

- (2) INFORMATION FOR SEQ ID NO:381:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GAATTCGGCC	TTCATGGCCT	ACATAACTCT	CCACAGGCTC	CCCTGGGAGG	GGTGCCCCCA	60
					TGGGCTGCCC	120
CCACCCTAGT	CATGATCTCG	CTCCTCTACT	CTCTCGTAGT	ACTTTATTTT	TACCTTGCTC	180
					TCTCCTTTTG	240
					CTCATCCCCT	300
		TACACATGTT				338

- (2) INFORMATION FOR SEQ ID NO:382:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

GAATTCGGCC	TTCATGGCCT	ACTTTCTCTC	CTTTTTTCCT	GTAACTGTGC	TGGTTTTGTT	60
					GGACTTCATT	120
					TTGATAAAAT	180
					CTTTTTCTTT	240
					CAGAAGAACT	300
	GGTGCCCATC					334

- (2) INFORMATION FOR SEQ ID NO:383:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

GCAGAAAATA	TGGTATCGGT	TTCATTTAAT	AAAAATGAAA	AAATAATTTT	CAGTTATCAG	60
TAATTTCTCA	GTTACACAAC	CTCTGCCTTC	ATTTCCGCTT	AGCCATGAAC	TTTTTACTGC	120
ACAAAGGAAT	TTAAAATAGC	CAAATTCTAC	AATTCTGGCT	GGGTGTGGGG	GCTCATGCCT	180
GGGATCTCAG	TAGTATGGGA	CCCCGAGGCA	GGTCTAGAAT	TCAATCCTCG	AG	232

- (2) INFORMATION FOR SEQ ID NO:384:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

GCCTCTGCTT	TTAATTCATT	GGCAACTGTT	ACGATGGAAG	ACCTGATTCG	ACCTTGGTTC	60
CCTGAGTTCT	CTGAAGCCCG	GGCCATCATG	CTTTCCAGAG	GCCTTGCCTT	TGGCTATGGG	120
CTGCTTTGTC	TAGGAATGGC	CTATATTTCC	TCCCAGATGG	GACCTGTGCT	GCAGGCAGCA	180
ATCAGCATCT	TTGGCATGGT	TGGGGGACCG	CTGCTGGGAC	TCTTCTGCCT	TGGAATGTTC	240
TTTCCATGTG	CTAACCCTCC	TGGTGCTGTT	GTGGGCCTGT	TGGCTGGGCT	CGTCATGGCC	300
TTCTGGATTG	GCATCGGGAG	CATCGTGACC	AGCATGGGCT	TCAGCATGCC	ACCCTCTCCC	360
TCTAATGGGT	CCAGCTTCTC	CCTGCCCACC	AATCTAACCG	TTGCCACTGT	GACCACACTT	420
CTCGAG						426

- (2) INFORMATION FOR SEQ ID NO:385:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

GAATTCGGCC TTCATGGCCT AGGC	CCTTAA ACTGGATTCA AAAAATGCTC TAAACATAGG	60
AATGGTTGAA GAGGTCTTGC AGTC	TTCAGA TGAAACTAAA TCTCTAGAAG AGGCACAAGA 1	20
ATGGCTAAAG CAATTCATCC AAGG	GCCACC GGAAGTAATT AGAGCTTTGA AAAAATCTGT 1	80
TTGTTCAGGC AGAGAGCTAT ATTT	GGAGGA AGCATTACAG AACGAAAGAG ATCTTTTAGG 2	40
AACAGTTTGG GGTGGGCCTG CAAA	ATTTAGA GGCTACCTCG AG 2	82

- (2) INFORMATION FOR SEQ ID NO:386:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

PCT/US98/06955 WO 98/45436

GATTGAATTC TAGACCTGCC TCGAAGGCCG AGAGGGAAAG TTGAAAGGTC CCAAATTCAA	60 120
GATGCCTGAG ATGAACATCA AAGCCCCCAA GATCTCCATG CCTGACATTG ATCTTAACCT	
GAAAGGACCC AAAGTGAAGG GTGATATGGA TGTGTCTCTG CCAAAAGTGG AAGGTGACAT	180
GCAAGTTCCT GACTTGGATA TTAAAGGCCC CAAAGTGGAT ATTAATGCCC CAGATGTGGA	240
TGGACTCGAG	250
•	
(2) INFORMATION FOR SEQ ID NO:387:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 344 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
, ==, :	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:	
TOTAL COMMISSION OF THE PARTY O	60
GAATTCTAGA CCCACCTCCA CCTTTAACTC GAAGTAACAC TGCAAATCGT TTAATGAAAA CACTCTCAAA ACTGAATTTA TGTGTTGATA AAACAGAGAA AGGAGAAAGT AGTAGTCCTT	120
CACTCTCAAA ACTGAATTTA TGTGTTGATA AAACAGAGAA AGGAGAAAGT AGTAGTCCTTCATCAGC TGAAAAAGGA AAGATTCTAA ATGTTTCAGT GATTGAAGAA AGTGGCAATA	180
CTCCATCAGC TGAAAAAGGA AAGATTCTAA ATGTTTCAGT GATTGAAGAA AGTGGCAATA AAAACGATCA AAAGTCTCAA AAAATTATGA AGAAGAAAGA GTCATCTTCT ATGTTGGCTA	240
CAGTTAAAGA AGAAGTCTCT GGTAGTTCAG CAGCTGTTAC GGAGAATGCT GATAGTGATA	
	344
GAATTTCTGA TGAAGCAAAT AGTAATTTTA ACCAAGGGCT CGAG	344
(2) INFORMATION FOR SEQ ID NO:388:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 165 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:	
GGAGTAATCA GAGGTGTTCT TGTGTTGTGA TAAGGGTGGC AGGAGTGGAC ATTCTTCACA	60
GGAGTAATCA GAGGTGTTCT TGTGTTGTGA TAAGGGTGGC AGGAGTGGAC ATTCTTCACA	

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs(B) TYPE: nucleic acid

TTTAGAATGA AAACCACAAG AGTTTTATTG TTGGCTGTAC TCGAG

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

CAATTCGGCC	TTCATGGCCT	AGAACAGAGC	TTACTTATTC	TTTCTGAAAC	CAAGGCTTCT	60
					GTTTCATTTC	120
					TTTAATTTT	180
						240
TTCACAGTTC	AGATTTTTAT	GTTTTTGGTT	CATCACTCTT	TTAAAAATGC	TGTGGTTCCC	
ATCAAACTCG	AG					252

TACACCCATT ATTGTTTTGA AGTGTTTAAT TACCTTTTTA GCTACATTTT TGCAGCTGAG 120

165

- (2) INFORMATION FOR SEQ ID NO:390:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GAATTCGGCC	TTCATGGCCT	AGGATGTTCA	CTTGCATGCC	TCTGGATTTT	AAAATTATTG	60
TTCACATGAC	TCCTTTTCTG	TGCGTTGGGA	AGCAGCTACA	GAGCAGTAGA	ATCCACTGAA	120
TTGGTACACT	GAAGCAGGCA	TGCCATTTAA	ATGAAGGCAG	TTAACCTTGA	CTGTTGTATC	180
ACCAGAGTTA	AAGAATTCTG	GTGCCCCTCT	TTAAGTCTTC	AGGAAGTGTT	TAGAGGCTTA	240
TTCACATTAG	TTAAAACAGG	CCCCCCCAC	CTTCCCCAAG	GCAACAGAAA	ACATAACCAT	300
TAGCTCTCTT	CCTGTTTTCC	TTCCTCATTT	CATGCTTGCT	TCGGCTGCTA	AACTGAATTT	360
TTGTTACTTA	GAATATTATA	AAGTGTGGAT	GCTTTCTATA	ATGCTATTGG	TCTAAGTGTG	420
ATTAAATTTC	ATTAAGGTGT	ATAAGCCTCT	AATTATTACA	TAACTGGCAC	TGGCTCGAG	479

- (2) INFORMATION FOR SEQ ID NO:391:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GAATTCGGCC	TTCATGGCCT	AGCCTATTAC	ACAGTAAGTT	AATAATTGTG	TCCTTGCAAA	60
TAAGCATTGT	GTTCTGAAAT	GGAATCAGCA	TATTTCCCTA	TAAAGACACT	TCCACTCATT	120
CATTAATTGA	GCAGCCCCAG	TTGATAAAGA	ATCAGTATAT	CATGTTCTGA	TATTTAATCA	180
GCAAACTCAT	TTATTCAGTA	GAAATTTGAA	TTCCTGTGAT	GTGCCAGGCT	TGTGAGGAGG	240
GAGACTCGAG						250

- (2) INFORMATION FOR SEQ ID NO:392:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

GAATTCGGCC	TTCATGGCCT	AGTCGACTCC	TGTGAGGTAT	GGTGCTGGGT	GCAGATGCAG	60
TGTGGCTCTG	GATAGCACCT	TATGGACAGT	TGTGTCCCCA	AGGAAGGATG	AGAATAGCTA	120
CTGAAGTCCT	AAAGAGCAAG	CCTAACTCAA	GCCATTGGCA	CACAGGCATT	AGACAGAAAG	180
CTGGAAGTTG	AAATGGTGGA	GTCCAACTTG	CCTGGACCAG	CTTAATGGTT	CTGCTCCTGG	240
TAACGTTTTT	ATCCATGGAT	GACTTGCTTG	GGTATGGAGA	GTCGGCTTGA	CTACACTGTG	300
TGGAGCAAGT	TTTAAAGAAG	CAAAGGAACT	CCTCGAG			337

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 216 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:	
GCGATTGAAC TCCTGACCTC AAGTGATCTG CCCACTTGTG CCTCCCAGAA CTGGGATAAA	60
AAAAAAAAA ATAGATCCTT GGTATTATTC CATTACATAC GGATTGTAAA ATTCAGTTAA	120
ACATTCATCT CTTGGTGGGC ATTTATGTAT TTCTTTTGTT TGTTTTGTTT	180
CTGTTAAACC TTTTTATAAG TACATCTCGA CTCGAG	216
(2) INFORMATION FOR SEQ ID NO:394:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 248 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:	
GAATTCGGCC TTCATGGCCT ACCACATTTG TAACGGAGCC ATTGAAGCAT ATTGGAAAAG	60
GAACTGGGGA ATTTATTAAA GCACTCATGA AGGAAATTCC AGCGCTGCTT CATCTTCCAG	120
TGCTGATAAT TATGGCATTA GCCATCCTGA GTTTCTGCTA TGGTGCTGGA AAATCAGTTC ATGTGCTGAG ACATATAGGC GGTCCTGAGA GCGAACCTCC CCAGGCACTT CGGCCTGGGA	180 240
TACTCGAG	248
(2) INFORMATION FOR SEQ ID NO:395:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 238 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:	
GAATTCGGCC TTCATGGCCT AGCCTTCCTC TACCATTTTT AATTTTTTTA GACTTCATTT	60
TGTGATTTAT TGCTGCTCTG GGGGCTTCAC ATCCAATCCT TTTATGGTTT CATCTTTCCT	120
TTCCTTACAT TTGTTGCATA TAACAATGGC GTGTTTAGCT ACTGCAGTGA AAAATCAATC	180
AAGCCTATTC CATATTCACA GGCTTGCAAT GGCACCAACG GCTCCTGGAT CTCTCGAG	238
(a) Typopus Troy For Gro Tr vo 206	
(2) INFORMATION FOR SEQ ID NO:396:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 188 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA

217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GAATTCGGCC	TTCATGGCCT	AAGTTGATCC	GGATACACAC	CTGCTAAAAC	TGCTTAAAAC	60
ATTAGAAGGA	CATGCTTATG	GCGTTTCTTA	TATTGCATGG	AGTCCAGATG	ACAACTATCT	120
TGTTGCTTGT	GGCCCAGATG	ACTGCTCTGA	GCTTTGGCTT	TGGAATGTAC	AAACAGGAGT	180
CTCTCGAG						188

- (2) INFORMATION FOR SEQ ID NO:397:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GAATTCGGCC	TTCATGGCCT	ACAGGCATGT	TGAGATTTGG	AAAAGTGGAT	GTAACTGAAA	60
TTCAGATAGC	TTTAGTGATT	GTCTTTGTGT	TGTCTGCATT	TGGAGGAGCA	ACAATGTGGG	120
ACTATACGAT	TCCTATTCTA	GAAATAAAAT	TGAAGATCCT	TCCAGTTCTT	GGATTTCTAG	180
GTGGAGTAAT	ATTTTCCTGT	TCAAATTATT	TCCATGTTAT	CCTCCATGGT	GGTGTTGGCA	240
AGAATGGATC	CACTATAGCA	GGCACCAGTG	TCTTGTCACC	TGGACTCCAC	ATAGGACTAA	300
TTATTATACT	GGCAATAATG	ATCTATAAAA	AGTCAGCAAC	TGATGTGTTT	GAAAAGCATC	360
CTTGTCTTTA	TATCCTAATG	TTTGGATGTG	TCTTTGCTAA	AGTCTCACAA	AAATTAGTGG	420
TAGCTCACAT	GACCAAAAGT	GAACTATATC	TTCAAGACAC	TGTCTTTTTG	GGGCCAGGGC	480
TCGAG						485

- (2) INFORMATION FOR SEQ ID NO:398:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GAATTCGGCC	TTCATGCCTA	GTGGATCCGG	AAACTCTGTG	GCTCTAGACT	TTCAACTATT	60
TTATTTTTTC	TTTTGTATTT	TTTGTTTGTT	GCTTGCTTTT	TTACAATGGG	AACTAGAATG	120
TAAGATGCCA	AACTCAGCCT	GTGGGGAACA	TGGATTTTCA	CAACAGCAAC	CACAGAGCGT	180
GGTTTCCATT	TCTATTCCCT	GTTCATGTGG	GAGGCAGAGA	AGGAAATCAG	GTGCTCAGTT	240
CCAGGGACAT	CACAGGACAG	GACTCGAG				268

- (2) INFORMATION FOR SEQ ID NO:399:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEO ID NO:399:

GAATTCGGCC	TTCATGGCCT	ACACCTCTTC	TGCCAACCAG	CTGCTTGGGA	TGACTGCGAT	60
CCCGTGTGCT	TGTCTGGGTA	TCTTCCTGGG	AGGTCTTTTG	GTGAAGAAGC	TCAGCCTGTC	120
TGCCCTGGGG	GCCATTCGGA	TGGCCATGCT	CGTCAACCTG	GTGTCCACTG	CTTGCTACGT	180
CTCCTTCCTC	TTCCTGGGCT	GCGACACTGG	CCCTGTGGCT	GGGGTTACTG	TTCCCTATGG	240
AAACAGCACA	GCACCTGGCT	CAGCCCTGGA	CCCCTACTCG	CCCAAG		286

- (2) INFORMATION FOR SEQ ID NO:400:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

GAATTCGGCC	TTCATGGCCT	ACCTGCCTCG	AGATGATCAT	TCTTTTCTTG	CTTCTAGGCT	60
CTGTGTCCTC	CTGGTTTCCT	CCAACCTCTC	TGGTCCTGTT	TCATTTGCTG	TGGGTTCCTT	120
TTGCCTTTGC	CACCCCTCAA	ATGGGGCTTC	TCACTCACAC	TAGTGAGTTT	TCAGTGCTTG	180
CAGACCCAAC	ACCCTCTTTT	TATAACAAAT	TAATTTTTTA	ACGTCCTTTT	CCACAACTCG	240
AG						242

- (2) INFORMATION FOR SEQ ID NO:401:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

GAATTCGGCC	TTCATGGCCT	AGTCCCATCA	GAGGGAGCTG	ATGAAGAATG	GTCCCTGTAA	60
GTAAGTCACT	AGGTTCAACA	ACTGCCTGGC	CGAGCACTCA	GCCCGTGGAG	CTCAGGCCAA	120
CACCAGAGCC	CCGGTTTTAG	GGGCCAGGAG	AGCAGGTGAC	CAATTATTTG	GGGAGTCTTG	180
GGTAGAATTT	CCGCCACACA	TTCTCCCCAG	GGCTGCAGGG	GTCTTCCGAG	GCAGGGCGGT	240
GGAGCAGGAT	TCAGGATGTG	GTGGGAATAG	AGTGAGGGGC	AGTGGGTGGT	GCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:402:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

GAATTCGGCC	TTCATGGCCT	AAAAAACTAG	AATAATGGAA	GAGTAAATAA	ACACAATTCT	60
TAATGTATTA	CAAGAAATAA	AAGGTTTAAA	AGTAGATTTT	TTAATTGAAA	AGAATTAAAT	120
CAGATAAAAA	TATTTGAGAG	GTAATGCAAA	CATTTAAGTT	TGTCAAAGAA	GCTTCAACAT	180
CTGGATAATA	GGAAAGAAAA	AAACCAAAGC	AAAAGAAAAA	TAAGCCACAA	ACTAAAAAAT	240
GTTTAGTTCT	TGAAATTTAA	AAAAGTAAAT	ATTGAAAGAG	CATGCTGTGT	ACCTGAGATT	300

ATTTACCCAA AACTCGAG	318
(2) INFORMATION FOR SEQ ID NO	403:
(i) SEQUENCE CHARACTERI (A) LENGTH: 355 (B) TYPE: nuclei (C) STRANDEDNESS (D) TOPOLOGY: li	base pairs c acid : double
(ii) MOLECULE TYPE: cDN	A
(xi) SEQUENCE DESCRIPTI	ON: SEQ ID NO:403:
GCAGCAGCCT GAGCCGGGCC AAGTCTG/ ATGCCATCTG CCGCAGCTAC CCAGGGCT CCCTGCAGCG CGTGTCCCGC TGCTATCC GCGGGCGGTC CAAGGCGGTG CTGCTGCC	ATT CTAGACCTGC CTCGAGTCTG GGCACCCTGA 60 AGC CCTTCCGCAT TTCTCCGGTC AACCGCATGT 120 AGC TGATCGTGCC CCAGAGTGTC CAGGACAACG 180 AGC AGAACCGCTT CCCCGTGGTC TGCTGGCGCA 240 AGCT CTGGAGGCCT GCATGGCAAA GGTGTCGTCG 300 AGCT CAGGCCAGTC CCAGGCGGAC TCGAG 355
(2) INFORMATION FOR SEQ ID NO	:404:
(i) SEQUENCE CHARACTER) (A) LENGTH: 346 (B) TYPE: nuclei (C) STRANDEDNESS (D) TOPOLOGY: li	base pairs c acid : double
(ii) MOLECULE TYPE: cDM	A
(xi) SEQUENCE DESCRIPT	ION: SEQ ID NO:404:
AGTATTACTG AAACAGATGA ACAAATG TATGAAACCC CACAAGATGA GGGTTAT GTCTTATAAA GAAAAAAAA AAAAGAA	GAA CAAGTCCTTG CTAAACTAGA AAACAGGACT 60 CAA GCATATGATC ACCTTTCATA TGAAACACCT 120 GAT GGTCCAGCCT GGGTGACAGA GCGAGACTCT 180 GTG GCAGCTCTGT CTGCTTCTCA CAGAGTTGCT 240 CCC TTGGGCTCCC CGGGTGGGCT GCTATTTGCC 300 GTC CCCGGGGTGG CTCGAG 346
(2) INFORMATION FOR SEQ ID NO	:405:
(i) SEQUENCE CHARACTER (A) LENGTH: 247 (B) TYPE: nucle: (C) STRANDEDNES: (D) TOPOLOGY: 1:	base pairs ic acid S: double
(ii) MOLECULE TYPE: cD	NA
(xi) SEQUENCE DESCRIPT	ION: SEQ ID NO:405:
GGAAGTCAGG TGAGAAGCTG TCAACTC TGTACTTTTT TGTTTTGTTC AAAAAAA	GAAC AGGGAACTTT CAAACAAAAG ATATATCATA 60 GGGC AGGCAGTGAT GAGAATCGTA GTTGTCTTAC 120 CCTA AAGCATCACG CATTTTGAAA GCAGAGTTTG 180 FTGC CAAGAGCGAC TGATATTTCT AGAATCCCAC 240 247
(2) INFORMATION FOR SEQ ID NO	D:406:

220

(i) SEQUENCE CHARACTERISTICS:

(1) DEQUERCE CHEECETHIEFTED.	
(A) LENGTH: 442 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:	
GAATTCGGCC TTCATGGCCT ACAACATCAA AACTCCCAAG CAAATGGATG AATTCATTGA	60
GATCCAAAGT TCAACAGGAA CCTGGTACCA GCGCTGGCTG GTCAGATTCA AGACCATTTT	120 180
CAAGCAGGTC TGGGATAATG CCCTGTACTG TGTGATGGGG CCCTACAGAA TGAATACACT	240
GATTCTGGCC GTGGTTTGGT TTGCCATGGC ATTCAGTTAC TATGGACTGA CAGTTTGGTT TCCTGATATG ATCCGCTATT TTCAAGATGA AGAATACAAG TCTAAAATGA AGGTGTTTTT	300
TCCTGATATG ATCCGCTATT TTCAAGATGA AGAATACAAG TCTAAAATGA AGGTGTTTT TGGTGAGCAT GTGTACGGCG CCACAATCAA CTTCACGATG GAAAATCAGA TCCACCAACA	360
TGGGCCTCGA CCTGACTTTG CCCCCTTGCC CATCAGCCAT TTGCCATCAC CCCAAACAAC	420
TCAGCTTCGG GGAAGTCTCG AG	442
(2) INFORMATION FOR SEQ ID NO:407:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 154 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
A LA CHOMBE DECONTRACTOR OF A NO. 407.	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:	
CCGAGTGACC TTCTTGATGC TGGCTGTTTC TCTCACCGTT CCCCTGCTTG GAGCCATGAT GCTGCTGGAA TCTCCTATAG ATCCACAGCC TCTCAGCTTC AAAGAACCCC CGCTCTTGCT TGGTGTTCTG CATCCAAATG CGAAGCTCCT CGAG	60 120 154
(2) INFORMATION FOR SEQ ID NO:408:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 146 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:	
GAATTCGGCC TTCATGGCCT AGTTTACTTC TGCTTGATCT TTATTCTTCC TTGCTACTAA	60
TTTTGGATTT AGTTTGTTCT TTTCTAGACA TTCATTGTTA GATTGTTTAT TTACAATTTT	120
TCTAGTTTTT TTGATGTAGA CATTTA	146
(2) INFORMATION FOR SEQ ID NO:409:	
(i) SEQUENCE CHARACTERISTICS:	
(1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 285 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
221	
221	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GAATTCGGCC	TTCATGGCCT	AGATGTTGCC	AGTTTTCATG	GAGGAAGTAG	ACATGAAAGC	60
TTGTTTGTAA	TGTGTTTGAC	AGAGTAGAAA	GACATTGAAG	AAGGTGATGG	TATACATCAC	120
TTGAATATTT	TTATTGAAAA	GGGAGGGAGG	AAATGGAGCG	TTAGTTGTAG	GACCAGATGA	180
TGTAAAGAGA	GTTTTTTAAA	GTGTACAAAA	CAATGGCATG	TTGTGATACT	AATGAGAAGG	240
AGCCAATAGA	GAACAAAAA	TTGATGATGC	AGGAGACGAC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:410:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

CTCGAGGGAT	CTGGCTTTCT	CTGTCTTCTC	ATTTACTACA	TNACGCTGGT	GAATTAATAG	60
					CTTAAGAAGC	120
					TGTATAACTC	180
			CAGCTNCAAG			240
			TTTTGCAATC			300
TCTTCAAAAG	CAAAGGAGTT	NGTTAGCAAC	ATATTAGGCC	ATGAAGGCCG	AATTC	355

- (2) INFORMATION FOR SEQ ID NO:411:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 226 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

GAATTCTAGA	CCTGCCTCTG	TATGTTGCTT	TAGCCAGGAT	TCAGAGCTAA	AGTGTAAGTG	60
TGTGCTTCTG	CTTTCTGGAT	GTATCTCTCA	AAATTGCTCT	GTCTGTTTAT	TCAGCTCCTG	120
GATCTACCTT	CTCTTTTCTT	TGAATTGGAC	ACCATTCATG	TCATTGCTCA	CTCAGAACTT	180
CAGCTGTTCT	CATGATCACA	TGCTTTCTTC	CCTGTTTATG	TCCAAT		226

- (2) INFORMATION FOR SEQ ID NO:412:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 218 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

GAATTCGGCC TTCATGGCCT AGTCTGCTGC TTAGCTTGTA TTTTCAGTTT AATATATTCG TGATCATTAA CAAAACAGCG AAGTGAATAA TGGGCATAAA TTTTCCTAAG AAGAATCATT	60 120
TTCCATACTT ATTTTTCAAT ATTATCAAAA AGTATGTAAT TTTGGGGGGT TTTTTGGTTT TTTTTTTTTT	180 218
(2) INFORMATION FOR SEQ ID NO:413:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 260 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:	
GAATTCGGCC TTCATGGCCT ACTTTGAACA ATTCGGCATG AATTGAAACC AGGTTTTCCT	60
GTGGAAAGTT ATAGCTTGAT TGGGAGATAG AAGTTGAATT GAGTTCTTTC TTGCAACTCT TAGTGTTTAT TTTTATATCT CAGTAAGACG AGGATACCTT CAGTTTGAAT CTGCATAATG	120 180
TTCACTGCCA AACTCCTTCT CATTTAATGC TTATGGCCTT CACATTTCTG TATAATAAAG ATCAATTATC AGCACTCGAG	240 260
(2) INFORMATION FOR SEQ ID NO:414:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 258 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:	
GAATTCGGCC TTCATGGCCT AAGCATATGA ATTTTGGAGA GACAGACATA CAGACCATAA	60
CAGTTCTATT TTCTATAACT ATAGTAGAAT ATCGAAATGA GAACATTGAC ATTGGTAAAA GGTGTATGTA TAGTTTATAT GTTATCTTAT CAAAAGGGTA GATTTACAGA ACCAACACAA	120 180
GTAAGCTATA GAACTAGCCC ATTACCACAA AGATCTCCCA CAAGCTACAG CTTTACAGTC	240
ATACCCACCC GGCTCGAG	258
(2) INFORMATION FOR SEQ ID NO:415:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 281 base pairs(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:	
GAGGACCTTT ATAATCTACT ACTAATTACT GTGAAAGTAA ACATTGTTTA ATATACCAGT	60 120
TCTTAAAGAA ATATTTTGTC TAGTCATTAA TATTCTAGTT CATCTCAAAG CTTCCATTTG ACAATTTAAA ATTACTTAAA TTTTAATATT AAAGGAAACA GTTTTCCTGA TTCTCATGAA	180
AGTTCCTATT TGCACTGAAG ATGACTAAAC CTTTTAGTCA TAGTTTTAGA AGAATTGGCT	240
TTTTTATAGC CATTTTATTT ACATATGGGT ACGGACTCGA G	281

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 118 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:	
GAATTCGGCC TTCATGGCCT ACTCAGAAAA GAAAATGAAA ATACCTCTAC ATGTGGTCTT CCTGCTAATC TCTCTGACCT TCCTATTCAC CACCCTCCCC ACTGCCCACT TACTCGAG	60 118
(2) INFORMATION FOR SEQ ID NO:417:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 273 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:	
GCGAGGATGG CATGGACGCT TATCGAGCAG CTTCAGGGTG GCAGCTACAA GAAGATTGGC TACTATGACA GCACCAAGGA TGATCTTTCC TGGTCCAAAA CAGATAAATG GATTGGAGGG TCCCCCCCAG CTGACCAGAC CCTGGTCATC AAGACATTCC GCTTCCTGTC ACAGAAACTC TTTATCTCCG TCTCAGTTCT CTCCAGCCTG GGCATTGTCC TAGCTGTTGT CTGTCTGTCC TTTAACATCT ACAACTCACA TGTCCGTCTC GAG	60 120 180 240 273
(2) INFORMATION FOR SEQ ID NO:418:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 145 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:	
GAATTCGGCC TTCATGGCCT AAGCAGTTGC TAATGCCAGC AGTACATAAA TTGAGGATGG AGCAAAAGGA TCGACACCAC CAATGGCTGC ATTGTGATAG GTGTGGACAG AGCCTGCCAG AATTAAACAC ACGCCAGGAC TCGAG	60 120 145
(2) INFORMATION FOR SEQ ID NO:419:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 290 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GGATTCGGCC	TTCATGGCCT	AGTGTTTATA	ATTAATCCTT	TAATATTATG	GTTATTAACC	60
TCTTAAACAT	GAATGAATTC	TTGATTGTTT	TAACACAGTA	CCTAAGACTA	ATGCTTTCTG	120
TGGACACCAC	TGAGCTCTGC	CTCAACTCCA	CCCTCTGCGA	CCGGAGGACT	ATGCCCCTAG	180
TAACTGCTGT	CGGTGTGGAC	GCTGTGCTGG	TTCTGTTTTC	TAAAGGAGCA	GAAGGACAGG	240
TCTCTGAGAC	ACCATCCTTC	TCCCTACAGG	AGGAACAGTG	GCCACTCGAG		290

- (2) INFORMATION FOR SEQ ID NO:420:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GCGATTGAAT	TCTAGACCTG	CCTCGAGCCT	CCCAAAGTGC	TGTGATTACA	GGAGTGAGCT	60
GCCACGCCCA	GCCTACAAGT	TTTTCTTTAA	CTACTGCTTT	AGTCAACCAT	ATCCTCTAGC	120
TTCTGATATT	TTCATTGTTT	GTTGTCATTT	TCTAGATATT	CAACAATTTC	AAATTAGATT	180
TTCTCTTCGA	CTAAAGTGGA	AGAATTTTTT	CCCGTTTATT	TTCTACATGC	TAAAGATTTT	240
TATTTTCATT	TTGTTATTAA	TTTCTAGTGT	TACCGTATTG	TCATTAGAAA	ATATGGGCTG	300
GCTCGAG						307

- (2) INFORMATION FOR SEQ ID NO:421:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GAATTCTGAA	AATATTAAGA	TTTATCCTAG	CACTTACGTT	CAACATACCA	TAATTTTTAT	60
ACTTCTCCAT	CTAAATAAAA	CCAAGTTTGT	TCCTACACTA	GTCCAGCCTG	CATTCTCAAG	120
AACTCCAGTG	ATTATACATC	AACATCTAGA	GATCAGGTAT	CCCAATCCTT	TCTTCCTATA	180
TCTAAGCTAA	CTCCTTCTTA	GCCAAATGGT	ACCCTTTGAT	TTTGTGTTAA	TCCTTTCCTT	240
CCCTCCACTC	TTAACCCCTC	TCATTCCATC	TTCTCCCTCC	CTTTTCCACC	CCACTCTCGA	300
G						301

- (2) INFORMATION FOR SEQ ID NO:422:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GAATTCGGCC TTCATGGCCT AGGTTAAAGT TGTCTGGTAA TAAGGTGGAG TGGATTTGGG GCAGGTTTTA TGTTTGTGT CTTCTCTTAG AAGTCAAAGA GTTGGTGAGG TAACTGCAAT CCTGTCTATA TCAGTGTAGT GATAATGCAC TAGTGTAATG AAGAATGAG CTGCACGTGT GAGGTTTTTC AAGTCCACAA AGATCAGGTA TTGTCTACGG TCAATAAAGA TTTTTTTAAA AAACCCTCTT AACTAAAGAG AGGTAACTTC CTTTTCAAAA CTCTGAAATT TACATGTGCT GACTTATAAT ATGTGTGATC CTCGCTGCTT TTCTGATCCC TGGTGGTTGG GGTGTGTGT TGTGTGTGTC TGTGTGATGG GCTCTCGAG	60 120 180 240 300 360 389
(2) INFORMATION FOR SEQ ID NO:423:	
(2) INFORMATION FOR SEQ ID NO:423:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 326 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:	
GAATTCGGCC TTCATGGCCT AATCTTAAGT GTTTTACATG CTCTACCTGC CGGAATCGCC TGGTCCCGGG AGATCGGTTT CACTACATCA ATGGCAGTTT ATTTTGTGAA CATGATAGAC CTACAGCTCT CATCAATGGC CATTTGAATT CACTTCAGAG CAATCCACTA CTGCCAGACC AGAAGGTCTG CTAAAAGGTC AGAGTAATGC AGAATGCGTG CCTTCATCTC AGATTTGTTC ATCACAGGTG GATCCCATGT GTCTTCAGTA GACAAGTCAC CTTTGTAGCT AGCACCAGTG CCAGCTCCAT GCCATTGCAC CTCGAG	60 120 180 240 300 326
(2) INFORMATION FOR SEQ ID NO:424:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 178 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:	
GCGATTGAAT TCTAGACCTG CCTCGAGCCA ATCATTTTTA AATCTAATCT	60 120 178
(2) INFORMATION FOR SEQ ID NO:425:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:	

60

120

127

GAATTCGGCC TTCATGTACA TAGATCTTCC TAGTGTCATT GACAAAGGTG ACATTTGCAA

GGCTTTTTCT TCATCAGATG CAGGGATCTG GACTTCATGT GTATCCTTTT ATCCACTCCT

CCTCGAG

PCT/US98/06955 WO 98/45436

- (2) INFORMATION FOR SEQ ID NO:426:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GAATTCGGCC	TTCATGGCCT	AGAATTTAAT	TGCAGAAAAT	TATTCATATT	CTTATAATCC	60
TTTTAATGTC	TATAGGATTT	ATGATGATAT	CTCCCCTTCC	ATCCTGATTT	TTTCAAGTTT	120
						180
						240
						300
						325
	TTTTAATGTC TTGTTTTTTC AAAGAACCAG TCTACTCTTT	TTTTAATGTC TATAGGATTT TTGTTTTTTC TTTTTTTTTTTA AAAGAACCAG CTTTTGGTTT TCTACTCTTT ATTATTTCCT	TTTTAATGTC TATAGGATTT ATGATGATAT TTGTTTTTTC TTTTTTCTTA TAAATTCTGG AAAGAACCAG CTTTTGGTTT CATAAAGTTT	TTTTAATGTC TATAGGATTT ATGATGATAT CTCCCCTTCC TTGTTTTTTC TTTTTTCTTA TAAATTCTGG TAAATGTTTA AAAGAACCAG CTTTTGGTTT CATAAAGTTT TATAATTTTT TCTACTCTTT ATTATTTCCT TCATTTTGTT TACTTTGGGT	TTTTAATGTC TATAGGATTT ATGATGATAT CTCCCCTTCC ATCCTGATTT TTGTTTTTC TTTTTCTTA TAAATTCTGG TAAATGTTTA TTAATTTTAT AAAGAACCAG CTTTTGGTTT CATAAAGTTT TATAATTTTT TTGTTTTCAC TCTACTCTTT ATTATTTCCT TCATTTTGTT TACTTTGGGT TTGTTTTGCC	GAATTCGGCC TTCATGGCCT AGAATTTAAT TGCAGAAAAT TATTCATATT CTTATAATCC TTTTTAATGTC TATAGGATTT ATGATGATAT CTCCCCTTCC ATCCTGATTT TTTCAAGTTT TTGTTTTTTC TTTTTTCTTA TAAATTCTGG TAAATGTTTA TTAATTTTAAT AAAGAACCAG CTTTTGGTTT CATAAAGTTT TATAATTTTT TTGTTTTCAC TTTCATTAAT TCTACTCTTT ATTATTCCT TCATTTTGTT TACTTTGGGT TTGTTTTGCC ATTTTTTCC TAGTTTCTTA AGGTGCCAGC TCGAG

- (2) INFORMATION FOR SEQ ID NO:427:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GAATTCGGCC	TTCATGGCCT	AGGCACACAG	GGCGGGCAGC	AACATAAACG	GCACCCATTA	60
AAAAGCAAGA	CTCGCTCTTG	AGACTAAAGG	AGAAGTTACC	TAAATTTCTG	TATAAACTCA	120
GTAATTCATT	CACTTTACTA	GTATTACATT	TATGAAATTC	ACCTTTGTGG	AAAAAGGAGC	180
GGGAGAGGGA	TAAGAAAATG	CCTGTTTCTA	GAAAACGCTC	GAG		223

- (2) INFORMATION FOR SEQ ID NO:428:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

GAATTCGGCC TTC	ATGGCCT AAATTCATAC	AGAAGACCTT	ATTGTGATAA	AGTTCAACGG	60
	CAACAAA AAAACTATCA				120
	TAATATT TTATACACAT				180
	TCTAGAT CATTATTTT				240
•	AGTTTTT GTGAGTGTA				277

- (2) INFORMATION FOR SEQ ID NO:429:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

AAATGAGCCC T	TATCACTGAG	AAATACGTGT	TTCATGATTT	AACTCTGTGT	GTGTGTGTGT	60
GTGTATTTTT T	TTTTGGTTG	TCTTCAGCTG	ACAGTATGAA	AAATGAAACT	GCTGAAAAAG	120
CTGAGCACCT G	GTCACCCTT	GGCCTTCCAT	TGCTTTGGCC	TTCAGTAAAA	AGCAGCCTCC	180
CTTCTAGGTC A	AGGGAACCAT	GCCATTGAGA	CTAGTAACGG	GCGTTCTGGG	CACAGTCCCA	240
CTGTGCACAG G	TTTGAGAGG	ACAAGTTCAT	CAGAAGGAAG	GCAGTCCTTA	GAAGTCACAT	300
ACGTTGAGCC C	CTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:430:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 271 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GAATTCGGCC	TTCATGGCCT	ACATTCAGAA	AACAGAAAAG	TTTCAAGAAG	CAGGAAGAAA	60
AGACTCACCT	ATGATCCCAA	CACCCAGAGG	TAATAATTTA	CCATTTTTGG	TGTATCTTCT	120
TTGTCTTTTC	CTATGTGTTG	CCTTATGTAG	ATATGTAACA	GGTTGTGGTT	TAAACCGAAG	180
CTATACCCAT	TGTTTGGAGT	CAGGCAGGTG	CGATAAATTT	GTAGGTGGCT	CACCAGAAAT	240
CTATTTGCAT	GATGAACCTA	CAGGACTCGA	G			271

- (2) INFORMATION FOR SEQ ID NO:431:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double .
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

TGGTCACCAA	TCTCTCATAT	ACCACTACTG	GATATTTACA	ACATGCTTCA	60
AGACACTGCT	GCTTTGCAAA	GATGACCTGG	AATGCCAAAA	GGTCTCTGTT	120
CTTATTGGAG	TACTTTCTCT	AGTGTTTCTT	TTTGCTATGT	TTTTGTTTTT	180
GACTGGCTGC	CAGGCAGAGC	TGGATTCAAA	GAAAACCCTG	TGACATACAC	240
TTTCGGTCAA	CAAAAAGTGA	GACAAACCAC	AGCTCCCTTC	GGAACATTTG	300
GTCCCTCAAA	CCCTGAGGCC	TCAAACAGCA	ACTCTCGAG		349
	AGACACTGCT CTTATTGGAG GACTGGCTGC TTTCGGTCAA	AGACACTGCT GCTTTGCAAA CTTATTGGAG TACTTTCTCT GACTGGCTGC CAGGCAGAGC TTTCGGTCAA CAAAAAGTGA	AGACACTGCT GCTTTGCAAA GATGACCTGG CTTATTGGAG TACTTTCTCT AGTGTTTCTT GACTGGCTGC CAGGCAGAGC TGGATTCAAA TTTCGGTCAA CAAAAAGTGA GACAAACCAC	AGACACTGCT GCTTTGCAAA GATGACCTGG AATGCCAAAA CTTATTGGAG TACTTTCTCT AGTGTTTCTT TTTGCTATGT GACTGGCTGC CAGGCAGAGC TGGATTCAAA GAAAACCCTG	TGGTCACCAA TCTCTCATAT ACCACTACTG GATATTTACA ACATGCTTCA AGACACTGCT GCTTTGCAAA GATGACCTGG AATGCCAAAA GGTCTCTGTT CTTATTGGAG TACTTTCTCT AGTGTTTCTT TTTGCTATGT TTTTGTTTTT GACTGGCTGC CAGGCAGAGC TGGATTCAAA GAAAACCCTG TGACATACAC TTTCGGTCAA CAAAAAGTGA GACAAACCAC AGCTCCCTTC GGAACATTTG GTCCCTCAAA CCCTGAGGCC TCAAACAGCA ACTCTCGAG

- (2) INFORMATION FOR SEQ ID NO:432:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GAATTCGGCC	TTCATGGCCT	ACCTGGATTT	CTCAATTTAT	TAAGTTGTAC	TTACCTGATG	60
CTGATGATGA	TTACTGTATT	TACACATTGT	CTCAGAGCTC	ACTCTTGCGG	AGGTTGTGGC	120
CTCGAAAATG	CCTTGTTGTC	CCTCTGGAAT	CTGTCTTTTC	AGCTTCATCT	CCTCCTCCTC	180
ACCTCCTGCT	GTGGTGCACA	GATACCTATA	GGCAGGCTCC	ATCTCCTCCT	CCCCAGCTCC	240
TCCCCTAGTG	CACACCTCGA	G				261

- (2) INFORMATION FOR SEQ ID NO:433:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

GAATTCTAGA	CCTGCCTCGA	GTCCTACGGG	AAACCTCCAG	GGTTTTAGGA	AGCTGACGAT	60
GCAAGTTTAT	CCAAATGGGA	ATGATAATAA	TCATGTTTAT	TATCCTGGGG	TGCTTTCTCC	120
ATAGCAAGTA	CTCACTTAGG	TCCTGTTCAT	TAGTCAGTCT	TTTAATCTGT	ACTGAAATAG	180
GTGCTGTCGC	ATCCATGGGG	AATGAACTCG	AG			212

- (2) INFORMATION FOR SEQ ID NO:434:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

GGTTGCAGTG	AGCTGAGATC	GCACCACTGC	ACTCCAGCCT	GGGCAACAGA	GTGAGACTTC	60
ATCTCCAAAA	АААААААА	AAAAAAAAGA	CAACCACAAC	AAAAACGAAA	CACCACCACC	120
AAAAAAGTTT	ACTGGTAGAG	TCTCCTCTAG	ATTGTTTTCT-	TTTCAATACT	TGTTTCATAT	180
TCTCCAACTG	CCCTCGTCCC	ATAATGTTGG	CTGTGCTTTT	CTTTGTGCTT	ACAGCTCATT	240
GCTGGGATGG	ATATGGTGAG	TTTTCATGTA	CATTGACCAA	ATACAATCTC	GAG	293

- (2) INFORMATION FOR SEQ ID NO:435:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

GAATTCGGCC TTCATGGCCT AGGCTTGAAA GGAAATGAGG GAAATTTCAG TGAGTTTGAG 60

GAATGGCAGA CTGGGTATGT GACAAATGAG TGGGTAAATA AGGAAATCTC AGATTGAGAA TCCTGGCAGA TCTTTCAATG GGTTAGACTG CAGGAAATATT GATTTTAAAG CCAGACTGAA GCAAATTCTA GTGATAAAGG AAGGGGAAAG GGTGGCTGAA TCAAATGTTC TACCAATACT CCTTTTTTTA GTATTTGAGT TAAAATTCAG ATTANATGCT TGGCTTAGAA GAATGCAAAG CTTCACTGAG CCTAATAATA TGGATCCCAG TGGGTGAGTG GAGGTGAGTT CACTCGAG	120 180 240 300 358
(2) INFORMATION FOR SEQ ID NO:436:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 258 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:	
GCTCGAGAGA GCTTTTTTT TTTTTTTAA ACATTGTATC ATTAATTTAT CACGTGTATC CAAGCTCCTT TGAGTTTCCC TGCCCCCATC CCTGTGTCAT TCCAGCCATA TCCAGCTACT CCTTCCATGC TTCCCCCATT CTTGTTTCTG ACTCTATTAC TCCCAGTCCA AATCTTGCTC TTCACTGTCT GCACCTTGTG CTCTCCTCTC	60 120 180 240 258
(2) INFORMATION FOR SEQ ID NO:437:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 299 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:	
CAAGCCGGCC ATATTAGAGA GATGGAAATA AAGCTTCCTT AATGTTGTAT ATGTCTTTGA AGTACATCCG TGCATTTTT TTTAGCATCC AACCATTCCT CCCTTGTAGT TCTCGCCCCC TCAAATCACC CTCTCCCGTA GCCCACCCGA CTAACATCTC AGTCTCTGAA AATGCACAGA GATGCCTGGC TACCTCGCCC TGCCTTCAGC CTCACGGGGC TCAGTCTCTT TTTCTCTTTG GTGCCACCAG GACGGAGCAT GGAGGTCACA GTACCTGCCA CCCTCAACGT CCACTCGAG	60 120 180 240 299
(2) INFORMATION FOR SEQ ID NO:438:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 238 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:	
GAATTCCTAC TAAATAATAT TAAGCAGGAA TTTTTTAGGT GTTGCTTTTT AGCTCCTTTT TATCAGTTCT GGGAAGCAAA CAGTGCTGCA TCTCCTTTGC TCTCATAGAA TTCTGTAATT TTTATACCAC AGGTCTCTGC TAAAAGGCGG CATGTGTTTA GAAATTCTAA AAATGAGGGC TCTGAACTTT GTAACTGTCC TGATACGTTT TCCCTTTTTT AATCCCAACC CCCTCGAG	60 120 180 238

(2)	INFORMATION	EOD	CEO	TΠ	MO. 420
21	INFORMATION	ror	SEU	11	NU:439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

GAATTCGGCC	TTCATGGCCT	ACAACTTGCA	CTTCGCTCCA	GCATCACTGG	CCTCCTGCTG	60
TTATTTAGGT	ATACTAGGCA	TTTCCTGTTT	TAGGGCCTTT	GTACCTCCAG	TTCCCTCTGT	120
TTGGAATGCT	TTTCCCCAGA	TAGCCCTGTG	GTTAAATCTC	TTACTTCCTT	TGGGTCTGTG	180
CTCAGATGTT	ACTTTCTCAG	AGGGTCCCCC	AAGCCCCCAT	GCACTCGAG		229

- (2) INFORMATION FOR SEQ ID NO:440:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

GAATTCGGCC	TTCATGGCCT	AGAGTCTATT	AACTATTTTT	CTGTTATACC	CTGCCAGAAA	60
AGAATTTTAA	AAGTTAGTTT	ATGTTTTGTG	TAACCATGTT	CTTCAGAATG	CAGGTATGTG	120
AGCATCATGG	TTTCTGGGTA	ATTCTGCTGC	TCCTGTCTTT	GAAAATGGAG	ATACCACTTG	180
CAGCTTATCC	CACTGCTGAG	TATTCCAGCA	TTGGTAGTGG	TTTCACTCCA	TTGCATCCAT	240
CCAGAACTTT	CACACAGGCC	TCCCCATTAC	CCAGCATCCT	CGAG		284

- (2) INFORMATION FOR SEQ ID NO:441:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GAATTCGGCC	TTCATGGCCT	AATAAAATAA	AAATTGGAAG	AATGGCATTT	TATTACAGTA	60
TAGTTAAGAG	ATTGGCTAAG	GCAGTAAATA	AAACTTAGAA	ATGCTCAAAT	TTATTGTAAA	120
TTGCTTTTAT	AATCATTGAT	ATATAAAGCA	TGCTACTGCT	AATCAATTAG	TTTTATGTAT	180
TAAGACCTAT	CAGCATGTCT	TTTTTTTAGT	ATCTGGTTGA	CTTAAACATG	ATGTTCTCTG	240
TACCATTTAA	CATTTTCAAG	ACATATTCTC	CCCAAACTCG	AG		282

- (2) INFORMATION FOR SEQ ID NO:442:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

G						241
TGATCATCCT	ACATGTCAAG	CACTGCCAAC	GTTTACTCAA	GAAAGCTTGG	TTAGAACCCA	240
ATTCCTTTCC	AAATGTGATT	CCAGACAGTA	TATCCAAACA	TGTCTTTCTT	TTCCCATTCC	180
TCTATTCTTT	CTGCATCAAA	TAATGAATAG	CTCATTTTGT	GTTGCCTTCA	AGTATGACAA	120
GAATTCGGCC	TTCATGGCCT	ACTCACCTGC	AATCTATTGT	TTATATTGTT	GCTATGTATC	60

- (2) INFORMATION FOR SEQ ID NO:443:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (E) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

GCAAGCACAA	ATCTAACCAT	GAGCTTCAGC	AATCAGCTCA	ATACAGTGCA	CAATCAGGCC	60
AGTGTTCTAG	CTTCCAGTTC	TACTGCAGCA	GCTGCTACTC	TTTCTCTGGC	TAATTCAGAT	120
GTCTCACTAC	TAAACTACCA	GTCAGCTTTG	TACCCATCAT	CTGCTGCACC	AGTTCCTGGA	180
GTTGCCCAGC	AGGGTGTTTC	CTTGCAGCCT	GGAACCACCC	AGATTTGCAC	TCAGACAGAT	240
CCTCTCGAG						249

- (2) INFORMATION FOR SEQ ID NO:444:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

GAATTCGGCC	TTCATGGCCT	AGGGATTTTT	TTTCTTTTTT	TTCCTCATAT	GTGAAGTAAT	60
AGTCTCTTCA	CAACAGAAGA	AGCCACAAAA	CTAAACTTAT	TGGTCACTGA	ATTTTCTTCA	120
AGGTTACGTA	CCTCTTTGGT	ATTTTAAATC	TAGATTATGT	TGATTTTTAT	ATTTTTGTTC	180
TCATTTTTCT	ATTTCTTTGT	TTTCTTTACT	GCAAATGGGC	TCGAG		225

- (2) INFORMATION FOR SEQ ID NO:445:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

GAATTCGGCC	TTCATGGCCT	AGTTTTGGAG	AGCTCTACCT	ACTAGCTGGT	TATTTCTTAC	60
ATTAAATTAA	TACCTTTAAA	AAGTATTATG	AAAATAACAC	ACTCAGTAAA	AGAAATTTTA	120
AAAAACAAAT	GCAATAAAAA	TGTGTTTCTT	TTCAACCTTT	GACTTGTCAC	TTCCTCCAGC	180
TTTTCCCTTA	TTTAACTGTG	AGAGGTATTC	TCTATTAGCA	GTTACTTATC	CCCTTCCTCA	240
AACTCGAG						248

- (2) INFORMATION FOR SEQ ID NO:446:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

GGATTGAATT	CTAGACCTGC	CTCGAGCGAC	CTCTAGAATC	CTACATTTGA	AATATTCTGG	60
CAGTGAGGTG	TTCATCCTAA	CTCAGTCAGG	TAGCTGTGGA	CAGCCTTCAC	CTGTTAGGAG	120
CTCCTTAGAA	ATAAATTCTG	AATACCTTTG	GTTTTCTTTT	ATCCTCCAGA	GGAATTTCCA	180
CTATCTCCGA	AGCTGTTCCT	TGTTCCACTG	ACAATTCGCT	TAGTTAATGT	TCTTTTTTAG	240
CCTGTACTAT	CTCGAG					256

- (2) INFORMATION FOR SEQ ID NO:447:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

GAAGGCAAGA	AAATCTATGG	AAAGAGAAAGG	CTACGAGTCC	TCGGGCAATG	ATGACTACAG	60
GGGTAGTTAC	AACACCGTGC	TCTCACAGCC	TTTATTTGAA	AAGCAGGACA	GAGAAGGTCC	120
AGCCTCCACG	GGAAGCAAAC	TCACCATTCA	GGAACATCTG	TACCCCGCGC	CTTCATCACC	180
TGAGAAAGAA	CAGCTGCTGG	ACCGCAGACC	CACTGAATGT	ATGATGTCGC	GATCAGTAGA	240
TCACCTCGAG						250

- (2) INFORMATION FOR SEQ ID NO:448:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GAATTCGGCC	TTCATGGCCT	AGCTGGGGGG	AATAGGTTAT	GTGATAAGGA	GTCAGTCGGA	60
CAGAGTGGGG	TGAAAGATGT	TCAGACAGGG	AAACACACAT	GCAANAGAGG	GAAGGTGGGA	120
CACAGCATAT	GCNTCCAACA	TTTGGTAGGG	CCGAGGCCCC	ACATGGGAGC	AGTGAGAGGT	180
TAGGGATCGA	CGCTCGAG					198

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 163 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:	
GAATTTTCCT TACCAGGAAA ATTCATGCTT TACAATTTGT CAGAGGTGCA CATTACTAAT TACAATAGGT CACACTTTTT CTATGCGCTT CATTATAATA TTGGCAACTT TATTATGCCC CATTACATAC TGTATTATGC TCTTACTTTA TATGCATTTT GAG	60 120 163
(2) INFORMATION FOR SEQ ID NO:450:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 122 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:	
GAATTGCTGA TATCTTATAA AGGGGACCTT TTTTCTTTAC ATTTCTGACG GTTTTTATCA GAATGTATGT ATTAATGCTA TTTGTCTTTG TATATTTATT TTATTTCCAG CCACTTCTCG AG	60 120 122
(2) INFORMATION FOR SEQ ID NO:451:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 302 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:	
GAATTCGGCC TTCATAGCCT AACTCAAGAT CTCCCATCTA TTAAAGCAGA GGAATAACTT TTGTAGGCTT AATACTGCTT TCTCACTTAG GAAAAGTTGA AATTAAGAAC ACACAGGAAG GGATCATTTC CTAAGGTTTA TGTCCTCAAC ATCAAATTGA GTTGAAACTT GACTACAGGC CATCTGCTCA TTCAAAGCAT TACAATAAAT CTGTCCTATT GATGATCAAA ATGAGAGCTG AATTGGATGC AGGATTGGAC ATTGCAAGCT GTTCTCCCAA GTGGGATGGA AAGGTGCTCG AG	60 120 180 240 300
(2) INFORMATION FOR SEQ ID NO:452:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 265 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GAATTCGGCC	TTCATGGCCT	ACAAAAATAT	TTATTTGACT	GAATGATTTA	ATATGCAGTT	60
ATGGTGTTTA	ATATATCATG	TGTTATTTGT	TTGTTTAAAT	ACAGACATAA	CCCACAGTTA	120
TCTTGAACAA	GAAACTACGG	GGATAAATAA	AAGTACGCAG	CCAGATGAGC	AACTGACTAT	180
GAATTCTGAG	AAAAGTATGC	ATCGGAAATC	CACTGAATTA	GTTAATGAAA	TAACATGTGA	240
GAACACAGAA	TGGCCCGGAC	TCGAG				265

- (2) INFORMATION FOR SEQ ID NO:453:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GAATTCGGCC	TTCATGGCCT	ACTTTAATTT	CTCTGAGCAG	TATTTTACAG	TTTTGATGTA	60
TAAACCTGGC	ACAGATTATG	TTCAGTTTAT	TTCTAAGTTT	AAGTCATGTT	TTTGAATGTT	120
ATATTAAAGG	ATATTTTCTT	TTTTAAAAAA	TCTACAATGT	TTATTTTATT	TTTATTATTA	180
TTAATCTCGC	TTCATCACCA	AGGCTGGAGT	AAAGTGACGC	GACCTCAGCT	CGAG	234

- (2) INFORMATION FOR SEQ ID NO:454:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GAATTCGGCC	TTCATGGCCT	ACGCACATCC	GCAGTCAGCC	ACCTCGCGCG	CGCCTCCAGG	60
AGCAAGGATG	GAGAGGCTGG	TGATCAGGAT	GCCCTTCTGT	CATCTGTCTA	CCTACAGCCT	120
GGTTTGGGTC	ATGGCAGCAG	TGGTGCTGTG	CACAGCACAA	GTGCAAGTGG	TGACCCAGGA	180
TGAAAGAGAG	CAGCTGTACA	CACCTGCTTC	CTTAAAATGC	TCTCTGCAAA	ATGCCCAGGA	240
AGCCCTCATT	GTGACATGGC	AGAAAAAGAA	AGCTGTAAGC	CCAGAAAACA	TGGTCACCTT	300
CAGCGAGAAC	CATGGGGTGG	TGATCCAGCC	TGCCTATAAG	GACAAGATAA	ACATTACCCA	360
GCTGGGACTC	CAAAACTCAA	CCCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:455:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

GAATTCGGCC	TTCATGGCCT	AGCTGATATT	ATTTCTGAGT	TTTTGCTTAT	TTGCTTTCTA	60
CATAGAATCA	ATAAAATTGA	CAACTAGCAT	TGCCTATATA	TGCAGGTGTG	ATACTATTCA	120
GGGTACTAGT	ATATTGGCCA	CTCATTATGA	AACTTTCAGG	TCCTCATATA	TTTTCTTTTA	180
TTACAATGAT	CTACTTATTT	CTGATAAATA	TTGGATTCAT	AGAGGCTAAA	GGGCTGGGAA	240
AGGAAAACAT	TCGTGACTAC	TTACAACCAT	TTGATACGAG	TTGTGTCAAT	ACAGACCTCA	300
CACAGCAGCA	CCTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:456:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GAATTCGGCC	TTCATGGCCC	ACAAAATGGT	AATACAAATA	AACCACTACT	TACTGCTTTT	60
AATGGTAGTT	TGTTTTTTT	TTTTTGAGAC	AGAGTCTCGC	TGTGTCGCCC	AGGCTGGAGT	120
GCAGTGGCGC	GATCTTGGCT	CACTGCAAGC	TCCGCCTTTC	GGGTTCACAC	CATTTTCCTG	180
CCTCAGCCTC	CCGAGTAGCT	GGGACTGCAG	GCGCCCGACT	CCCGGGTTCA	CACCATTCTC	240
CTCCCTCAGA	CTCGAG					256

- (2) INFORMATION FOR SEQ ID NO:457:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

GAATTCGGCC	TTCATGGCCT	AGGAGAATCG	TGAGACCTCT	ATTTCCATAT	CTTTTTCTAC	60
TACTGGAATT	TTTATTTTTA	CCATACCCAT	AAATTACTTT	CTATTTTAAG	AAGCAAATAT	120
ATAATTCCTC	AGTTTAGTAA	AAAGTTCTCA	CTTGAAAAGC	TGGTATATGA	ACTTTAGAGG	180
GCAGATTAAT	CAACTGCTAA	AATTATTAA	TCTTTCTTCT	TGGAACTTTC	CAACACAAAA	240
GACAGTTTAT	AGAAAACAAA	GTCAGTGTTC	AAAACAGCTG	AATGAACTAT	CTTTTGATAT	300
TTTATTTGTT	TTTGTTTTGT	TTTGTTTTGT	TGAGACAGAG	TCTTGCTCTG	TTGTCCAGGC	360
TGGAGAGTAA	TGGCACGATG	ACTGCAACCT	CTGCCTCCCG	GGCTCAAGTG	ATTCTCCTGC	420
CTCAGTCTCT	CGAG					434

- (2) INFORMATION FOR SEQ ID NO:458:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

GAATTCGGCT TCATGGACGA GGAGATCGTG TCCGAGAAGC AAGCCGAGGA GAGCCACCGG 60

CAGGACAGCG CCAACCTGCT CATCTTCATC CTGCTGCTCA CCCTCACCAT TCTCACAATC TGGCTCTTCA AGCACCGCCG GGCCCGCTTC CTGCACGAAA CCGGCCTGGC TATGATTTAT GGTCTTTTGG TGGGCCTTGT GCTTCGGTAT GGCATTCATG TTCCGAGTGA TGTAAATAAT GTGACCCTGA GCTGTGAAGT GCAGTCAAGT CCAACTACCT TACTGGTAAA TGTTAGTGGA AAATTTTATG AGTATATGCT GAAAGGAGAG ATACTCGAG	120 180 240 300 339
(2) INFORMATION FOR SEQ ID NO:459:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 256 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:	
GAATTCGGCC TTCATGGCCT ACTTATTTT GTTTCTGTGT GTTTGTTTTA AATGTGTGTG CGCTCATGTG AGTTTGAAGG GAGTTAGATG CAACAGCAGG AGCTGTGCTC AGGGCAGTGG TGTTAATTAT GGAGGGCGTG GGAAGGGCTG GGAAGAGGAG GGGGTTGTAA GACTCCCCTT TTCCCTCGCA TGTAAACAGA TGCTGGTGAC TGAAAGTCTG TCTGCGGTTA TTGGCAAGAG TGACGGAAAG CTCGAG	60 120 180 240 256
(2) INFORMATION FOR SEQ ID NO:460:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 320 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:	
GAATTCGGCC TTCATGGCCT AATTTGAAAA TTCATAAGTT TCTACCAATA CTTCCAATTT CAATCCAACA TCTGAGGATC TCCCTAGATT TCCTATTTCC ATGATTATAA CTCTTGTACC AGATGATAAG AAACATGGAT CTGACTATAC TCAATTTATT CACATATTTT CTCAGTGAAC TAACTTATTT GCTGAATATA ACCAGTCCCC AGCCTTCCAA CTGCCTCTCT CACTTGCCAC CTCTGCATCT TCCCCCACTG TCTTCCTCAG CAATCAGACT GCCTCTTGCC AAGTCATCAC CACAGCACCC CACTCTCGAG	60 120 180 240 300 320
(2) INFORMATION FOR SEQ ID NO:461:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 307 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:	

60

120

180

240

GAATTCGGCC TTCATGGCCT ACCCTCTACT ATTTTTGAAC CAAATCAACA ACAACCTATT

TAGCTGTTCC CCAACCTTTT CCTCCGACCC CCTAACAACC CCCCTCCTAA TACTAACTAC

ACGAAAAAA CTCTACCTCT CTATACTAAT CTCCCTACAA ATCTCCTTAA TTATAACATT

CTGACTCCTA CCCCTCACAA TCATGGCAAG CCAACGCCAC TTATCCAGTG AACCACTATC

CACAGCCACA GAACTAATCA TATTTTATAT CTTCTTCGAA ACCACACTTA TCCCCACCCA

300

TCTCGAG	307
(2) INFORMATION FOR SEQ ID NO:462:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 254 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:	
GAATTCGGCC TTCATGGCCT AGTACAATTT AATATAATTT CTTACAAGTT TATTACCTAA AACTTTGCAA ATAATTGAAG TTAGAAGCTT TGGATTTTGT TTTTAGAGCT TAATCCTTTT CTGTAAGTGG AAATCCTTTC CACTGGTTTA TTTTCCTTTT GATTTTATTT TACTTTGACA CCCTAAAGGT TTAGTGTTCC TGTTTTTAAA TCTACTGATC GTTTCTTATG AGATTCCTTA GAGTACCCCT CGAG	60 120 180 240 254
(2) INFORMATION FOR SEQ ID NO:463:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 283 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:	
GAATTCTAGA CCTGCCTCGA GAGGACGCCG GAGAGAAATG AGTAGCAACA AAGAGCAGCG GTCAGCAGTG TTCGTGATCC TCTTTGCCCT CATCACCATC CTCATCCTCT ACAGCTCCAA CAGTGCCAAT GAGGTCTTCC ATTACGGCTC CCTGCGGGGC CGTAGCCGCC GACCTGTCAA CCTCAAGAAG TGGAGCATCA CTGACGGCTA TGTCCCCATT CTCGGCAACA AGGTAGCGCA GCTGCTTTGG GGAGCTCCTC CCTACTGCCC AGCAAAACTC GAG (2) INFORMATION FOR SEQ ID NO:464:	60 120 180 240 283
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 233 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:	
GAATTCGGCC TTCATGGCCT AAAAAGTGGT TCCTATTTTC CTGGTTGAAC CTTGAGTGAT ACACCCAGTA TTGTACCACC CAATTAGTAG ACATTATTTC TTCTTAGGTC ATATTATTCT CAGCTTATAG AGCAAGAAGT TGAAGCTTAA AGGGTTAGAT TACTTGCCCA AGGTAATACA GCAAGAATCT TATTTCATCC AACCTAGAGT GAATATTTCC CCCACATCTC GAG	60 120 180 233
(2) INFORMATION FOR SEQ ID NO:465:	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GAATTCGGCC	TTCATGGCCT	ACTGATGTTG	AAGACGACAC	CACGGCTTTG	ATGGAATATC	60
AGATATTGAA	AATGTCTCTC	TGCCTGTTCA	TCCTTCTGTT	TCTCACACCT	GGTATTTTAT	120
GCATTTGTCC	TCTCCAATGT	ATATGCACAG	AGAGGCACAG	GCATGTGGAC	TGTTCAGGCA	180
GAAACTTGTC	TACATTACCA	TCTGGACTGC	AAGAGAATAT	TATACATTTA	AACCTGTCTT	240
ATAACCACTT	TACTGATCTG	CATAACCAGT	TAACCCAATA	TACCAATCTG	AGGACCCTGG	300
ACATTTCAAA	CAACAGGCTT	GAAAGCCTGC	CTGCTCACTT	ACCTCGGTCT	CTGTGGAACA	360
TGTCTGCTGC	TAACAACAAC	ATTAAACTTC	TTGACAAATC	TGATACTGCT	TATCAGTGGA	420
ATCTTAAATA	TCTGGATGTT	TCTAAGAACA	TGCTGGAAAA	CGTTGTCCTC	ATTAAAAATTA	480
CACTAAGAAG	TCTCGAG					497

- (2) INFORMATION FOR SEQ ID NO:466:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GAATTCGGCC	TTCATGGCCT	AGCCCCGACT	AGCTTTGCCC	TAACTCCTTC	ATCAAAAGAC	60
CCCCCCCCAG	CTTCCCACAC	CTCATACGCA	GCCACATCTG	CCCTATTCTC	CATGCTTTCC	120
AGCTTGCCTG	CCCTTCCTCA	TCTCTCCCTG	CCTGTGCAGA	CCTCCACCCT	TCTTTCCTCC	180
ACCCCTCCAT	CCCCCAATGC	TTGTAGACCT	TCCATTCATT	CCGTCTCATC	GTGCGTGGTC	240
TCTGATCGTC	CATCACCTGA	CCTCGAG				267

- (2) INFORMATION FOR SEQ ID NO:467:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

GTTTACATAA	ATATTATACT	AGCATTTACC	ATCTCACTTC	TAGGAATACT	AGTATATCGC	60
TCACACCTCA	TATCCTCCCT	ACTATGCCTA	GAAGGAATAA	TACTATCGCT	GTTCATTATA	120
GCTACTCTCA	TAACCCTCAA	CACCCACTCG	AG			152

- (2) INFORMATION FOR SEQ ID NO:468:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

CAATATTTCA AGCTATACCA	AGCATACAAT	CAACTCCAAG	CTCGGAATTT	TAACTTCATG	60
GCAAACAGAA AAGCTAGACT	GAGTTATCAG	TGTTGTGAGA	GGAATATTTG	GCCCAACAAG	120
AGTTGTTGGG GTGGGAGGAG	GGAGAGACAA	AAGGAAAGGA	CTGCCAGCTC	TCAGAGGGTG	180
GAGATGGGGG ACCTCGAG					198

- (2) INFORMATION FOR SEQ ID NO:469:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (J) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

GAATTCGGCC	TTCATGGCCT	ACTGCTATAT	TCAAGTTTCT	CCCACTACTG	TGGTTTCTTT	60
TTTTTTTTT	TTTTTTTTTT	TTTTGAGACA	GGGTCTTGCT	CTGTCACCCA	GGCTGGGGTG	120
CAGTGGTGCG	ATCTCGGCTC	ACTGCAAATT	ACACCTCCTG	GATTCGAGCA	ATTCTCATGC	180
CTCAGCTTCC	TGAGTAGCTG	GGATAACAGG	TATGCACCAC	CACCCCTGGC	TAATTTTTGT	240
GTTTTTAGTA	GAGACAAGTT	CTCACCATGT	TGTCCAAGCC	ACCTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:470:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

GAATTCGGCC	TTCATGGCCT	AAAAGAAGAA	TACTAATTAG	AATTTGAGTT	CTAGGGGTTT	60
TTCCTAGGTT	TTTCATTCTA	GACTTAGCTT	TTATTCAAAC	CTGTTGATCC	TGCATAGGGG	120
TAGTCTAGCT	TTAAAAAATA	AAACAATAAA	CATAAATGAG	CCTATTGAGT	TCAATCAGAG	180
TAGGGAGCAG	TTTTATTGAA	CAGCACATTT	TCAAATTCTT	CAGTTGTGTT	TTGTTTTTCA	240
GCTACGTGTC	TCTCTGTGAT	AATGAAAAGA	CAGGTTGCAA	AGCCCGGGAA	CTAAAATCAG	300
TTTATGTGGA	TGCAGTAGGA	CTCGAG				326

- (2) INFORMATION FOR SEQ ID NO:471:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

GAATTCGGCC	TTCATGGCCT	AGTGTAAAGT	GTTTTTGCAC	AGTGCCCAGA	AATTTGCAGT	60
ATTTAATGGT	CCTTCCTCCT	TATTTATTTT	TATTACTTGT	TTTTGTTTTT	TTGAGACAGT	120
GTCTTGCTCT	GTCGCCCAGG	CTGGAGAGCA	GTGATATTAT	CGTGACTCAC	GGCAGCCTCG	180
ACCTCCCAGA	CTCAGGTGAT	CCCTTCACCT	CAGCCTCCCA	GGCAGCTGGG	ACCATAGCTA	240
TGAACAAACA	CGTCCAGCTA	TGTTTTGTAT	TTTTTGTGAA	GACGGAGTCT	CACCATGTTG	300
CCCAGGCTGA	TCTCCAACTC	CTCGAG				326

- (2) INFORMATION FOR SEQ ID NO:472:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

GGAAAGGTGT	TGTCCCTTGT	AACATTTTGG	TTGGCTATAA	AGCTGTATAT	CGTTTGTGCT	60
TTGGTTTGGC	TATGTTCTAT	CTTCTTCTCT	CTTTACTAAT	GATCAAAGTG	AAGAGTAGCA	120
GTGATCCTAG	AGCTGCAGTG	CACAATGGAT	TTTGGTTCTT	TAAATTTGCT	GCAGCAATTG	180
CAATTATTAT	TGGGGCATTC	TTCATTCCAG	AAGGAACTTT	TACAACTGTG	TGGTTTTATG	240
TAGGCAACCT	CGAG					254

- (2) INFORMATION FOR SEQ ID NO:473:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GAATTCGGCC	TTCATGGCCT	ACAGAAATCT	AATTCCTGGT	GCTATTTGCA	ACTACATATA	60
TTTAAAATAC	AAGGAGATAA	ATACCCAGAA	CACATTAAGC	CTACTGATTT	AAACAGAACA	120
TTTCAAGACT	GCTACACAGA	AAGGGAAGGA	AGCTGTTAAC	CCAGCACAGC	AGCACACCTC	180
ACATATTTAC	GTCTCAGAGA	TTAAATGGAA	AGAAAGGATC	AATCAAAACC	TTTAATGCTC	240
AGTTTTCACA	AACACAGTCA	AGTCTATCAA	ATTTCCAGAT	TTACAG		286

- (2) INFORMATION FOR SEQ ID NO:474:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

GAATTCGGCC	TTCATGGCCT	ACAATTAAAA	GGTTCTGTTA	AATTACGTCT	TTCAGTCTGA	60
AATTACTCTG	AGAATTTACT	TAAAATTTTT	CCATTTAAAA	ACAGGTATAA	AATTAATTGC	120
TAGTTTCCAT	AATCACCCAG	TATAAAGATA	GAAAAGACCT	GTAAGACAAC	TGTGTGGTTA	180

AATACATGAT AACACATTTA CGTGCCTTTT ATAGAAATCC ACTTATTATG TACATACTGG CTTGTTTTTT TTCCCACTTC TCCAGTACAC TATTTCAGGC ACAGGCTCAA AATTTGAACC CAAATGGTCT GTTAGGTCTC TTGACTTTTT CAGTTCAAAG CTCTGCTAAT CTGCTAAACC TAGCCCCAAA CCCACTCGAG	240 300 360 380
	/
(2) INFORMATION FOR SEQ ID NO:475:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 254 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:	
GAATTCTAGA CCTGCCCGGA GCCCTGACCT AGTCCGGCGT GGAGAGAGGA ATGGAAAGCA GTGTCCCTTT TGAGAAGGCA AATTTACAGC TGGCTTTTGT AATCCTAGCT ATTTTTTGTT TGTTTGCTAA GTCTTTGATA GTCCCCAGTG TGGTTTGTCT GCCAGTGATC TCAGCACCAC CAGAGAGCTT GTTAGAAATG CGGCATCCCA ACCCCACCAC AGCCCTCCCA AGTCAGATAC TCCCCCCTCT CGAG	60 120 180 240 254
(2) INFORMATION FOR SEQ ID NO:476:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 389 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:	
GAATTCGCTG TGGAGCTGGG CGTGCTGTTC GTCCGGCCCC GGCCCGGAAC CGGGCTGGGT AGAGTGATGC GGACCCTCCT GCTGGTGCTG TGGCTGGCGA CGCGCGGAAG CGCGCTCTAC TTTCACATCG GAGAGACGGA GAAGAAGTGC TTTATTGAGG AGATCCCGGA CGAGACCATG GTCATAGGAA ACTACCGGAC GCAGCTGTAT GACAAGCAGC GGGAGGAGTA CCAGCCGGCC ACCCCGGGGC TTGGCATGTT TGTGGAGGTG AAGGACCCAG AGGACAAGGT CATCCTGGCC CGGCAGTATG GTTCCGAGGG CAGGTTCACT TTCANTTCCC ATACCCNTGT GTGAGCACCA GATCTGTTTT CANTCCAATT CCACTCGAG	60 120 180 240 300 360 389
(2) INFORMATION FOR SEQ ID NO:477:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 431 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:	
GAATTCGGCC TTCATGGCCT AGAAGGAAAT AAAGGCCCCG ATTTCTGGAG TTCTGAGCCT ACTTTTTTTG GGTGCATTTT GAAACATACG GATTTTACCG CTAGTATATT CAGTGAGGAA	60 120

180

240

GGAAGGCTTC TGAAGGATTG ATGATCCCCA AACTGGATTA TGTGTTCATG ATAATGGTGT

ATTTGGTGGC CTAGCATAGT GAGGTGAGGT AGGTCTTTAA AATGGCTCAT TATAAACATC

ATTGTTCCTG AGCTCACTTG CCCTTGCATC TCCTGCCAGA GTGCTTTGTA CATAGTAGGC CCTCATCAAT GCTTGTAGAT TTTAAATTCG GAGGCACACT TGGAAGACAA TGGTGGCTGG TAAATTAATT ATCAGGGTTA GCAACTTCAT TTCTGCTNAC GCTTAAAAAG TGCTGCGCGA GGAAACTCGA G	300 360 420 431
(2) INFORMATION FOR SEQ ID NO:478:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 426 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:	
GCCTCTGNTT TTAATTCATT GGCAACTGTT ACGATGGAAG ACCTGATTCG ACCTTGGTTC CCTGAGTCT CTGAAGCCCG GGCCATCATG CTTTCCAGAG GCCTTGCCTT	60 120 180 240 300 360 420 426
(2) INFORMATION FOR SEQ ID NO:479:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 325 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:	
GAATTCGGCC TTCATGGCCT AAATTTCAG GCAGTTTGAA GTATCTGGCA GAAAAAGTAA ATTGAAATCA TTGGGACGTT GATTTTTAAA TTACCTAGAA GCAATCCCAA TGCTTTATGT AATACTAAAA TTTCTCCTCT CTCTTTTCTT TATCTCTCTC	60 120 180 240 300 325
(2) INFORMATION FOR SEQ ID NO:480:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 406 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:	
GGCAAGTAAC AGGTTGCAAG AATTGGAGGC AGAGCAACAG CAGATCCAAG AAGAAAGAGA ATTACTGTCC AGACAAAAGG AAGCTATGAA AGCAGAGGCA GGCCCAGTTG AACAACAATT	60 120

ACTACAGGAG ACAGACAAAT TAATGAAGGA AAAACTAGAA GTACAATGTC AAGCTGAAAA AGTACGTGAT GACCTTCAAA AACAAGTGAA AGCTCTAGAA ATAGATGTGG AAGAACAAGT CAGTAGGTTT ATAGAGCTGG AACAAGAAAA AAATACTGAA CTAATGGATT TAAGACAGCA AAACCAAGCA TTGGAAAAAGC AGTTAGAAAA AATGAGAAAA TTTTTAGATG AGCAAGCCAT TGACAGAGAA CATGAGAGAA ACAGGAAATA CTCGAG	180 240 300 360 406
(2) INFORMATION FOR SEQ ID NO:481:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 357 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:	
GAATTCGGCC AAAGAGGCCT AGTCGGTGCC TCATTGGTAT AAATGTTATG TCTGCATGGG TTTTTTCTAC AATTCTTTC TAAGATTATT TCTCCCCAAA GCTCAGCACT TTTGGAATTT TTCATTCTCA TCCAAAAATG GAAGCAATTT TATGTAAATG TCTCTTGGAA GCAGTGTTGG AATTCATATT TTGGGTAGCA GAAGCAGTAG TTACAAGGGT AGTGGTGTCT TTTGTGGTGG TGGTGGCACC TGCTGCAGTT GTTCATATTT GGGGTGCAGG AGTAGGGAGG GTAGGATCAG TTGGAGAATT TACAGGGAAA AATGGAGGTC CAGGTGGATA GGGTCTAGAA TTCAATC	60 120 180 240 300 357
(2) INFORMATION FOR SEQ ID NO:482:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 303 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:	_
GAATTCGGCC AAAGAGGCCT AAGTGACTCC AGAGCCTCCT GCAAGATGCT GTTGATTCTG CTGTCAGTGG CCTTGCTGGC CCTGAGCTCA GCTCAGAACT TAAATGAAGA TGTCAGCCAG GAAGAATCTC CCTCCCTAAT AGCAGGAAAT CCACAAGGAG CACCCCCCACA AGGAGGCAAC AAACCTCAAG GTCCCCCATC TCCTCCAGGA AAGCCACAAG GACCACCCCC ACAAGGAGGC AACCAGCCTC AAGGTCCCCC ACCTCCTCCA GGAAAACCAC AAGGACCACC CCCTATTCTC GAG	60 120 180 240 300 303
(2) INFORMATION FOR SEQ ID NO:483:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 469 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:	

60

120

180

GAATTCGGCC AAAGAGGCCT AAGCAGACAC AATGGTAAGA ATGGTGCCTG TCCTGCTGTC

TCTGCTGCTG CTTCTGGGTC CTGCTGTCCC CCAGGAGAAC CAAGATGGTC GTTACTCTCT

GACCTATATC TACACTGGGC TGTCCAAGCA TGTTGAAGAC GTCCCCGCGT TTCAGGCCCT

TGGCTCACTC	AATGACCTCC	AGTTCTTTAG	ATACAACAGT	AAAGACAGGA	AGTCTCAGCC	240
CATGGGACTC	TGGAGACAGG	TGGAAGGAAT	GGAGGATTGG	AAGCAGGACA	GCCAACTTCA	300
GAAGGCCAGG	GAGGACATCT	TTATGGAGAC	CCTGAAAGAC	ATCGTGGAGT	ATTACAACGA	360
CAGTAACGGG	TCTCACGTAT	TGCAGGGAAG	GTTTGGTTGT	GAGATCGAGA	ATAACAGAAG	420
CAGCGGAGCA	TTCTGGAAAT	ATTACTATGA	TGGAAAGGAC	AAACTCGAG		469

- (2) INFORMATION FOR SEQ ID NO:484:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GAATTCGGCC	AAAGAGGCCT	ACTACTTCTG	TAGTCTCATC	TTGAGTAAAA	GAGAACCCAG	60
CCAACTATGA	AGTTCCTTGT	CTTTGCCTTC	ATCTTGGCTC	TCATGGTTTC	CATGATTGGA	120
GCTGATTCAT	CTGAAGAGTA	TGGGTATGGC	CCTTATCAGC	CAGTTCCAGA	ACAACCACTA	180
TACCCACAAC	CATACCAACC	ACAATACCAA	CCTGCCTCAA	GGTCCTCCAC	CTCCTCCAGG	240
AAAGCCACAA	GGACCACCCC	CACAAGGAGG	CAACAAACCT	CAAGGTCCCC	CACCTCCAGG	300
AAAGCCACAA	CGACCACCCC	CACAAGGAGG	CAGCAAGTCC	CGAAGTTCTC	GATCTCCTCC	360
AGGAAAGCCA	CAAGGACCAC	CCCCACAAGG	AGGCAACAAA	CCTCAAGGTC	CCCCACCTCC	420
AGGAAAGCCA	CAAGGACCAC	CCCCACAAGG	AGGCAGCAAG	TCCCGAAGTG	CCCGATCTCC	480
TCCAGGAAAG	CCACAAGGAC	CATCCCACAA	CTCGAG			516

- (2) INFORMATION FOR SEQ ID NO:485:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

GAATTCGGCC	AAAGAGGCCT	ACTTCACTTC	AGCTTCACTG	ACTTCTTGAC	TCTCCTCTTG	60
AGTAAAAGGA	CTCAGCCAAC	TATGAAGTTT	TTTGTCTTTG	CTTTAGTCTT	GGCTCTCATG	120
ATTTCCATGA	TTAGCGCTGA	TTCACATGAA	AAGAGACATC	ATGGGTATAG	AAGAAAATTC	180
CATGAAAAGC	ATCATTCACA	TCGAGAATTT	CCATTTTATG	GGGACTGTGG	ATCAAATTAT	240
CTATATGACA	ATTGATATCC	TTAGTAATCA	TGGGGCATGA	TTATAGAGGT	TTGACTGGCA	300
ል <u>አጥጥር አርጥጥ</u>	тастсаттта	TTCTCATTCA	TCACACCGCA	AGTCTAGGCC	TCTCGAG	357

- (2) INFORMATION FOR SEQ ID NO:486:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

GGTTACCATC CTCAAAGGA	T TGGCTAAAAG	CAAGCAACTG	GATTGAACAC	CCTAAGAAGA	60
AAGATTCACA CTGCACCAG	G AGACATCAGA	AAGAATGAAA	ACTCTGCCGC	TGTTTGTGTG	120
CATCTGTGCA CTGAGTGCT	T GCTTCTCGTT	CAGTGAAGGT	CGAGAAAGGG	ATCATGAACT	180
ACGTCACAGG AAGGCATCA	T CACCAATCAC	CCAAATCTCA	CTTTGAATTA	CCACATTATC	240
CTGGACTGCT AGCTCACCA	G AAGCCGTTCA	TTAGAAAGTC	CTATAAATGT	CTGCACAAAC	300
GCTGTTAGGC CTAAGCTTC					360
CAGCCACCTA AACATCCAG	A TAAAAATAGC	AGTGTGGTCA	ACCCTACCTT	AGTGGCTACA	420
ACCCAAATTC CATCTGTGA	C TTTCCCATCA	GCTTCCACCA	AAATTACTAC	CCTTCCAAAT	480
GTGACTTTTC TTCCCCAGA	A TGCCACCACC	ATATCTTCAA	GAGAAAATGT	TAACACAAGC	540
TCTTCTGTAG CTACATTAG	C ACCCAGTGAA	TTCCCCAGCT	CCACAAGACA	CCACAGCTGC	600
CCCACCCACA CCTTCTGCA	A CTACACCAGC	TCCACCCCTC	GAG		643

- (2) INFORMATION FOR SEQ ID NO:487:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GAATTCGGCC	AAAGAGGCCT	ACAAGATGCT	GCTGGTCCTG	CTCTCAGTGG	TCCTTCTGGC	60
TCTGAGCTCA	GCTCAGAGCA	CAGATAATGA	TGTGAACTAT	GAAGACTTTA	CTTTCACCAT	120
ACCAGATGTA	GAGGACTCAA	GTCAGAGACC	AGATCAGGGA	CCCCAGAGAC	CTCCTCCTGA	180
AGGACTCCTA	CCTAGACCCC	CTGGTGATAG	TGGTAACCAA	GATGATGGTC	CTCAGCAGAG	240
ACCACCAAAA	CCAGGAGGCC	ATCACCGCCA	TCCTCCCCCA	CCTCCTTTTC	AAAATCAGCA	300
ACGACCACCC	CAACGAGGAC	ACCGTTCATC	TCGAG			335

- (2) INFORMATION FOR SEQ ID NO:488:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

GAATTCGGCC AAAGAGGCCT	AGACACATTG	CCTTCTGTTT	TCTCCAGCAT	GCGCTTGCTC	60
CAGCTCCTGT TCAGGGCCAG	CCCTGCCACC	CTGCTCCTGG	TTCTCTGCCT	GCAGTTGGGG	120
GCCAACAAAG CTCAGGACAA	CACTCGGAAG	ATCATAATAA	AGAATTTTGA	CATTCCCAAG	180
TCAGTACGTC CAAATGACGA	AGTCACTGCA	GTGCTTGCAG	TTCAAACAGA	ATTGAAAGAA	240
TGCATGGTGG TTAAAACTTA	CCTCATTAGC	AGCATCCCTT	CTACAAGGTG	CATTTAACTA	300
TAAGTATAAC TGCCAACCTC	GAG				323

- (2) INFORMATION FOR SEQ ID NO:489:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

GAATTCGGCC	AAAGAGGCCT	AGTGACACCA	GAGCCTCCTG	CAAGATGCTT	CTGATTCTGC	60
TGTCAGTGGC	CCTGCTGGCC	TTCAGCTCAG	CTCAGGATTT	AAATGAAGAT	GTCAGCCAGG	120
AAGATGTT						128

- (2) INFORMATION FOR SEQ ID NO:490:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

GAATTCGGCC	AAAGAGGCCT	AATTTTGACC	AGCAGATTAA	TCAACTGTAA	GACGGATCCT	60
CACACAAAGA	GGCAACTGAA	AGGATGAAAT	CACTGACTTG	GATCTTGGGC	CTTTGGGCTC	120
TTGCAGCGTG	TTTCACACCT	GGTGAGAGTC	AAAGAGGCCC	CAGGGGACCA	TATCCACCTG	180
GACCGCTGGC	TCCTCCTCAA	CCTTTTGGCC	CAGGATTTGT	TCCACCACCT	CCTCCTCCAC	240
CCTATGGTCC	AGGGAGAATC	CCACCTCCTC	CTCTGCAGAG	AAAACCTTTG	AAGAAAAGCA	300
GGAACAGAGA	TCGATGGCGA	TCTATTTCCC	TGTACTATAC	TGGAGAGAAA	GGTCAAAATC	360
GTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:491:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

GGTTTCCCGT	TTGTCCCTCC	TTCAAGGTTT	TTTTCAGCAG	CTGCAGCACC	CGCTGCCCCA	60
CCTATTGCAG	CTGAGCCTGC	TGCAGCTGCA	CCTCTTACAG	CCACACCTGT	AGCAGCTGAG	120
CCTGCTGCAG	GGGCCCCTGT	TGCAGCTGAG	CCTCCTGCAG	AGGCACCTGT	TGGAGCTGAG	180
CCTGCTGCAG	AGGCACCTGT	TGCAGCTGAG	CCTGCTGCAG	AGGCACCTGT	TGGAGTGGAG	240
CCAGCTGCAG	AGGAACCTTC	ACCAGCTGAG	CCTGCTACAG	CCAAGCCTAG	GCCTCT	296

- (2) INFORMATION FOR SEQ ID NO:492:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 535 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

CTCGAGTCCT TGT	GGCTTTC CTGGAGGTG	GGGACCTTGA	GGTTTGTTGC	CTCCTTGTGG	60
GGGTGGTCCT TGT	GGCTTTC CTGGAGGAG	TGAAGGACCT	TGAGGCTGGT	TGCCTCCTTG	120

TGGGGGTGGT	CCTTGTGGCT	TTCCTGGAGG	AGATCGGGGA	CTTCGGGGAC	TTGTCTCCTT	180
	TCCTTGTGGC					240
GTGGGGGTGG	TCCTTGTGGC	TTTCCTGGAG	GAGGTGGGG	ACCTTGAGGC	TGGTTGCCTC	300
CTTGTGGGGG	TGGTCCTTGT	GGCTTTCCTG	GAGGAGATGG	GGGACCTTGA	GGTTTGTTGC	360
	GGGTGCTCCT					420
	ATTTAAGTTC					480
TCAACAGCAT	CTTGCAGGAG	GCTCTGGAGT	CACTTAGGCC	TCTTTGGCCG	AATTC	535

- (2) INFORMATION FOR SEQ ID NO:493:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GAATTCGGCC	AAAGAGGCCT	AGTCGGTAAT	CACAACAAAC	ACGGAGCAAT	CTCAATGCTG	60
	GGACAGTCTG					120
	TCATAATGAT					180
	GATCCTTTCC					240
ACCAGCAGGA	CCTTCTCCAG	TCGAATTCTC	TCTCCACACG	CAAGGTCTAG	TTCATTTCCA	300
ATTAAGATCA	GGTCTTCAGA	G				321

- (2) INFORMATION FOR SEQ ID NO:494:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 basé pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

GAATTCGGCC	AAAGAGGCCT	AACCTGCCTT	GGTTCTTGCT	CCTCTTTCCA	CGTTGGATAA	60
CAATTTTTTG	GTTGTTTTGT	TTAAGTTGGT	GCTCTGAAGC	TTAATCTCAG	TACCCTTTAC	120
TCTGAATTGT	CAAATTTTGA	TAAAACGTGC	CATTTTCTTT	GGTAAGAGAA	AGCAGGTCTT	180
AATGTCTGCC	AGAACACAAT	TTATATGCCT	TATTGGCTTC	ATTAAACTTT	TAGAAAACTT	240
TAGCATTTGT	TACTTTTTTC	CATTGCATTT	ACTTTCAAAT	GCACCTAATG	AATTCGTCAC	300
CCAGTCGCAA	CTTTTCCCTT	CTCTGTCCCA	TTGCTTTCTC	CTTTCCCCAA	CGCAGCTCGA	360
G						361

- (2) INFORMATION FOR SEQ ID NO:495:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

GAATTCGGCC	AAAGAGGCCT	AAAGCGACCA	AGATAAAAGT	GGACAGAAGA	ATAAGCGAGA	60
CTTTTTATCC	ATGAAACAGT	CTCCTGCCCT	CGCTCCGGAA	GAGCGCTACC	GCAAAGCCGG	120
GTCCCCAAAG	CCGGTCTTGA	GAGCTGATGA	CAATAACATG	GGCAATGGCT	GCTCTCAGAA	180
GCTGGCGACT	GCTAACCTCC	TCCGGTTCCT	ATTGCTGGTC	CTGATTCCAT	GTATCTGTGC	240
TCTCGTTCTC	TTGCTGGTGA	TCCTGCTTTC	CTATGTTGGA	ACATTACAAA	AGGTCTATTT	300
TAAATCAAAT	GGGAGTGAAC	CTTTGGTCAC	TGATGGTGAA	ATCCAAGGGT	CCGATGTTAT	360
TCTTACAAAT	ACAATTTATA	ACCAGAGCAC	TGTGGTGTCT	ACTGCACATC	CCGACCAACT	420
AGGCCTCTTT	GGCCG					435

- (2) INFORMATION FOR SEQ ID NO:496:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

GAATTCGGCC AAA	AGAGGCCT AGAA	ATATAT TTTCTAC	STGA ATTCTTATTG	GAAGCCAGGT	60
CTCTCCTCTC ATT	TAGATCAA AAGG	GACTTA TGTACAT	raca acaattgaaa	GTGTTACTCG	120
AG					122

- (2) INFORMATION FOR SEQ ID NO:497:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

GAATTCGGCC	AAAGAGGCCT	AAGAAAATCA	GCCTGTCTGC	TCTCTCCTTG	GCTCAACAAG	60
GCCTCTAACA	GTCTTCTGTC	CTCTATTCTG	CACACGGCAT	ATTTGGGAAC	GAGAAACAAA	120
AGTTTTCCCA	AATGAAGAGA	ACTCACTTGT	TTATTGTGGG	GATTTATTTT	CTGTCCTCTT	180
GCAGGGCAGA	AGAGGGGCTT	AATTTCCCCA	CATATGATGG	GAAGGACCGA	GTGGTAAGTC	240
TTTCCGAGAA	GACCCTCGAG					260

- (2) INFORMATION FOR SEQ ID NO:498:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

GAAAGAGGCC TACCAACATG CCAGAGGCCG TACCCATATC CGCAGCAG

(2) INFORMATION FOR SEQ ID NO:499:

249

48

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

GAATTCGGCC	TTCATGGCCT	ACCCTGTCAA	AATTTTGCCT	CCTCTTGATT	TTCAATATAT	60
ATATATTTT	TTGTCTTACT	CTGTTGCCCA	GGCTAGAGTG	CAGTGACGTG	ACCTTGGCTC	120
ACTGCAACCT	CTGCCTCCTG	GGCTCAAGCA	ATCCTCCCAC	CTCAGCCTCC	TCAGTAGCTG	180
GGACCACAGG	CATATGCTAC	AAAGCCCAGA	TTTTTTTTTT	ATAGAAACAG	GGTTTCACCA	240
TGTTGCCCAG	GCTTGTCTCG	AACCCCAGAA	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:500:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

GAATICGGCC TICATGGCCT ACAAATGCCC ATCAAAGACT GGATAAAGAA AATGTAGTAT	60
ATATATAT ACCATGGAAT ACTGTGCAGC CATAAAAAAG GAATGAGATC ATGTGTTTCA	120
CAGGGATGTG GATGAAGCTG GAAGCCATCA TCCCCAGCAG ACTAACACAG GAACAGAAAA	180
CCAAACACTG CATGTTCTCA CTCATAAGTG GGAGCTGAAC AATGAGAACA GGTGGGCACA	240
GGGACGGGAA CAACACACA CAGGGCCTGT TGTGTGGTGG GGGTGAGGGT TGGAACTCGA	300
G	301

- (2) INFORMATION FOR SEQ ID NO:501:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

GCGAGGCAGG	GAAACTCACT	TCACGTCTCT	TTCCTTGTAG	AGCATCATGC	TTATTTCTGG	60
CTCACTCACA	TCTTTGTCTC	GGGAGTTCTC	TGCCGAGCCA	TTGCCCCCTA	CAGCAGAGAG	120
CACAGCTGGC	TGCACTAGTG	CTGAAGGAGC	CAGCCCCAGA	GCAGGGCATT	TCCAGGGGCT	180
CTTGTCCCAG	AGCGGCAGGC	GTTGTGTGCA	GAGAACGCCC	CTCCCACGCA	GCACAGAGAA	240
CGCGGGGTGG	GTGTGTGGCT	CCGGGCCTGT	GGGGCTTAGG	CTGCCTGAAC	CACCGCCGAC	300
TGGCACCATG	ACTCGGCATT	CCTGGAAGTG	CCTTACCAAG	TTGTTGTTGT	TGTTTTGTTG	360
TTTTTTAAGA	GACGGGCTTG	CTCTATCATC	CAGGCTCGAG			400

- (2) INFORMATION FOR SEQ ID NO:502:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear .
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

GAGATAAACA	AAATTGATTG	CCCCATTCTC	TCACTTCCCC	ATCTTGTCTT	CCTAGACCCC	60
ACAGAGTTAA	AACTTGGGAT	TCCCCTGGCC	CCCCCAGAAC	ACTTGTATAT	TGTTTGTTTG	120
AGGTTCGTGC	CGCAGTAACA	GACACAGTAT	TTAATTGCAC	ATACAGATGT	TTGCTGGGTA	180
TATTCACTGT	AAATTTTATT	TAATCTGTTT	TTTTGTTTGT	TTGGGGGTTA	TTTGGGGGGA	240
GGTTGGTTTT	GTTTTTAAAT	AAAAAAAA	AAATCTGTCA	CTCGAG		286

- (2) INFORMATION FOR SEQ ID NO:503:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

GGCCTCACCT	TACCCCAGGA	CTCCGCTATG	ACACCGCCTC	TGCCCCTACA	AGACACAGAT	60
CTCTCGTCAG	CCTCAAAGCC	TGTGGCTGCA	GCCACGCCTG	TGTCCCAGCA	GGCTGAAGAG	120
GGCCTCACCT	TACCCCAGGA	CTCCGCTATG	ACAGCACCTC	TGCCTCTGCA	AGACACAGGC	180
CCCACCTCAG	GTCCAGAGCC	TCTGGCTGTG	GCCACCCCTC	AAACCTTGCA	GGCAGAAGCA	240
GGCTGTGCCC	CAGGGACAGA	GCCTGTGGCC	ATACTCGAG			279

- (2) INFORMATION FOR SEQ ID NO:504:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

GCAATGGCAG	GAATTCGAAA	TATTGGCATA	TGGTTCTTTT	GGATTAGATT	ATATAAAATC	60
AGAAGAGGTA	GAACCAGGCC	CCAAGCACTC	CTTTTTCTCT	GCATGATACT	TCTGCTTATT	120
GTCCTTCACA	CTAGCTACAT	GATTTATAGT	CTTGCTCCCC	AATATGTTAT	GTATGGAAGC	180
CAAAATTACT	TAATAGAGAC	TAATATAACT	TCTGATAATC	ATAAAGGCAA	TTCAACCCTT	240
TCTGTGCCAA	AGAGATGTGA	TGCAGAAGCT	CCTGAAGATC	AGTGTACTGT	TACCCGGACG	300
CTCGAG						306

- (2) INFORMATION FOR SEQ ID NO:505:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

GAATTCGGCC	TTCATGGCCT	AAGGAGAATG	GCGTGCACCC	GGGAGGCGGA	GCTTGCAGTG	60
AGCCAACATC	ACGCCACTGC	ACTCCAGCCC	GGGCGACTGA	GCGAGACTCT	CTCTCNAAAA	120
ААААААААА	AAAGAAAAAG	AAAAAGAAAA	AGAAAAAGAA	AAGAAAATAT	ATANATACAC	180
ACAGAGAGTG	AGAGAGAGAG	AGAGAGAGAG	ACCAGAAAAA	GAGAGAAGGA	GAAAGAGAGA	240
ATGCAAAAAC	CAAGAGGANA	GAATGATCCA	CTCTCCAACT	AGAAAGGTAG	CTCTCAATCT	300
GAAAAGTCAC	TTGATTACTT	TGTCTATTTT	GCTTATCTGC	TACATCAATG	GTTCCCTCGA	360
G						361

- (2) INFORMATION FOR SEQ ID NO:506:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

GAATTCGGCC	TTCATGGCCT	AGGCCTTTTC	TTTTTAAAGG	AATTCAAGCA	GGATACGTTT	60
TTCTGTTGGG	CATTGACTAG	ATTGTTTGCA	AAAGTTTCGC	ATCAAAAACA	ACAACAACAA	120
AAAACCAAAC	AACTCTCCTT	GATCTATACT	TTGAGAATTG	TTGATTTCTT	TTTTTTATTC	180
TGACTTTTAA	AAACAACTTT	TTTTTCCACT	TTTTTAAAAA	ATGCACTACT	GTGTGCTGAG	240
CGCTTTTCTG	ATCCTGCATC	TGGTCACGGT	CGCGCTCAGC	CTGTCTACCC	GCAGCACACT	300
CGAG						304

- (2) INFORMATION FOR SEQ ID NO:507:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GGGGCTGCGG	GGATTGACCT	CCTCACTTCT	GGGTTGCCAC	TCGAAGCTTG	CTCCGGGCAA	60
CGACCCTGCT	GCTTCCCAGA	GGGAAACTGT	AGCCCACAGA	CCAGGAGAGA	AGCCAAAGCA	120
CCTGCTCCAC	GTCCACATCA	CCCCAGGCTT	CTAGCCCCCA	GGGGCTTCAT	CAGTGCTTCA	180
GCGCTCTCTC	CCATCCCCCA	CTCCCCATGT	CCCTCGTGAT	CCGAACTCCT	AGGGCTCCGT	240
GTCCCACAGG	TCACCACTTC	CGGCTGTCTC	GAG			273

- (2) INFORMATION FOR SEQ ID NO:508:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GAATTCGGCC	TTCATGGCCT	ACATCAATAA	AATACATTCT	ACACAGAATA	CGCCAACCAT	60
ACACTACTCT	TTTTTGATAA	TAAAAAATGT	ATTTACTGAG	CCAGTTGTGG	TGGCTCGCGC	120
CTATAATCCC	AGCACCTTGG	AAGGCCAATG	GGAGTGGATC	GGTTGAGGCC	AGGAGTTTGA	180
GACCGGCCTG	GCCAACATGG	TGGAATGCCG	TCTCTACTGA	GAATGCAGAA	ATGAGCCGGG	240
CACGGTGGCA	CGCACCTGTA	GTCCCAGGTA	CTCCGATTCC	TCTCGAG		287

- (2) INFORMATION FOR SEQ ID NO:509:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

AAGAGGCGAT	GGCGGCGATG	GCATCTCTCG	GCGCCCTGGC	GCTGCTCCTG	CTGTCCAGCC	60
TCTCCCGCTG	CTCAGCCGAG	GCCTGCCTGG	AGCCCCAGAT	CACCCCTTCC	TACTACACCA	120
CTTCTGACGC	TGTCATTTCC	ACTGAGACCG	TCTTCATTGT	GGAGATCTCC	CTGACATGCA	180
AGAACAGGGT	CCAGAACATG	GCTCTCTATG	CTGACGTCGG	TGGAAAACAA	TTCCCTTGTC	240
CACTCGAG						248

- (2) INFORMATION FOR SEQ ID NO:510:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

GGCGATGATT	AGGCCAGACC	CTCCCCATCC	TCGTGAGGGC	CAGAAGCTGT	TGCTACACTG	60
TGAGGGTCGC	GGCAATCCAG	TCCCCCAGCA	GTACCTATGG	GAGAAGGAGG	GCAGTGTGCC	120
ACCCCTGAAG	ATGACCCAGG	AGAGTGCCCT	GATCTTCCCT	TTCCTCAACA	AGAGTGACAG	180
TGGCACCTAC	GGCTGCACAG	CCACCAGCAA	CATGGGCAGC	TACAAGGCCT	ACTACACCCT	240
CAATGTTAAT	GACCCCAGTC	CGGTGCCCTC	CTCCTCCAGC	ACCTACCACG	CCATCATCGG	300
TGGGATCGTG	GCTTTCATTG	TCTTCCTGCT	GCTCATCATG	CTCATCTTCC	TCGGCCACTA	360
CTTGATCCGG	CACAAAGGAA	CCTACCCTAC	ACTCGAG			397

- (2) INFORMATION FOR SEQ ID NO:511:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

GCCTGCCTCC AGGCCTTTGC TCCCACTGTT GCCTCCACTT AGAATAACAT TCCACCCCAT CTCTATAAAT ATCCTACAGA CAAATACTAC CTTCCCCTTA AGGCCAGTTC TAACCCTAAC TGACAACAAA TCATCTCTAC ATGATCTTTT CCTTCTGGGA ATGCCTGCAG CACTGTTTAA TCCTGCCCCA CCACCATCCC CTCACCCAGC ACCCTCTCCC AGACCAGACA GGGTGGCTCA TGCCTGCAAT CCCAGCACCT TGGGAGGCTG AGGCAGGAGG ATTGCTCGAG	60 120 180 240 290
(2) INFORMATION FOR SEQ ID NO:512:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 304 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:	
GAATTCGGCC TTCATGGCCT ACTATGCCGT CATGATAGAG AAGATGATCC TGAGAGACCT GTGCCGTTTC ATGTTTGTCT ACGTCGTCTT CTTGTTCGGG TTTTCCACAG CGGTGGTGAC GCTGATTGAA GACGGGAAGA ATGACTCCCT GCCGTCTGAG TCCACGTCGC ACAGGTGGCG GGGGCCTGCC TGCAGGCCC CCGATAGCTC CTACAACAGC CTGTACTCCA CCTGCCTGGA GCTGTTCAAG TTCACCATCG GCATGGGCGA CCTGGAGTTC ACTGAGAACC ATGAACTTCT CGAG	60 120 180 240 300 304
(2) INFORMATION FOR SEQ ID NO:513:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 314 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:	
GAATTCGGCC TTCATGGCCT AGGAACCTGG ACCGCGGCGG CGCCGGGTTT CCCTCATGAT CCCGGGCGGG CGCGGCGGCGC GGCAGAGGCG GCGGGAGGAT GACCTCTTAC CGGGAGCGGA GTGCCGACCT GGCCCGTTTC TACACTGTCA CCGAGCCCCA GCGACACCCG AGGGGCTACA CAGTATATAA GGTCACCGC CGGGTTGTTT CACGAAGAAA TCCAGAGGAT GTCCAGGAGG GAGAATCCTG AACCAACCTA TCCATGAACA TACTCTCTGC CATTTCTTA GTCCTTTTTT CGGAAAAAACT CGAG	60 120 180 240 300 314
(2) INFORMATION FOR SEQ ID NO:514:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 529 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:	
GAATTCGGCC TTCATGGCCT ACGAACTTAA GAAAATGAGA CTGAGCAATC TCATGGTTCT TGGACAGTTA GTCTATGGCC AATTGATGGA ACCAGTAAAT CGAGAGAACT TTACGCAGAC CTTGCCCAAA ATGCCAATTC ATTCTCATGC ACAGCCCCCA GATGCCAGGG AAGAGGATAT	60 120 180

CATACTTGAA	GGTCAACAGA	GCCTGCCATC	CCAGGCTTCA	GATTGGAGCC	GATACTCAAG	240
CAGCTTACTG	GAATCCGTCT	CTGTTCCTGG	AACACTAAAT	GAGGCTGTTG	TAATGACTCC	300
		GAATTTCAGA				360
GCCCTCCCCG	CATCCCAGAG	CCTGGTTTGT	GTCTCTTGAT	GGAAAGCCAG	TTGCACAAGT	420
					ACACCAGTCT	480
4		ATGAGCTTCA				529

- (2) INFORMATION FOR SEQ ID NO:515:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GGAGATGAAA	GTTAAAAGTG	AAAACCTTAA	AGAGGAGCCT	CAGTCTTCTG	AAGAAGAATC	60
		GGACACTAAT				120
TGTTTTACCA	CAGGCTACTG	GAGACCAGAA	ATCTGGTGGA	AAATGTGAAA	CAGACAGACG	180
		AACCCCTAAC				240
		CTAGTTCTGA				300
		CCTCATCATC				352
TICITCCMON	10.11011011		4	+		

- (2) INFORMATION FOR SEQ ID NO:516:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GTCTACACCN	TTCCGAGTTG	GCTGCAGATT	TGTGGTGCGT	TCTGAGCCGT	CTGTCCTGCG	60
		ATTAAAAACA				120
		ATAGGAATGG				180
		AAGGCTTTGA				240
		CATGTGAAAG				300
AGCCGTGTTA	GATGGGGAGC	GTGGAACGTC	ACTGTACACT	TGTATAAGTA	CCGTTTACTT	360
CATGGCATGA	ATAAATGGAT	CTGTGAGATG	CACTGCTACC	TGGTACTGCT	TTCAGTGTGT	420
TCCCCCTCAG	CCCCTCCGGC	GTGTCAGGCA	TACTCTGAGT	AGATAATTTG	TCATGCAGCG	480
CATGCAATCA	GAATCTCGAG					500

- (2) INFORMATION FOR SEQ ID NO:517:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GAATTCGGCC	TTCATGGCCT	AGATGCTCAA	CACCTCCTCC	TTGGTGGAGC	AGCTGAACGA	60
GCAGTTTAAC	TGGGTGTCCC	GGCTGGCAAA	CCTCACGCAA	GGCGAACACC	AGTACTATCT	120
GCGGGTCACC	ACGGTGGCTT	CCCACACTTC	TGACTCGGAC	GTTCCTTCCG	GTGTCACTGA	180
GGTGGTCGTG	AAGCTCTTTG	ACTCTGATCC	CATCACTGTG	ACGGTCCCTG	TAGAAGTCTC	240
CAGGAAGAAC	CCTAAATTTA	TGGAGACCGT	GGCGGAGAAA	GCNCTGCAGG	AATACCGCAA	300
AAAGCACCGG	GAGGAGTGAG	ATGTGGATGT	TGCTTTTGCA	CCTACGGGGG	CATCTGAGTC	360
CAGCTCCCCC	CAAGATGAGC	TGCAGCCCCC	CAGAGAGAGC	TCTGCACGTC	ACCAAGTAAC	420
TCTCGAG						427

- (2) INFORMATION FOR SEQ ID NO:518:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GAATTCGGCC TTCATGGCC	AATCTTAAGG	GACCTTTCCT	TACTACAGAT	TCAAATGCGA	60
GATCTTGAGG GTTACAGGG	AACGAGGTAT	CAGTTACTTC	AGCTTCGACC	TGCGCAGAGA	120
GCATCATGGA TTGGTTATG	TATTGCTTAC	CATTTATTAG	AAGATTATGA	AATGGCAGCA	180
AAGATTTTAG AAGAATTTAG	GAAAACACAA	CAGACATCCC	CTGACAAGGT	GGATTATGAA	240
TATAGTGAAC TACTCTTATA	TCAGAATCAA	GTTCTTCGGG	AAGCAGGTCT	CTATAGAGAA	300
GCTTTGGAAC ATCTTTGTA	CTATGAAAAG	CAGATTTGTG	ATAAACTTGC	TGTAGAAGAA	360
ACCAAAGGGG AACTTCTGT	GCAACTATGT	CGTTTGGAA			399

- (2) INFORMATION FOR SEQ ID NO:519:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GAATTCGGCC TTC	ATGGCCT ACTTATCTTA	ATCCAATGGG	TGACATCTTC	AACAACCCTG	60
TTCCAAATAA GGC	TGCATTC TAAACACTAC	GGATTAAGAC	ATCAACATGT	GAATTTTGGA	120
GGAATGTAGT TCT	AACCATA ACAGCAGTG	ATGAGATGAC	AGACTATTGC	TCTCAAAAGA	180
TAGCCAGGTT TCT	AGTTTCC TTAGGCATT	TCTGGAGGTT	TGCGAGCAGT	TCATTATTAT	240
CTTAAAAATA TTA	TCCAGAG CTGTGGTCTA	TCAGCAGCTC	ATTACCAGAC	TGGCAGATAC	300
ATTTAATCAG CAA	AAGAGTT GTTCCTGTG	TTAGCATCCT	CCTGGTTTCC	CAGCTCAAGA	360
GTTCTTCTGA GTA	ATAGTAA TCCTTCCCC	ATGCTCGAG			399

- (2) INFORMATION FOR SEQ ID NO:520:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GCTGAAGTGG TGACTTTTGA GAGAGGACAC AAAATTATCA TCAGCTCCAG TCGGAGAATC CAGAAAGGAG AAGAGGTAAG AGTGTGAGAG ATTGCATCTG CCATGTTGTT CAGATCCTGG GCGAATAGTT CCCTCCAC ACAGGTCACT TACTCACTTG TTTCCCAAATT CTTTGTTGTG ATAAAAACTC TGTCCATAAT AGGCCAGATG TTCCCACCCT GCAGTATCTC ACCCTTCAGG CACTCCAGTT CACCTTCCTC CACATCCCTC GAG	60 120 180 240 273
(2) INFORMATION FOR SEQ ID NO:521:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 323 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:	
GCTTTAAGAA TTAACGAAAG CAGTGTCAAG ACAGTAAGGA TTCAAACCAT TTGCCAAAAA TGAGTCTAAG TGCATTACT CTCTTCCTGG CATTGATTGG TGGTACCAGT GGCCACTACT ATGATTATGA TTTTCCCCTA TCAATTTATG GGCAATCATC ACCAAACTGT GCACCAGAAT GTAACTGCCC TGAAAGCTAC CCAAGTGCCA TGTACTGTGA TGAGCTGAAA TTGAAAAGTG TACCAATGGT GCCTCCTGGA ATCAAGTATC TTTACCTTAG GAATAACCAG ATTGACCATA TTGATGAAAA	60 120 180 240 300 323
(2) INFORMATION FOR SEQ ID NO:522:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 274 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:	
GGAAAAAGAA GAGAAAGCCA AGGAAGACAA GGGCAAACAA AAGTTGAGGC AGCTTCACAC ACACAGATAC GGAGAACCAG AAGTGCCAGA GTCAGCATTC TGGAAGAAAA TCATAGCATA TCAACAGAAA CTTCTAAACT ATTTGCTCG CAACTTTTAC AACATGAGAA TGTTAGCCTT ATTTGTCGCA TTTGCTATCA ATTTCATCTT GCTCTTTTAT AAGGTCTCCA CTTCTTCTGT GGTTGAAGGA AAGGAGCTCC CCACGAGGCT CGAG	60 120 180 240 274
(2) INFORMATION FOR SEQ ID NO:523:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:	
GCCCCAGTCC AGATCCAGGA CTGAGATCCC AGAACCATGA ACCTGGCCAT CAGCATCGCT CTCCTGCTAA CAGTCTTGCA GGTCTCCCGA GGGCAGAAGG TGACCAGCCT AACGGCCTGC CTAGTGGACC AGAGCCTTCG TCTGGACTGC CGCCATGAGA ATACCAGCAG TTCACCCATC	60 120 180

CAGTACGAGT TCAGCCTGAC CCGTGAGACA AAGAAGCACG TGCTCTTTGG CACTGTGGGG GTGCCTGAGC ACACATACCG CTCCCTCCTC GAG	240 273
(2) INFORMATION FOR SEQ ID NO:524:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 456 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:	
GAATTCGGCC TTCATGGCCT ACTCTCCTAT AAAGCAGACG CCGCGCCGCG	60 120 180 240 300 360 420 456
(2) INFORMATION FOR SEQ ID NO:525:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 452 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:	
GAATTCGGCC TTCATGGCCT AATGGGACAA CTCCTCGCCC TCTACCTGTC CCCTCCCCT TTGGTTGTAT GATTTTCTTC TTTTTTAAGA ACCCCTGGAA GCAGCGCCTC CTTCAGGGTT GGCTGGGAGC TCGGCCCATC CACCTCTTGG GGTACCTGCC TCTCTCTCC CTGTGGTGTC CCTTCCCTCT CCCATGTGCT CGGTGTTCAG TGGTGTATAT TTCTTCTCC AGACATGGGG CACACGCCCC AAGGGACATG ATCCTCTCCT TAGTCTTAGC TCATGGGGCT CTTTATAAGG AGTTGGGGG TAGAGGCAGG AAATGGGAAC CGAGCTGAAG CAGAGGCTGA GTTAGGGGGC TAGAGGACAG TGCTCCTGGC CACCCAGCCT CTGCTGAGAA CCATTCCTGG GATTAGAGCT GCCTTTCCCA GGGAAAAAGT GTCCGACTCG AG	60 120 180 240 300 360 420 452
(2) INFORMATION FOR SEQ ID NO:526:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 366 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:	
GCGATTGAAT TCTAGACCAG ACTCGTCTCA GGCCAGTTGC AGCCTTCTCA GCCAAACGCC GACCAAGGAA AACTCACTAC CATGAGAATT GCAGTGATTT GCTTTTGCCT CCTAGGCATC	60 120

ACCTGTGCCA	TACCAGTTAA	ACAGGCTGAT	TCTGGAAGTT	CTGAGGAAAA	GCAGCTTTAC	180
AACAAATACC	CAGATGCTGT	GGCCACATGG	CTAAACCCTG	ACCCATCTCA	GAAGCAGAAT	240
CTCCTAGCCC	CACAGACCCT	TCCAAGTAAG	TCCAACGAAA	GCCATGACCA	CATGGATGAT	300
ATGGATGATG	AAGATGATGA	TGACCATGTG	GACAGCCAGG	ACTCCATTGA	CTCGAATCGA	360
CTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:527:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

GCCCCAGTCC	AGATCCAGGA	CTGAGATCCC	AGAACCATGA	ACCTGGCCAT	CAGCATCGCT	60
CTCCTGCTAA	CAGTCTTGCA	GGTCTCCCGA	GGGCAGAAGG	TGACCAGCCT	AACGGCCTGC	120
CTAGTGGACC	AGAGCCTTCG	TCTGGACTGC	CGCCATGAGA	ATACCAGCAG	TTCACCCATC	180
CAGTACGAGT	TCAGCCTGAC	CCGTGAGACA	AAGAAGCACG	TGCTCTTTGG	CACTGTGGGG	240
GTGCCTGAGC	ACACATACCG	CTCCCGAACC	AACTTCACCA	GCAAATACAA	CATGAAGGTC	300
CTCTACTTAT	CCGCCTTCAC	TAGCAAGGAC	GAGGGCACCT	ACACGTGTGC	ACTCCACCAC	360
TCTGGCCATT	CCCCACCCAT	CTCCTCCCAG	AACGTTACAG	TGCTCGAG		408

- (2) INFORMATION FOR SEQ ID NO:528:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GTAGGTCACA	GCAGAAGCAG	CCAAAATGGA	TCCCCAGTGC	ACTATGGGAC	TGAGTAACAT	60
TCTCTTTGTG	ATGGCCTTCC	TGCTCTCTGG	TGCTGCTCCT	CTGAAGATTC	AAGCTTATTT	120
CAATGAGACT	GCAGACCTGC	CATGCCAATT	TGCAAACTCT	CAAAACCAAA	GCCTGAGTGA	180
GCTAGTAGTA	TTTTGGCAGG	ACCAGGAAAA	CTTGGTTCTG	AATGAGGTAT	ACTTAGGCAA	240
AGAGAAATTT	GACAGTGTTC	ATTCCAAGTA	TATGGGCCGC	ACAAGTTTTG	ATTCGGACAG	300
TTGGACCCTG	AGACTTCACA	ATCTTCAGAT	CAAGGACAAG	GGCTTGTATC	AATGTATCAT	360
CCATCACAAA	AAGCCCACAG	GAATGATTCG	CATCCACCTC	GAG		403

- (2) INFORMATION FOR SEQ ID NO:529:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

GAATTCCTCT TCTTTACCCT CGTCCTGCCG GGCACTTTCC TTAGGTTTGG TTTCATCTAC

60

AGCTTCTATG	TTCTCTTCAG	CTTGGCTGCT	CTCCCCAGTC	TCCGTTGGAG	GCTGGGCTGT	120
TGCCTTGGCA	GCAGCATCCT	CTGCGGCAGG	${\tt GGTGGTGGCA}$	GCAGCAGCAG	TGACAGCAGC	180
AGGCACATCG	GCTTGTTTAG	GCTCCTCCTT	${\tt GGCTGGGGCA}$	TCTTCAGCCT	TGGAGGACGG	240
CGAGTTATCA	GTGGAAGCTT	TAGTGGCACT	TTCTGTCTCA	GCTGAGCCGG	CCTTCTCCTC	300
TGAGGATGCA	GGAGCCTGGG	GGGCTACCTG	CTCTGTGGCA	GCATCACCCT	CCCCCTTTTT	360
CTCCTCGGAA	GGAGTTTCTC	CTGCTTTGCC	GGGCTCATCA	GGCTTGGAGC	CAGTGGCTGG	420
GGCTGCTTCG	GCAGTAGTGG	TGCCTTCTCC	CTTCTTCTCC	ACCCCATCGC	TCGAG	475

- (2) INFORMATION FOR SEQ ID NO:530:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

GTGCTGGCGG	ACATGGACGT	GGTGAATCAG	CTGGTGGCTG	GGGGTCAGTT	CCGGGTGGTC	60
AAGGAGCCCC	TCGGCTTTGT	GAAGGTGCTG	CAATGGGTCT	TCGCCATCTT	CGCCTTTGCC	120
ACATGCGGCA	GCTACAGTGG	GGAGCTCCAG	CTGAGCGTGG	ATTGTGCCAA	CAAGACCGAG	180
AGTGACCTCA	GCATCGAGGT	CGAGTTCGAG	TACCCCTTCA	GGCTGCACCA	AGTGTACTTT	240
GATGCACCCA	CCTGCCGAGG	GGGCACCACC	AAGGTCTTCT	TAGTTGGGGA	CTACTCCTCG	300
TCAGCCGAAT	TCTTTGTCAC	CGTGGCCGTG	TTTGCCTTCC	TCTACTCCAT	GGGGGCTCTG	360
GCCACCTACA	TCTTCCTGCA	GAACAAGTAC	CGAGAGAATA	ACAAAGGGCC	CATGCTGGAC	420
TTTCTGGCCA	CGGCTGTGTT	CGCCTTCATG	TGGCTAGTTA	GCTCATCGGC	ATGGGCCAAG	480
GGGCTGTCAG	ATGTGAAGAT	GGCCACAGAC	CCAGATGAAC	TCGAG		525

- (2) INFORMATION FOR SEQ ID NO:531:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

GCAAACAGAC	AAGGCTTACA	GGTTAGTTCA	GGATCTGCGC	CTTATCAAGC	AAATTGTTTT	60
GCCTATCCAA	CCTGCGGTGC	CAAACCCATA	TACTCTCCTA	TCCTCAATAC	CTCCCTCCAC	120
AACCCCTCCA	TAACCCATTA	TTCGGTTCTG	GATCTCAAAC	ATGCTTTCTT	TGCTATTCCT	180
TTGCATCCTT	CATCCCAGCC	TCTCTTTGCT	TTCACTTGGG	CTGGCCCTGA	CACCCATCAG	240
CCTCAGCAAC	TTACCTGGGC	TGTACTGCCA	CAAGCCTTCA	CGGACAGCCC	CCATTACTTC	300
AGTAGCCCTC	GAG					313

- (2) INFORMATION FOR SEQ ID NO:532:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GAGACTATCG	CCTATACTTT	ATTTGGGTAA	ATGGTTTGGT	TAAGGTTGTT	TGGTGGTAGC	60
TGGTTGGGTT	GCTGGGGCTC	GGTTGTTGTA	GTCGCGATGT	TCTTCTCCGA	GGCCAGAGCC	120
AGGTCGCGGA	CGTGGGAAGC	CAGTCCCTCG	GAACACAGGA	AGTGGGTGGA	AGTATTTAAA	180
GCATGTGATG	AAGATCACAA	AGGATATCTC	AGCAGAGAGG	ACTTTAAAAC	TGCTGTTGTA	240
ATGCTGTTTG	GGTACAAGCC	CTCCAAGATA	GAAGTGGATT	CTGTGATGTC	TTCAATAAAT	300
CCAAATACTT	CTGGTATATT	ACTCGAG				327

- (2) INFORMATION FOR SEQ ID NO:533:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

GCCTGCCCCC	ACCTTACAGG	TCTGGGATGT	ACCTTTCCAT	CTGTTGCTGC	TTTCTTCTAT	60
GGGCCCCTGC	CCTCACTCTC	AAGAACCTCA	ACTACTCCGT	GCCGGAGGAG	CAAGGGGCCG	120
GCACGGTGAT	CGGGAACATC	GGCAGGGATG	CTCGACTGCA	GCCTGGGCTT	CCGCCTGCAG	180
AGCGCGGCGG	CGGAGGGCGC	AGCAAGTCGG	GTAGCTACCG	GGTGCTGGAG	AACTCCGCAC	240
CGCACCTGCT	GGACGTGGAC	GCAGACAGCG	GGCTCCTCTA	CACCAAGCAG	CGCATCGACC	300
GCGAGTCCCT	GTGCCGCCAC	AATGCCAAGT	GCCAGCTGTC	CCTCGAG		347

- (2) INFORMATION FOR SEQ ID NO:534:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

GGTAGGACCG	GCGAGGAATA	GGAATCATGG	CGGCTGCGCT	GTTCGTGCTG	CTGGGATTCG	60
CGCTGCTGGG	CACCCACGGA	GCCTCCGGGG	CTGCCGGCAC	ATTCTTCACT	ACCGTAGAAG	120
ACCTTGGCTC	CAAGATACTC	CTCACCTGCT	CCTTGAATGA	CAGCGCCACA	GAGGTCACAG	180
GGCACCGCTG	GCTGAAGGGG	GGCGTGGTGC	TGAAGGAGGA	CGCGCTGCCC	GGCCAGAAAA	240
CGGAGTTCAA	GGTGGACTCC	GACGACCAGT	GGGGAGAGTA	CTCCTGCGTC	TTCCTCCCCG	300
AGCCCATGGG	CACGGCCAAC	ATCCAGCTCC	ACGGGCCTCC	CAGAGTGAAG	GCTGTGAAGT	360
CGTCAGAACA	CATCNACGAG	GGGGAGACGG	CCATGCTGGT	CTGCAAGTCA	GAGTCCGTGC	420
CACCTGTCAC	TGACTGGGCC	TGGTACAAGA	TCACTGACTC	TGAGGACAAG	GCCCTCATGA	480
ACGGCTCCGA	GAGCAGAGTT	CTCGAG				506

- (2) INFORMATION FOR SEQ ID NO:535:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

60	TTTCATCTAC	TTAGGTTTGG	GGCACTTTCC	CGTCCTGCCG	TCTTTACCCT	GAATTCCTCT
120	GCTGGGCTGT	TCCGTTGGAG	CTCCCCAGTC	CTTGGCTGCT	TTCTCTTCAG	AGCTTCTATG
180	TGACAGCAGC	GCAGCAGCAG	GGTGGTGGCA	CTGCGGCAGG	GCAGCATCCT	TGCCTTGGCA
240	TGGAGGACGG	TCTTCAGCCT	GGCTGGGGCA	GCTCCTCCTT	GCTTGTTTAG	AGGCACATCG
300	CCTTCTCCTC	GCTGAGCCGG	TTCTGTCTCA	TAGTGGCACT	GTGGAAGCTT	CGAGTTATCA
360	CCCCCTTCTT	GCATCACCCT	CTCTGTGGCA	GGGCTGCCTG	GGAGCCTGGG	TGAGGATGCA
420	CAGTGGCTGG	GGCTTGGAGC	GGGCTCATCA	CTGCTTTGCC	GGAGTTTCTC	CTCCTCGGAA
475	TCCAC	ACCCCATCCC	CAACAACACC	TECCTTCTC	GCAGTAGTGG	CCCTCCTTCC

- (2) INFORMATION FOR SEQ ID NO:536:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

GAATTCGCCT TCATGGCCTA	CAAGCTCTAG	CCTAGACCTT	TAGTGTGCCA	TGCAGTCACA	60
GGTCTGAAAA GCAGCATCAT	CCAAACCTTA	CTTAATCTCT	AAAATCTCAG	CTGGTGGACA	120
GCTCATGATT AGTTCAGCCC	ACTTCCTCCC	CCTTAGTTGA	GTTTGCAGCA	GGACGCAGGA	180
GATAAGCACT TCCAAGCAAG	TCTGATTTAT	ATATCAAACT	CGGTCTCCAT	CCCAGGCCAG	240
CTGACCCTCA GAGCCAGCAA	TGCTCTGTGC	TTCCTCCCTG	CGTCACGGCT	TGGCAAGAGC	300
TGCCTCTGCT GAGCAGTGTG	TGTGATGGAG	ACGGAGGCCG	CTGAAGGCCG	AGTGCTTGCA	360
GGCTTGTGAA CTGCCATCGA	ACACAATCCA	AACTCTGGAA	ATGTTCCTGA	CCACCTAAGC	420
CCTCAACAAC GTAATGCCTG	TATGTGCTNT	TTNTCAGTAA	ACTCCTTGCT	CATGTCNATA	480
AAGTATCCCT GAACACTCGA	G				501

- (2) INFORMATION FOR SEQ ID NO:537:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

GCGGGCACCA	TTTCCAGTAT	GTACCAAACC	AAAGCCGTCA	TCATTGCAAT	GATCATCACT	60
GCGGTGGTAT	CCATTTCAGT	CACCATCTTC	TGCTTTCAGA	CCAAGGTGGA	CTTCACCTCG	120
TGCACAGGCC	TCTTCTGTGT	CCTGGGAATT	GTGCTCCTGG	TGACTGGGAT	TGTCACTAGC	180
ATTGTGCTCT	ACTTCCAATA	CGTTTACTGG	CTCCACATGC	TCTATGCTGC	TCTGGGGGCC	240
ATTTGTTTCA	CCCTGTTCCT	GGCTTACGAC	ACACAGCTGG	TCCCGGGGAA	CCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:538:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

GCTCCACCAG	CTACTGAGAA	AATGGCCTGT	AAAGATCCAG	AAAAACCCAT	GGAGGCCTGT	60
			CCTGAAGCCA			120
					TGGCCCTGTG	180
					TGATTCATTG	240
		AGCAGAACAA				276

- (2) INFORMATION FOR SEQ ID NO:539:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

GAATTCGGCC	TTCATGGCCT	AGCCAGACAA	CTTGTACTGA	TCTTTCTTTG	CTTTGCCTAC	60
TAATCACACA	CACCCTCTCT	TCTAGCCTGT	GAAGACTTAA	CTGATTTTCT	ACGGATGAAG	120
GTTTCAGTGT	CCCAAGGCCC	CATACCGTAT	CTGATTTTAC	TTTATTTTTG	TTTGTTAAGC	180
CTAACAGCTT	CTGAGGAGCC	ACGTAGAGCT	CAAGAAGCAA	AAGCTACTGA	GAGTAGATGC	240
TATGTAAACT	GCACAAGACG	TCTCGAG				267

- (2) INFORMATION FOR SEQ ID NO:540:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

GAATTCGGCC	TTCATGGCCT	ACAAAAAGAT	GCTGGACAAG	GCGTTTGCAG	AGCGGATCAT	60
CCATGACTAC	AAGGATATTT	TCAAACAAGC	AACTGAAGAC	AGGCTCACCA	GTGCCAAGGA	120
ACTGCCCTAT	TTTGAAGGTG	ATTTCTGGCC	CAATGTGTTA	GAAGAGAGCA	TTAAGGAACT	180
AGAACAAGAA	GAAGAGGAGA	GGAAAAAGGA	AGAGAGCACT	GCAGCCAGTG	AAACCACTGA	240
GGGCAGTCAG	GGCGACAGCA	AGAATGCCNA	GAAGAAGAAC	NACNAGAAAA	CCAACAAGAA	300
		CCAACAAGAA				360
CCTGTCCCAG	AAACTCGAG					379

- (2) INFORMATION FOR SEQ ID NO:541:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

GAATTCGGCC	TTCATGGCCT	ACATAATTTG	AATCAACACA	ACCACCCACA	GCCTAATTAT	60
TAGCATCATC	CCTCTACTAT	TTTTTAACCA	AATCAACAAC	AACCTATTTA	GCTGCTCCCC	120
AACCTTTTCC	TCCGACCCCC	TAACAACCCC	CCTCCTAATA	CTAACTACCT	GACTCCTACC	180
CCTCACAATC	ATGGCAAGCC	AACGCCACTT	ATCCAGTGAA	CCACTATCAC	GAAAAAAACT	240
CTACCTCTCT	ATACTAATCT	CCNNACAAAT	CTCCTTAATT	ATAACATTCA	CAGCCACAGA	300
TCTCGAG						307

- (2) INFORMATION FOR SEQ ID NO:542:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

GGATGGCGCC	GCGGAGGGTC	AGGTCGTTTC	TGCGCGGGCT	CCCGGCGCTG	CTACTGCTGC	60
TGCTCTTCCT	CGGGCCCTGG	CCCGCTGCGA	GCCACGGCGG	CAAGTACTCG	CGGGAGAAGA	120
ACCAGCCCAA	GCCGTCCCCG	AAACGCGAGT	CCGGAGAGGA	GTTCCGCATG	GAGAAGTTGA	180
ACCAGCTGTG	GGAGAAGGCC	CAGCGACTGC	ATCTTCCTCC	CGTGAGGCTG	GCCGAGCTCC	240
ACGCTGATCT	GAAGATACAG	GAGAGGGACG	AACTCGCCTG	GAAGAAACTA	AAGCTTGACG	300
GCTTGGACGA	AGATGGGGAG	AAGGAAGCGA	GACTCATACG	CAACACACTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:543:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

GGATACCCTA	AAAAAACAAT	CTATGTCAGA	GGCTTCACTG	GAGGTTACGT	CACGTTATCG	60
TATTAATTTA	GAAGATGAGA	CACAGGATTT	AAAGAAGAAA	TTAGGTCAAA	TCAGAAATCA	120
ATTGCAAGAA	GCACAGGATC	GACATACAGA	AGCTGTCAGA	TGTGCTGAGA	AGATGCAAGA	180
TCACAAGCAA	AAGCTTGAAA	AAGATAATGC	CAAGTTAAAA	GTTACAGTCA	AAAAGCAAAT	240
GGACAAAATT	GAGGAGCTTC	AGAAAAACCT	GTTAAATGCA	AATTTGTCTG	AAGATGAAAA	300
GGAACTCGAG						310

- (2) INFORMATION FOR SEQ ID NO:544:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

GTTTGGATGA	TTGGTGGCGT	GTACGCAGCT	GCTATGGCCT	GGGCCATCAT	CCCCCACTAT	60
GGGTGGAGTT	TTCAGATGGG	TTCTGCCTAC	CAGTTCCACA	GCTGGAGGGT	CTTCGTCCTC	120

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GTCTGCGCCT	TTCCTTCTGT	GTTTGCCATT	GGGGCTCTGA	CCACGCAGCC	TGAGAGCCCC	180
CGTTTCTTCC	TAGAGAATGG	AAAGCATGAT	GAGGCCTGGA	TGGTGCTGAA	GCAGGTCCAT	240
GATACCAACA	TGCGAGCCAA	AGGACATCCT	GAGCGACTCG	AG		282

- (2) INFORMATION FOR SEQ ID NO:545:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GAATTCGGCC	TTCATGGCCT	AGAACTTTGT	ACACCATGGA	ATGTTCTACT	TATTATTTTG	60
TGCTACAATA	TGTGCTGTTT	CTTTTGTTTG	AATTGCAGAT	TGTCTACTAT	GAAGCAGGGA	120
TTATTCTATG	CTGTGTCCTG	GGGCTGCTGT	TTATTATTCT	GATGCCTCTG	GTGGGGTATT	180
TCTTTTGTAT	GTGTCGTTGC	TGTAACAAAT	GTGGTGGAGA	AATGCACCAG	CGACAGAAGG	240
AAAATGGGCC	CTTCCTGAGG	AAATGCTTTG	CAATCTCCCT	GTTGGTGATT	TGTATAATAA	300
TAAGCATTGG	CATCTTCTAT	GGTTTTGTGG	CAAATCACCA	GGTAAGAACC	CGGATCCTCG	360
AG						362

- (2) INFORMATION FOR SEQ ID NO:546:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

TCGAGGGACA	TGAGGCTGAG	CTGGTTCCAG	GTCCTGACAG	TACTGTCCAT	CTGCCTGAGC	60
GCCGTGGCCA	CGGCCACGGG	GGCCGAGGGC	AAAAGGAAGC	TGCAGATCGG	GGTCAAGAAG	120
CGGGTGGACC	ACTGTCCCAT	CAAATCGCGC	AAAGGGGATG	TCCTGCACAT	GCACTACACG	180
GGGAAGCTGG	AAGATGGGAC	AGAGTTTGAC	AGCAGCCTGC	CCCAGAACCA	GCCCTTTGTC	240
TTCTCCCTTG	GCACAGGCCA	GGTCATCAAG	GGCTGGGACC	AGGGGCTGCT	GGGGATGTGT	300
GAGGGGGACC	TCGAG					315

- (2) INFORMATION FOR SEQ ID NO:547:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 449 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

GAATTTTAAT	TAAGAATTCG	GCCTTCATGG	CCTAATCGAG	GAGAATGGAG	ACCAAACCTG	60
TGATAACCTG	TCTCAAAACC	CTCCTCATCA	TCTACTCCTT	CGTCTTCTGG	ATCACTGGGG	120
TGATCCTGCT	GGCTGTTGGA	GTCTGGGGCA	AACTTACTCT	GGGCACCTAT	ATCTCCCTTA	180
TTGCCGAGAA	CTCCACAAAT	GCTCCCTATG	TGCTCATCGG	AACTGGCACC	ACTATTGTTG	240

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420

449



TGTTTCGTCA TGAGATCAAG GACACCTTCC TGAGGACTTA CACGGACGCT ATGCAGACTT ACAATGGCAA TGATGAGAGA ATGCTCGAG

ATGCCATGTT TCTGTCCCTG GTGTTCCTGG CTGAGCTCGT AGCTGGCATT TCAGGGTTTG

- (2) INFORMATION FOR SEQ ID NO:548:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

GGGCTTTAAA	GGCAGACATT	GATGCTACAT	TATATGAACA	AGTCATCCTG	GAAAAAGAAA	60
TGGGAACTTA	TTTGGGCACC	TTTGATGATT	ACTTGGAGTT	ATTCCTGCAG	TTTGGTTATG	120
TGAGCCTTTT	CTCCTGTGTT	TACCCATTAG	CAGCTGCCTT	TGCTGTGTTA	AATAACTTCA	180
CTGAAGTAAA	TTCAGATGCC	TTAAAAATGT	GCAGGGTCTT	CAAACGTCCA	TTCTCAGAAC	240
CTTCAGCCAA	TATTGGTGTG	TGGCAGTTGG	CTTTTGAAAC	GATGAGTGTT	ATATCTGTGG	300
TCACTAACTG	TGCGCTGATT	GGAATGTCAC	CACAAGTGAA	TGCAGTCTTT	CCAGAATCAA	360
AGGCAGACCT	CGAG					374

- (2) INFORMATION FOR SEQ ID NO:549:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

GTACAATCTG	AATCCAGGTC	TGACAGCTGG	CCATACAAAG	TCATACTTTC	CCCACATCCC	60
TCCTCTTTGA	TAGGCATTGT	CATCTAGAGC	AATAGCCTCG	AAATAGACTG	AACACCGTGG	120
CCCATAGCTT	AACTCCGTTC	CACCTCTATT	TCAAAGTAAA	CTTGGGCTGG	GATTACAGGC	180
ATGAGTATGT	TTTCATTTGT	ACATAAAGAC	TTTATACAAA	TGCTCTTCCT	AATATTTGCT	240
ACTTATTTTT	GCATTAGTTC	AAATTCTTTG	TCCTGTCATC	CCAAAACTCT	CGAG	294

- (2) INFORMATION FOR SEQ ID NO:550:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

GAATTCGGCC	TTCATGGCCT	ACACTGCACG	GGGAACCCCC	GAACCATCAT	CGTGCCACCC	60
CTGAAAACCC	AGGCCAGCGA	AGTATTGGTG	GAGTGTGATA	GCCTGGTGCC	AGTCAACACC	120
AGTCACCACT	CGTCCTCCTA	CAAGTCCAAG	TCCTCCAGCA	ACGTGACCTC	CACCAGCGGT	180
CACTCTTCAG	GGAGCTCATC	TGGAGCCATC	ACCTACCGGC	AGCAGCGGCC	GGGCCCCCAC	240

300 TTCCAGCAGC AGCAGCCACT CAATCTCAGC CAGGCTCAGC AGCACATCAC CACGGCCGTC 303 GAG (2) INFORMATION FOR SEQ ID NO:551: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:551: GCCACAAGCC TGTCAGCAAG TGGGGCTACT TGGGTCCTCG GGCCTCAATC CACTCCTGGC CAGAGACAAC TTCCTCTCCC ATGGGAAAGG CTAACGCATG CCCATAAATT AAGACATTTG 120 CTCTCCCTCC AAGCCCTGGA AACCTGGGAC TCTCTAACAT CTACCTCTGT TTTCTTTGGC 180 TGCATTCAAC TTTCCTGCAA TTAGTCAGGC CCTGGGGCAG CAGTTAGACG ACAGATGAGT 240 CAGAGGATTG CAGAATCTAA TCCAGAAGGA AGAGTTTATC CAAATGTTGG TGGCCTTTCT 300 CTTTTGGCGC ATTCTCTTCT GGTTCTGTCT TTTCTCAGGA GTCCTCTGAG CTTCCATGTA 360 375 CCGGGCCCCC TCGAG (2) INFORMATION FOR SEQ ID NO:552: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 390 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:552: GCAAGGGCAG GCGGGTCCCC CAGTCCCGCC ATTACGGGTT GTCAGACCGT CTGCGTGTGG CAGGGCTCCC AAGGGCAGGC GGGTCCCCCA GTCCCGCCAT TACGGGTTGT CAGACCGTCT 120 180 GCGTGTGGCA TTTTTTGGCT TATAAGCTTC ACCCACTCAC CCCCAACCCA CACCCCACAT CCCCCTGCCG GCAGCCCCTC AACCTAAGAA GGCCAGAGCA TATTTATTTT CGGAGGGAGC 240 AGATTACTTC TCCCAGAGAA AGGAAAATCT TGGAAAAGAT TTAAAAAACAC AAATCTAAGC 300 CTTGACGGTT TTTTTTCCC TTTTGACCCC CTTCCCATTT TTTCAGNATT TATTCCCATG 360 390 GCTTTTTTT TTCTTGTGCG TGTTCTCGAG (2) INFORMATION FOR SEQ ID NO:553: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 620 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:553: GAATTCGGCC AAAGAGGCCT AAGCAGGCGC GAGGGGGGG CAGCGAGCCG GGTCCCACCA TGGCCGCGAA TTATTCCAGT ACCAGTACCC GGAGAGAACA TGTCAAAGTT AAAACCAGCT 120 CCCAGCCAGG CTTCCTGGAA CGGCTGAGCG AGACCTCGGG TGGGATGTTT GTGGGGCTCA 180

TGGCCTTCCT GCTCTCCTTC TACCTAATTT TCACCAATGA GGGCCGCGCA TTGAAGACGG

240

CAACCTCATT	GGCTGAGGGG	CTCTCGCTTG	TGGTGTCTCC	CGACAGCATC	CACAGTGTGG	300
CTCCGGAGAA	TGAAGGAAGC	TGGTGCACAT	CATTGGCGCC	TTACGGACAT	CCAAGCTTTT	360
GTCTGATCCA	AACTATGGGG	TCCATCTTCC	GGCTGTGAAA	CTGCGGAGGC	ACGTGGAGAT	420
GTACCAATGG	GTAGAAACTG	AGGAGTCCAG	GGAGTACACC	GAGGATGGGC	AGGTGAAGAA	480
GGAGACGAGG	TATTCCTACA	ACACTGAATG	GAGGTCAGAA	ATCATCAACA	GCAAAAACTT	540
CGACCGAGAG	ATTGGACACA	AAAACCCCAG	TGCCATGGCA	GTGGAGTCAT	TCATGGCAAC	600
AGCCCCCTTT	GTTCCTCGAG					620

- (2) INFORMATION FOR SEQ ID NO:554:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

GAATTCGGCC AAAGAGGCC	T AGGACTTGTT	TCGGAAGGAG	CTGACTGGCC	AATCACAATT	60
GCGAAGATGA AGGCTCTGT	G GGCCGTGCTG	TTGGTCACAT	TGCTGACAGG	ATGCCTAGCC	120
GAGGGAGAGC CGGAGGTGA	C AGATCAGCTC	GAGTGGCAAA	GCAACCAACC	CTGGGAGCAG	180
GCCCTGAACC GCTTCTGGG	A TTACCTGCGC	TGGGTGCAGA	CGCTGTCTGA	CCAGGTCCAG	240
GAAGAGCTGC AGAGCTCCC	A AGTCACACAA	GAACTGACGG	CACTGATGGA	GGACACTATG	300
ACGGAAGTAA AGGCTTACA	A AAAGGAGCTG	GAGGAACAGC	TGGGTCCAGT	GGCGGAGGAG	360
ACACGGGCCA GGCTGGGCA	A AGAGGTGCAG	GCGGCACAGG	CCCGACTCGG	AGCCGACATG	420
GAGGATCTAC GCAACCGAC	T CGGGCAGTAC	CGCAACGAGG	TGCACACCAT	GCTGGGCCAG	480
AGCACAGAGG AGATACGGG	C GCGGCTCTCC	ACACACCTGC	GCAAGATGCG	CAAGCGCTTG	540
ATGCGGGATG CCGAGGATC	T GCAGAAGCGC	CTAGCTGTGT	ACAAGGCAGG	GGCAGTCGAG	600

- (2) INFORMATION FOR SEQ ID NO:555:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

GAATTCGGCC	TTCATGGCCT	AGTATTTCCT	TATCACAGAT	TTTGGGAGCA	ACAGTGTTTT	60
CCCATCTGGA	GGAGGCTGAG	TTAATTCTGT	GGAACACCCA	TTTGGTTGGA	AATAAAAACA	120
CAGCATGGAT	TTAATTCATG	CCACTTATTT	ATTTTTATTA	GGACTTGAGC	TTCTTTGTAT	180
TTTTTTTGCT	TTGCTTCCAC	TCAAAACCAG	ATTTGGTGGT	TGCTGTGTAA	ACAGTGAAAT	240
ACAACACAGG	CCAGGACTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:556:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

GAATTCGGCC	AAGAGGCCTA	GTATTCTTTC	GTTTCTCTCT	AAAAGAAGAA	AAATATAATT	60
TAGAAATACA	TTGCGTATTT	TCTAAAACAA	TAAATTTATA	GTGTTAATAT	TCATAGGGTC	120
AATCAAAATG	AAGCTTCTCC	TTTGGGCCTG	CATTGTATGT	GTTGCTTTTG	CAAGGAAGAG	180
ACGGTTCCCC	TTCATTGGTG	AGGATGACAA	TGACGATGGT	CACCCACTTC	ATCCATCTCT	240
GAATATTCCT	TATGGCATAC	GGAATTTACC	ACCTCCTCTT	TATTATCGCC	CAGTGAATAC	300
AGTCCCCAGT	TACCCTGGGA	ATACTTACAC	TGACACAGGG	TTACCTTCGT	ATCCCTGGAT	360
TCTAACTTCT	CCTGGATTCC	CCTATGTCTA	TCACATCCGT	GGTTTTCCCT	TAGCTACTCA	420
GTTGAATGTT	CCTCCTCTCC	CTCCTAGGGG	TTTCCCGTTT	GTCCCTCGAG		470

- (2) INFORMATION FOR SEQ ID NO:557:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GAATTCGGCC	AAAGAGGCCT	ATGCAGATTC	TGTGGTTATA	CTCACTCCTC	ATCCCAAAGA	60
ATGAAATTTA	CCACTCTCCT	CTTCTTGGCA	GCTGTAGCAG	GGGCCCTGGT	CTATGCTGAA	120
GATGCCTCCT	CTGACTCGAC	GGGTGCTGAT	CCTGCCCAGG	AAGCTGGGAC	CTCTAAGCCT	180
AATGAAGAGA	TCTCAGGTCC	AGCAGAACCA	GCTTCACCCC	CAGAGACAAC	CACAACAGCC	240
CAGGAGAGTT	CGGCGGCAGC	AGTTCAGGGG	ACAGCCAAGG	TCACGTCAAG	CAGGCAGGAA	300
CTAAACCCCC	TGAAATCCAT	AGTGGAGAAA	AGTATCTTAC	TAACAGAACA	AGCCCTTGCA	360
AAAGCAGGAA	AAGGAATGCA	CGGAGGCGTG	CCAGGTGGAA	AACAATTCAT	CGAAAATGGA	420
AGTTCCCTCG	AG					432

- (2) INFORMATION FOR SEQ ID NO:558:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

GAATTCGGCC AAAGAGGCCT AAAAAGTATA TACATTTTAG TACTGCTTTG ATTTTGTTTA 60 CATACTGAAA AATGTATCTG AAAATGAGTT ATTTTGGACT CGAG 104

- (2) INFORMATION FOR SEQ ID NO:559:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 203 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GAATTCGGCC AAAGAGGCCT ATTCACTTCA GCTTCACTGA CTTCTGGATT CTCCTCTTGA 60

GTAAAAGGAC TCAGCCAACT ATGAAGTTTT TTGTTTTTGC TTTAATCTTG GCTCTCATGC TTTCCATGAC TGGAGCTGAT TCACATGCAA AGAGACATCA TGGGTATAAA AGAAAATTCC ATGAAAAGCA ACATGATCTC GAG	120 180 203
(2) INFORMATION FOR SEQ ID NO:560:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 484 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:	
GAATTCGGCC ACAGAGGCCT AGCCCAGTCT CGGGTATGTC TTTATCAGCA GCATGAAAAT GGACTAATAC AGTTGCTATG ATTATTAGTT TTTTGCTACT GAGTTGTAGG AGTATCTGAT ATATATTTTG GTAACTAATC CCTTATAAAA TATATTGTTT CCAAATATTT TTTTCCCATT CCATAGGCTG CCTTTTCATT CTGTTGTTC CTTTGCTTCA GGTAAGGGAT TCTGAAACAA CTATTTGGGC AGCAGAACAG CTTCTTTTGT TTGCTTTCTC ATTGTCTACT GTGTTCTGCA TAAATAAGGT TATGAATTAG CTGTTGTTCA TATGGGTGAA AGATTTGCAT CTGTGGACGC TTAGATAGCA CATATGGTAA ACCATAGAAC TTCACCATTT ATAACCTTTG AACAACTGAT ACACTTAGAA AAGCAGTTTT TGGCTGGGCG CGGTGGCTCA TGCCTGTAAT CCCTAGGCCT CGAG	60 120 180 240 300 360 420 480
(2) INFORMATION FOR SEQ ID NO:561:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 176 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:	
GAATTCGGCC AAAGAGGCCT ATTGAATTCT AGACCTGCCT CGAGCTGACA ACTATGAAGT TTTTTGTTTT TGCTTTAATC TTGGCTCTCA TGCTTTCCAT GACTGGAGCT GATTCACATG CAAAGAGACA TCATGGGTAT AAAAGAAAAT TCCATGAAAA GCATCAAGGA CTCGAG (2) INFORMATION FOR SEQ ID NO:562:	60 120 176
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 475 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:	
GAATTCGGCC AAAGGGCCTA ATTTTATTAA TAACATTTTA AAAACAACAA TTATGAAAAA GCAATTCGGT TTACCGCTGA TGCTTGCGTC AGCCCTCGCC TTCTCTGCTT GTAGCTCTGA TGATGTGGCC GAGAATGGCC CAAAGGACAAT CGCAGCTCTT ACAGATGGTG GTTACTTGAA GATGTCTATC AATCTTCCTT CCCGTGCTGC TAATGGTGGC TTCAGAGCTA CGGAACAAGA CGGTTATGTT AACTTGGAAG ATGCTATCCT	60 120 180 240 300

CGTCCTTTTC CAAGGTGATA ATGAAGCAGA TGCCAAGTTC CATTCTGCAT ATGAACTTAC TACATCAATG CAGAAGGATG GCTCTACGCA AATCACTTCC ACAACGAAAC TTGTTAAGAA TGTGAATATT GGTGGTCAGG GAAATCCTCT TAAACCTGCT GATGTTAAGC TCGAG	360 420 475
(2) INFORMATION FOR SEQ ID NO:563:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 204 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:	
GAATTCGGCC AAAGAGGCCT ACAATTATGG GGCTTATGGG GAACATGCTC ATTGTGTTTT ACCAATCAGG ACATGGAACT TAAACAATAT TTGTTGACTT ATAGTGAAAC CTGGCTAATT AGGACTCTTA ACCAGCACTC TTAATTAACT GACTTATTTT TCTCTGTGTC CACCCCTCTT AAAGAAAAAG AAGCGAAACT CGAG	60 120 180 204
(2) INFORMATION FOR SEQ ID NO:564:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:	
GAATTCGGCC AAAGAGGCCT ATAGGCCTCT TTGGCCGTAG GCCTCTTTGG CCGATTGAAT TCTAGACGCG GCTCGAGGCA GGTCTAGGCC TCTTTGGCCG AA	60 102
(2) INFORMATION FOR SEQ ID NO:565: (i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 285 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:	
GAATTCGGCC AAAGAGGCCT ACTCAATTGT TCCTTTCTTC CATCACCACC CTTTGAAGGT CTCTTTGCCT ACTTGTAGAT TTAGGGGGAC ATAACATTGA GACTGAGCAG TTTCTTGAAC CTCTCCTCTC AGCAGCCACC AGCCTGGCTT TCGCAGACCA CTGGAAAGTA TCCCAGCTCA TTAGCTTTTG GAATGACGG AAGCCTTTTG ATGTTNGACG TCTTAATCTC AACTCTTCAA CTTAGCTCAT TCTGGAGCAG TCACGCGATG ACAGATGAGC TCGAG	60 120 180 240 285

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GATAACTTGA	GATCAAATCA	GTCATATTTG	ACTCTTCTCT	TTTTCACTCC	TTTTATATCT	60
GATCAGTCAG	CAGTTTTTTG	AAACCCTGTT	CGAAGCAGTT	CTCAACACTT	GTGCACCCAT	120
TCTTTCTCCT	ACACCACTCA	ATCTAGACCC	TCACATGTGG	CTGTCCTGCT	TTCCTTCTCT	180
CCTACTTCTA	AGCTATTCTG	TGGAGAGATG	TCAAAGTAAT	CTTCACAAAA	AATCTGATTG	240
CATCACTTCA	CATCTCGAG					259

- (2) INFORMATION FOR SEQ ID NO:567:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

GGGCTTTAAA	GGCAGACATT	GATGCTACAT	TATATGAACA	AGTCATCCTG	GAAAAAGAAA	60
TGGGAACTTA	TTTGGGCACC	TTTGATGATT	ACTTGGAGTT	ATTCCTGCAG	TTTGGTTATG	120
TGAGCCTTTT	CTCCTGTGTT	TACCCATTAG	CAGCTGCCTT	TGCTGTGTTA	AATAACTTCA	180
CTGAAGTAAA	TTCAGATGCC	TTAAAAATGT	GCAGGGTCTT	CAAACGTCCA	TTCTCAGAAC	240
CTTCAGCCAA	TATTGGTGTG	TGGCAGTTGG	CTTTTGAAAC	GATGAGTGTT	ATATCTGTGG	300
TCACTAACTG	TGCGCTGATT	GGAATGTCAC	CACAAGTGAA	TGCAGTCTTT	CCAGAATCAA	360
AGGCAGACCT	CGAG					374

- (2) INFORMATION FOR SEQ ID NO:568:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

GAATTCGGCC	TTCATGGCCT	AGATAAGTAA	ATAGACTTAC	AGAGGGAAAG	TAACTTGGCT	60
AAGGTGAACT	TGAACCAAGA	TGACTGACTC	CAGAGCTTCC	ATTTTTCTTT	TTCTTTCTTT	120
TTTTTTTTTT	NGGAGACAGA	GTCTCACTCT	GTCGCCCAGG	CTGGAGTGCA	ACGGCGCGGT	180
CTCCACTCAC	TGCAGCCTCC	AGCTCCTGGG	CTCAAGTGAT	CCTCCCACCT	CAGCACCCCC	240
ACGTCTCGAG						250

- (2) INFORMATION FOR SEQ ID NO:569:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

GAATTCGGCC	TTCATGGCCT	ACAGGGAGGG	AGGGGTTCTG	AGAGCCTCAG	ACCACAGGGC	60
CTGAGGCCCA	CAGTGGCCCA	GAGTCCATCT	GGCAGCCCCT	GCTCTGCTGG	CCCAGGGGGC	120
TCTCCCCAGG	GTGGAGTAGG	CAGGGGAGGG	TCGCTGGTCC	CCAGTCCCAG	CCTTCGAGAG	180
GTGGGGCCAG	ACAGCAGGGC	ACCCGTACCC	GAGACCACAG	TGCTCCCCAA	GGCCAGCTCT	240
CTCCCCAGTG	AGGTCACTCC	TACCTCCGGG	GCCATTTGGG	GCGGGGGATC	CTGTAGATCT	300
CTGACTCTGC	GGCGCCTTAT	CTTGATGGCC	TGGCNCAAGA	AGGGAGGGCG	CTGCCCACTT	360
CCTCGAG						367

- (2) INFORMATION FOR SEQ ID NO:570:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

TTTTGACTGA CTCTTT	AAAT TAGTACAATT T	TTCTACTTG TCATATA	ACT CCTGGAACAA 60
TAGTACGGGA AGCCGT	GATC CTTTTCCCTG A	CTCATGATT TTAGTCT	TTT TCCAAATCGC 120
TGTTTTTTTT TGGTTT	TTTT TTTTTTTGCT G	CTCCAACGA CCAGCAT	GTG TTGGAGCAGA 180
TCTCCATGGT AAGCCA	AAAG TGGACTTGTC A	GCCTATAAC TACTCTG	CAG CTGCCACTAA 240
CTCTACAGGC ACAGAG	CTCG AG		262

- (2) INFORMATION FOR SEQ ID NO:571:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

CAGAAACTCT	TGGACTCAAA	AGAGAAAGAA	AAAAGTCAAG	CCAAGGAAAG	CACAAGAGGT	60
AAGACAGGCC	TAGTGATCTC	AGCAGGCAGA	ATTTATGGAC	ATATTTTGCA	GGCAAGTGGT	120
TCTCAATCAG	GGGTGATTTT	TGGCTTGTAA	GGACATTTAG	CAATATCTGG	ACACATTTTT	180
TGGTTGTCGT	AAGTGGATGG	GGGTTGCTGC	TATCATCCTA	CAATGCATAG	GTGCATTAGT	240
CTGTTTTCAT	GCTGCTGATA	AAGACATACC	GGAGACTGGG	CAATTTGCAA	ATGAGAGATG	300
GCTCGAG						307

- (2) INFORMATION FOR SEQ ID NO:572:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 578 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

GAATTCGGCC	TTCATGCCTA	CAGCCATATT	AAAACTAAGT	AAACTCGTCC	CTGGGAACTA	60
CACTTTCAGC	TTGACTGTAG	TAGACTCTGA	TGGAGCTACC	AACTCTACTA	CTGCAAACCT	120
GACAGTGAAC	AAAGCTGTGG	ATTACCCCCC	TGTGGCCAAC	GCAGGCCCCA	ACCAAGTGAT	180
CACCCTGCCC	CAAAACTCCA	TCACCCTCTT	TGGGAACCAG	AGCACTGATG	ATCATGGCAT	240
CACCAGCTAT	GAGTGGTCAC	TCAGCCCAAG	CAGCAAAGGG	AAAGTGGTGG	AGATGCAGGN	300
TGTTAGAACA	CCAACCTTAC	AGCTCTCTGC	GATGCAAGAA	GGAGACTACA	CTTACCAGCT	360
CACAGTGACT	GACACAATAG	GACAGCAGGC	CACTGCTCAA	GTGACTGTTA	TTGTGCAACC	420
TGAAAACAAT	AAGCCTCATC	AGGCAGATGC	AGGCCCAGAT	AAAGAGCTGA	CCCTTCCTGT	480
GGATAGCACA	ACCCTGGATG	GCAGCAAGAG	CTCAGATGAT	CAGAAAATTA	TCTCATATCT	540
CTGGGAAAAA	CACAGGGACC	TGATGGGTGC	AGCTCGAG			578

- (2) INFORMATION FOR SEQ ID NO:573:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 623 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

GAATTCGGCC	TTCATGGCCT	AACTTTGTGT	GATCAGAGTT	TATGGGTTGG	GCTGCCCCAG	60
GCTTGGATAA	CTTAAAGGCT	TGATGAGGTC	ATCAATTTAT	GCTTGGCTAC	CCATGGCACA	120
GAAGCATAGC	CCCACTGTGA	TGGCTGGGGT	GGCTCCGGGC	ATCCTGGGCA	GTCAGGAGGA	180
AACTCCATGA	AGGAAGGAGC	TAACCTTTCT	GGGGGTACCC	CTATCCCAGC	ACAGACTTCC	240
TCATCTCATT	GGTCAGAACT	GGGTCACATG	AACATGCCTC	AGCCTATCAC	AGGCACAGGG	300
AATGAGACCA	TCATGGACCA	ATCAGGATTC	ACCACTCAAG	GTGGGGCCTG	CCATCCGGAT	360
GGATGCTCTC	CGCCACAGGG	AGGTGGGGGA	CCCAGAAGCT	GTGGGCAATG	GCCATGTGCA	420
CAGTAGGACT	GAGGCACTCA	GTCCCGTAGC	TGACCTACCT	GGGACAGGCC	TGGAGGCTGA	480
CTTAGGTGTG	AGGGGCAGAG	AGATTACTGT	GCACAGACCG	CTGTGTGACC	CCAGATCTAG	540
GTGGGATCCC	GGTGTGCCCC	ATCTGCCTGG	CTTACCCCAA	CCCCTCTGGA	ACCTGAACCA	600
TTGAATTCTA	GACCTGCCTC	GAG				623

- (2) INFORMATION FOR SEQ ID NO:574:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

GAATTCGGCC	TTCATGGCCT	ACTCCAGAAT	GAAGATCTTC	TTGCCAGTGC	TGCTGGCTGC	60
CCTTCTGGGT	GTGGAGCGAG	CCAGCTCGCT	GATGTGCTTC	TCCTGCTTGA	ACCAGAAGAG	120
CAATCTGTAC	TGCCTGAAGC	CGACCATCTG	CTCCGACCAG	GACAACTACT	GCGTGACTGT	180
GTCTGCTAGT	GCCGGCATTG	GGAATCTCGT	GACATTTGGC	CACAGCCTGA	GCAAGACCTG	240
TTCCCCGGCC	TGCCCCATCC	CAGAAGGCCT	GCTCGAG			277

- (2) INFORMATION FOR SEQ ID NO:575:
 - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 251 base pairs

(B)	TYPE: nucleic acid
• • •	STRANDEDNESS: double
(D)	TOPOLOGY: linear
(ii) MOLEC	ULE TYPE: cDNA
(xi) SEQUE	NCE DESCRIPTION: SEQ ID NO:575:
	GCCT AAGCTTTTGC TTTTTTAATA ACTTGTATAG CTAAAAACTT 60
	CAGA TCAAAGCTGA TCCTTCTGTC AGTAATGATT CTAAAAATAA 120
	GAAT ATATTTTATT TCATTCTTAT CTCAAACCTA GGTACTGTGG 180
TCGTTTTGAG TTCATT	TCGA GGCATTTTCA ATGTGCCTCA GGCCACATCC AACCTCTCCC 240
CAGAACTCGA G	251
(2) INFORMATION E	FOR SEQ ID NO:576:
(i) SEOUEN	CE CHARACTERISTICS:
(A)	LENGTH: 261 base pairs
(B)	TYPE: nucleic acid
(C)	STRANDEDNESS: double
(D)	TOPOLOGY: linear
(ii) MOLEC	TULE TYPE: cDNA
(xi) SEQUE	NCE DESCRIPTION: SEQ ID NO:576:
GAATTCGGCC TTCATO	GGCCT ACAGTCTAAG ACATTTCCTA TTCTGCCTTC TTGTCTTCCT 60
	FIGGIC AGACTIACAT CITGGACAGC TCTCCCAGCC ATCTTCTACT 120
	CCTCC CAGACTTTTC CCCGCAAAAC ATCTGTTGCA GGTGGTATTA 180
ATTTCCTATC ACGGCT	TGTGA CAAATTACCA CAAACTCAGT GGCTTAAAAC AATGCACATT 240
TATTATCTGA CAGTTO	CTCGA G 261
(2) INFORMATION	FOR SEQ ID NO:577:
(i) SEQUEN	ICE CHARACTERISTICS:
	LENGTH: 216 base pairs
(B)	TYPE: nucleic acid
(C)	STRANDEDNESS: double
(D)	TOPOLOGY: linear
(ii) MOLEC	CULE TYPE: cDNA
(xi) SEQUI	ENCE DESCRIPTION: SEQ ID NO:577:
СВАТТССССТ ТСАТС	GCCTA GCAAGACTCC ATCTCAAAAA AAGAAAGAAA GAAAAAAAGAA 60
	AGTAT TATAGTGAAA AATTCGCATT CTGGCTGATT TTAAGCCATT 120
	ACAAC CTTCCATAAA AATTTGACAG GTGCCCAGAT GTTGCTTTCT 180
CCATTTATTT TTTGT	TTTTT TTTAATCACA CTCGAG 216

- (2) INFORMATION FOR SEQ ID NO:578:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

GCGATTGAAT	TCTAGACCTG	CCTCGAGTAA	GTGCCGAAAA	CTTCACTGTG	CTCATCAAGA	60
ACAATATCGA	CTTCCCCGGC	CACAACTACA	CCACGAGAAA	CATCCTGCCA	GGTTTAAACA	120
TCACTTGTAC	CTTCCACAAG	ACTCAGAATC	CACAGTGTCC	CATTTTCCGA	CTAGGAGACA	180
TCTTCCGAGA	AACAGGCGAT	AATTTTTCAG	ATGTGGCAAT	TCAGGTTGGT	GGTGCTTTGT	240
ACACTGGGAT	GTGGGGCTGT	GTGTCTAGGG	ATGGAGGATG	TCAAACAACT	CGAG	294

- (2) INFORMATION FOR SEQ ID NO:579:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GAATTCGGCC	TTCATGGCCT	ACCTTCACAG	AAAAATGCAT	AGCTGGATGC	TGCAGACTCT	60
AGCGTTTGCT	GTAACATCTC	TCGTCCTTTC	GTGTGCAGAA	ACCATCGATT	ATTATGGGGA	120
AATCTGTGAC	AATGCATGTC	CTTGTGAGGA	AAAGGACGGC	ATTTTAACTG	TGAGCTGTGA	180
AAACCGGGGG	ATCATCAGTC	TCTCTGAAAT	TAGCCCCCCC	GATCTCGAG		229

- (2) INFORMATION FOR SEQ ID NO:580:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GAATTCGGCC	TTCATGGCCT	AGCTTACTTT	ACAATTCTGC	TGTTTGTCAA	GTGTTCCTAT	60
AGTTTTTTT	AAAGGTATGT	TAACTATTTT	TCCCTTTTGG	TTTATATTTG	TAGGAATCTT	120
TGCCTTTAAG	TGTGCCCGTG	CAGAAGAATT	ATTTAACATG	TTGCAAGAGA	TTATGCAAAA	180
TAATAGTATA	AATGTGGAGC	TCGAG				205

- (2) INFORMATION FOR SEQ ID NO:581:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GAAGTGTAAT	GTCAGACACA	CAAGAAAAGC	AAATCAGTGT	TGTAAGCTTA	AAGTACAATT	60
TCAAAGGTCA	TTACCAACAG	CAGGGTTTTT	TTTATACTTT	AAAAACATTA	TGCTACATAT	120
CATTGCCATT	TTCATATTTT	GGGGTTTTGC	TACTCTTATA	CAATGGAATC	AATGGAAATG	180
TCATCCAGCC	AGATCTCGAG					200

- (2) INFORMATION FOR SEQ ID NO:582:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

GAATTCGGCC	TTCATGGCCT	ACACAAATGT	TTGTTGAGTG	CTCATTGTAT	GTCTGGAGAC	60
CATTCTGTCT	TCTTCCCTAA	GAGTGTTCAT	GCTGTTGGAC	CAGGTGTTAT	GATTTTGCTC	120
TGGAGAATAA	GGTATTTCCA	CATGGAGCAT	GTGGAAAATA	TAGTGCCTAT	CTCCTGAAAG	180
GTCCAGGTGA	TGCAAAGATG	AATGAGACAT	GATTGGAGGT	TTTTCTTCTG	TCTGAAATGC	240
AGACAGTTCT	GGGTTGGGCA	GCTCTGTAAG	ATGCTGAACA	TGTGTCCTTC	CAAGAAGCAA	300
GGATCAGAAA	GCAGACTCCA	G				321

- (2) INFORMATION FOR SEQ ID NO:583:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GAATTCGGCC	TTCATGGCCT	ACACCATTGA	CTTCTTCTAC	CGGCCGCATA	CCATCACCCT	60
GCTCAGCTTC	ACCATCGTCA	GCCTCATGTA	CTTCGCCTTT	ACCAGGGATG	ACTCTGTTCC	120
AGAAGACAAC	ATCTGGAGAG	GCATCCTCTC	TGTTATTTTC	TTCTTTCTTA	TCATCAGTGT	180
GTTAGCTTTC	CCCAATGGTC	CGTTCACTCG	ACCTCATCCA	GCCTTATGGC	GAATGGTTTT	240
TGGACTCAGT	GTGCTCTACT	TCCTGTTCCT	GGTATTCCTA	CTCTTCCTGA	ATTTCGAGCA	300
GGTTAAATCT	CTAATGTATT	GGCTAGATCC	AAATCTTCGA	TACGGCCACC	TCGAG	355

- (2) INFORMATION FOR SEQ ID NO:584:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

GGAAACTTCT	AGAAATAATG	ACAAGGATTC	AAACTTATTG	TCAAATGAGT	CCAATGTCAG	60
ATTTTGGAAC	TCAACCCTAT	GAACAATGGG	CCATTCAAAT	GGAAAAAAA	GCTGCAAAAG	120
AAGGAAATCG	CAAAGAACGT	GTTTGTGCAG	AACATTTGAG	GAAGTACAAT	GAGGCCCTAC	180
AAATTAATGA	CACAATTCGA	ATGATAGATG	CGTATACTCA	TCTTGAAACT	TTCTATAATG	240
AAGAGAAAGA	TAAGAAGTTT	GCAGTCATAG	AAGATGATAG	TGATGAGGGT	GGTGATGATG	300
AGTATTGTGA	TGGTGATGAA	GATGAGGATG	ATTTAAAGAA	ACCTTTGAAA	CTGGATGAAA	360
CAGATAGACT	CGAG					374

(2) INFORMATION FOR SEQ ID NO:585:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GAATTCGGCC	TTCATGGCCT	AGAGAAACTG	AGAGGAAGTT	AAAGATTTGT	CTTACAAAGG	60
CTGTGTAGTG	ATAAGACCTA	AGGTTTTCTC	TGAGATTCAA	AATGGGTATT	ATTTGTTCTT	120
TAATCCTTCT	GATTATTCTT	TTGGAAAAAA	GGGAAGTAGA	GGAAAGGAAG	TAGAAAAATA	180
ATATTTCTTA	TACTTATTAT	GTACCAGACA	TGGTGCTAAG	TTCATTTAAA	ACACTGCCTC	240
ATTTAATCTT	TGCAACCAAT	TTATACCCAT	ACACATAAGG	CCACAAAAGC	TCGAG	295

- (2) INFORMATION FOR SEQ ID NO:586:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

GAATTCGGCC	TTCATGCCTA	AGGTAAGGGA	AAGTGAGAAG	CAGCAGGATA	GTCAGCCTGA	60
AGAAGTTATG	GATGTGCTAG	AGATGGTTGA	GAATGTCAAA	CATGTAATTG	CTGACCAGGA	120
GGTAATGGAA	ACTAATCGAG	TTGAAAGTGT	AGAACCTTCA	GAAAATGAAG	CTAGCAAAGA	180
ATTGGAACCA	GAAATGGAAT	TTGAAATTGA	GCCAGATAAA	GAATGTAAAT	CCCTTTCTCC	240
TGGGAAAGAG	AATGTCAGTG	CTTTAGACAT	GGAAAAGGAG	TCTGAGGAAA	AAGAAGAAAA	300
AGAATCTGAG	CCCCAACCAC	TCGAG				325

- (2) INFORMATION FOR SEQ ID NO:587:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

GAATTCGGCC	TTCATGGCCT	ACAAGGACGT	TAAAGGCATT	TTATTCCAGC	GTCTTCTAGA	60
GAGCTTAGTG	TATACAGATG	AGGGTGTCCG	CTGCTGCTTT	CCTTCGGAAT	CCAGTGCTTC	120
CACAGAGATT	AGCCTGTAGC	TTATATTTGA	CATTCTTCAC	TGTCTGTTGT	ATACCTACCG	180
TAGCTTTTTA	CCGTTCACTT	CCCCTTCCAA	CTATGTCCAG	ATGTGCAGGC	TCCTCCTCTC	240
TGGACTTTCT	CCAAAGGCAC	TGGACCCTCG	AG			272

- (2) INFORMATION FOR SEQ ID NO:588:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GAATTCGGCC TTCAT	GGCCT AGCATCCCT	AAACTGTGTA	ATTTTGAGGA	TCCTTCTGGT	60
CTTAAAGCCA ATTTA	GAAGG TGCTAATCT	AAAGGTGTGG	ATATGGAAGG	AAGTCAGATG	120
ACAGGAATTA ACCTG	AGAGT GGCTACCTT	A AAAAATGCAA	AGTTGAAGAA	CTGTAACCTC	180
AGAGGAGCAA CTCTG	GCAGG AACTGATTT.	A GAGAATTGTG	ATCTGTCTGG	GTGTTAGCTC	240
GAG					243

- (2) INFORMATION FOR SEQ ID NO:589:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GAATTCGGCC	TTCATGGCCT	AAATTATACT	CCAAATGTTT	TATCTAAAAT	GCATTTTCTG	60
TCTTTTCCTT	TTTACTCTTG	TCCTCACTTT	TAATGATCCA	TCGGCTGACA	GTGTCTTTAC	120
ATCCAAAATG	CAAAGCAGAC	AAATGGGCAT	ATCAGGGAAG	AACATGACAA	AAAGCACCAG	180
CATCAGTGGA	GACATGTGCT	CACTGGAGAA	GAATGATGGC	AGCCAGTCTG	ACACTGCAGT	240
GGGCACCTTG	GGCACCAGTG	GCAAAAAGCG	GCGCTCTAGC	CTTGGTGCCA	AAATGGTAGC	300
TATCGTTGGT	CTGTCACGGA	AAAGTCGCAG	TGCTTCTCAG	CTCAGCGGAC	TCGAG	355

- (2) INFORMATION FOR SEQ ID NO:590:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

GAATTCAAAT GCTTCAGGTA	AATGTTGAAG	CTCGGTGTAC	CGCGGGACAA	ATCCTGAGTC	60
ACCCCTGGGT GTCAGATGAT	GCCTCCCAGG	AGAATAACAT	GCAAGCTGAG	GTGACAGGTA	120
AACTAAAACA GCACTTTAAT	AATGCGCTCC	CCAAACAGAA	CAGCACTACC	ACCGGGGTCT	180
CCGTCATCAT GAACACGGCT	CTAGATAAGG	AGGGGCAGAT	TTTCTGCAGC	AAGCACTGTC	240
AAGACAGCGG CAGGCCTGGG	ATGGAGCCCA	TCTCTCCAGT	TCCTCCCTCA	GTGGAGGAGA	300
TCCCTGTGCC TGGGGAAGCA	GTCCCGGCCC	CCACCCCTCC	GGAATCTCCC	ACCCCGCTCG	360
AG					362

- (2) INFORMATION FOR SEQ ID NO:591:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

GAATTCGGCC TTCATGGCCT ACTCAGTCTG CACAACCTTT TTGCTGTGTG TCGGAATATG

TATAACTGGC TACTGCAGAA TCCCAAAAAT GTCTGTGTTG TCCACTGCTT GGATGGACGG

GCGGCATCAT CAATTCTGGT TGGTGCTATG TTCATTTTCT GTAATCTCTA CTCTACTCCT

GGCCCAGCCA TTCGATTGCT ATATGCAAAG CGACCAGGAA TTGGACTTC ACCATCCCAT

AGGAGATACC TGGGCTATAT GTGTGACCTA CTGGCAGACA AGCCCTACCG CCCTCGAG

298

- (2) INFORMATION FOR SEQ ID NO:592:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

GAATTCGGCC	TTCATGGCCT	ACCGTAAGCA	GATGAAGCTG	CTGCTGCTGC	TGCTGCTGCT	60
GAGCTGCGCC	GCGTGGCTCA	CCTACGTGCA	CCTGGGCCTG	GTGCGCCAGG	GACGCGCGCT	120
GCGCCAGCGC	CTGGGCTACG	GGCGAGATGG	TGAGAAGCTG	ACCAGTGAGA	CCGACGGCCG	180
GGGGGTCCAC	GCTGCGCCAT	CCACACAGAG	GGCTGAGGAC	TCCAGTGAGA	GCCGTGAAGA	240
GGAGACCAGC	GCAGACATGC	TGCGGCCAGA	TCCCAGGGAT	TACCTCGAG		289

- (2) INFORMATION FOR SEQ ID NO:593:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

GAGAGATGGT	GACTGAGGCA	GAAGCTAATA	GGGAAGATGA	TAGGAAAGAA	ATTTTACCCA	60
AGGAATTAGA	TTTAGCAAGA	GAGCGAAGGA	AAGCTGAGAG	GCCAAAAACA	TCTCTGAGGA	120
AAACTGACTC	TGAGAGAGAA	GAGGTGACAA	GGGCAAATGC	ACTCAAGGAT	GAAGATGCTT	180
TTAAAGAAGA	GCAAAAACTT	AAAGCGGAAG	AAGGGGAAAC	AGAGACAGAA	GTAAGAGCTG	240
AGGAAGAGAC	AAAAGCTCCC	CCAAATGAAA	TGGGATCTGA	TGCTGAGAAC	GAAACACTCG	300
AG						302

- (2) INFORMATION FOR SEQ ID NO:594:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

GAATTCGGCC TTCATGGCCT AGGATATTTA AACCTCTATT ATTTTAGACA AGACTGTCTA	60
GAACTTAAGT TTGATCTGTC AGCCAGTACT CCCATTAAAT TCAGTGTAGT TTCACTTGAT	120
AGAATCAGAT ATGTTATCGA AATGTTAGCA GCAGCTTCAT CCTCCTTCTG ATTAAAGTAA	180
GTAGAAATGG GATGTTTTGT TTAATAACAG CCATAGTGTG TGTTTAGACC ACAGCGGATG	240
TTGTAGACCA GGACCCTCGA G	261
(2) INFORMATION FOR SEQ ID NO:595:	
/ L COOMBAGE CHARACTERISTICS	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 370 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(C) STRANDEDNESS: GOUDTE (D) TOPOLOGY: linear	
(b) TOPOBOGI: Timear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:	
GAATTCGGCC TTCATGGCCT AGGGGCTTTT GTCAAGATAG AAGGGTATCA ACGGTTTCTG	60
TACAGCACAG ATTATGACAG CGTCTTTCTT AAGACTTATC ATTTGGAGCA CTGGCTCAGG	120
AGTCGAAATC ACCAATGGCT CATCCATCAA TCAACCAGAA GTGAAGACGA AAGCTTCAAA	180
GAAGAGAATG TTTAAATTTC ATCAAATGAA ACATATTTTT GAAATACTTG ATAAAATGAG	240
ATGCCTGAGA AAACGTTCTA CAGTGTCATT CTTGGGAGTT CTTGTCATTT TTCTCCTTTT	300
TATGAACTTG TACATTGAAG ATAGCTATGT TCTGGAAGGA GACAAACAAC TTATAAGGGA	360
AACTCTCGAG	370
(a) Turner of the Control of the Con	
(2) INFORMATION FOR SEQ ID NO:596:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 240 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(-,	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:	
GAATTCGGCC TTCATGGCCT ACTAACGACT CATCTTTGTT TTTAGTTTTT TTAATTAACA	60
ATCGTTCTGT TCACAATTTT TAATTTCCTT TCTTCCCCCT TCTCCGCAAA GCACTCAGGC	120

TTTTTTGGGT TTGCCGTGTG TTGCCCCCCT TTTCCTCTCC AACCCCCCC ATTCCTCGAG

(2) INFORMATION FOR SEQ ID NO:597:

ATCGGACACG CTATGGTAAA CAAACTACAT TGTCTGGTAG ATATCATTCT TATTGTCTCT

180

240

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

GAATTCGGCT	TCATGGCCTA	GTGTATTGGT	TGTGTGTGTT	TTCCTTTTTG	CATAAGAAAT	60
ATGTCCATTT	AGTCCAGAGG	CTCTTGCTTT	ATCCGGATGA	CGGAGGGTAC	ACGGGGCGTC	120
CGCCTCAGTT	CCCGCCGAAG	GACGTATTCG	CTGAACTGGG	ACGAGTCTAC	TCCTCCCCCA	180
CAGGAGCCCA	CGATTTCAAA	TCCTCTTTGC	TGCAACCTCT	CGAG		224

(2) INFORMATION FOR SEQ ID NO:598:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 272 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:	
GAATTCGGCC TTCATGGCCT AGATATTTTA AAGGAGTGAT GACATCTTTT TCCTATCATG TGAAGAGGGG AAAGAGAAAG GAAAGGGCCC ATATTATTGT GTTCCTGCTT GTGCCAGCTG TTCTATATCT GTTGATCTCA TTTAGTCCTC ATGACAGTTC TATGAGGAGG GCACTGTCAT CATCACCATT GCACAGATGC AGAAACTGTG GCTCACAGAG GATAAAGCTA GGTCACTCAC ACAACCCCCT GACTCCAGAG CCACCACTCG AG (2) INFORMATION FOR SEQ ID NO:599:	60 120 180 240 272
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 351 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:	
GAATTCGGCC TTCATGGCCT AGTAAGGGAG AAACTGAATG GTGATTCAGA GCATAGAGAT TATGTTTTTT TATGCACAGG GCTTCATCAG AAAAATGGAA GGAATTGTCA ATAACAATAA AATGTTCAGC TAGATCAACT CAGTATATAG TATGTATTAT ACAATTATTC AAAATAGTGT TTAACAGTAC TGTAATAACA TGAATAAATG TTTTGTCATA TTAAGTGAAA AAGAGCTATA TAAAAATTATC TAAGTTTATG GTATATGTAG ATTGTTGCAA AAATGTCTTC AATTCTTTAT CCCTCCCTGT ATCCACACCT GTATCAGTTT TCTCGGGGCA GCTGCCTCGA	60 120 180 240 300 353
(2) INFORMATION FOR SEQ ID NO:600:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:	

GAATTCGGCC TTCATGGCCT AGAATATTTT TATCATCCCA AAGCTAAAAC ATTAAAAAAAT 60
TTAAAGTTTA TTCTTAGAGA TTGATGCAAC TTGCATATCT AATCGAG 107

- (2) INFORMATION FOR SEQ ID NO:601:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

60	AGAAGAAAAG	CTTTTGTGAA	TTCACAAAAT	CACACAACGT	TTAAACGTTG	GGAAAATTAC
120	TCATGCCGAC	CAGCTTAACA	TAAGCTAATG	CAGCAGGAGT	GTGTGAGTCT	GAAATTCAGT
180	AGATGATTAG	TTCCTGTGCC	CCTGATTCTC	GCAGAGTGCC	TTATCTGCGG	AAAGAAGCGC
240	TAAATCCCCT	ATCACCCCGC	GCCTCCAACC	ATCTGGTACA	GTACCTCTTG	TGCACTGGAA
277			ACTCGAG	CATCCGTATT	CTCCTAAACA	AGAAGTCCCA

- (2) INFORMATION FOR SEQ ID NO:602:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

GAATTCAAAT	TAACATTTTA	CCTTGAAATA	GTTGGCTTCA	GATTAATATC	AACTTAGTTT	60
CAATAGCATA	GGAAATTTGC	TTCACTATAT	TTCCATTTTC	TCCCCGTCCT	TTGTGCTATT	120
ATTACTATAC	·CAATTAGATC	TCTACACAAT	ATAGGCATAT	CAACACATTT	TGTAATTATT	180
TCCTTATCCA	GTTGTCTTTT	AATATAGATC	TGTGAAGAAA	AGTATTACAC	AAATAGATCT	240
ATTCTGTTTT	TTATAATTAT	TTAATTACCT	TTGGTGGTGC	TGTTTATTTT	TCATGCATTT	300
GAGTTACTGT	CTAGTATTCA	TTCATTTCTC	TCTGAATCAC	TCCCCGGTAT	TGCTCGAG	358

- (2) INFORMATION FOR SEQ ID NO:603:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

GAATTCGGCC	TTCATGGCCT	AGCCATCTTA	TTTGAACTAT	ATTTTTCCTT	CAAAGAAGCA	60
ATAGGTCTCA	ACATAGTGTA	GGTAGCATCA	GGTGACAGAA	AGCCAATTTT	ATTTTCAAAT	120
TTAAGTTAAT	TATCTTCGTG	ATCCTATTTA	TCCACAATTT	CTTTCAGAAA	AGACTGAAAA	180
AACACATTAT	ATTCAGGAGA	TATAATGAAA	TTATTGGAAG	GCATCACTCG	AG	232

- (2) INFORMATION FOR SEQ ID NO:604:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

GAATTCGCCC	TTCATGGCCT	AAATATTTTC	CATCTTCCTC	TCCAGTAAAC	ATTCTTTTGT	60
CATCACAGTC	TGTCTCTGAC	ACCTTCGTTA	AAGAGGTCTT	AAAATGGAAA	TATGAAATGT	120
TTTTGAACTT	TGGTCAGTGT	GGGCCCCCTG	CAAGTCTTTG	TCAGTCCATC	TCAAGACCTG	180
TGCCTGTCAG	ATTTCACAAT	TATGGAGATT	ATTTTAATGT	TTTTTTCCCT	TTGATGGTAT	240
TGAATACTTT	TGAAACAGTG	GCACAAGCGG	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:605:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

GAATTCGGCC	AAAGAGGCCT	AAAAATATAA	TTTAAAAAATA	CATTGCGTAT	TTTCTAAAAC	60
ATTAAATTTA	TAGTGTTAAT	ATTCATAGGG	TCAATCAAAA	TGAAGCTTCT	CCTTTGGGCC	120
TGCATTGTAT	GTGTTGCTTT	TGCAAGGAAG	AGACGGTTCC	CCTTCATTGG	TGAGGATGAC	180
AATGACGATG	GTCACCCACT	TCATCCATCT	CTGAATATTC	CTTATGGCAT	ACGGAATTTA	240
CCACCTCCTC	TTTATTATCG	CCCAGTGAAT	ACAGTCCCCA	GTTACCCTGG	GAATACTTAC	300
ACTGACACAG	GGTTACCTTC	GTATCCCTGG	ATTCTAACTT	CTCCTGGATT	CCCCTATGTC	360
TATCACATCC	GTGGTTTTCC	CTTAGCTACT	CAGTTGAATG	TTCCTCCTCT	CCCTCCTAGG	420
GGTTTCCCGT	TTGTCCCTCC	TAATCTCGAG				450

- (2) INFORMATION FOR SEQ ID NO:606:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 614 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GAATTCGGCC	AAAGAGGCCT	ATCAGGTGAT	AATAATAATT	TTTAAAACTA	CTATAGAAAC	60
TGCAGAGCAA	AGGAAGTGGC	TTAATGATCC	TGAAGGGATT	TCTTCTGATG	GTAGCTTTTG	120
TATTATCAAG	TAAGATTCTA	TTTTCAGTTG	TGTGTAAGCA	$\mathbf{AGTTTTTTT}$	TAGTGTAGGA	180
GAAATACTTT	TCCATTGTTT	AACTGCAAAA	CAAGATGTTA	AGGTATGCTT	CAAAAATTTT	240
GTAAATTGTT	TATTTTAAAC	TTATCTGTTT	GTAAATTGTA	ACTGATTAAG	AATTGTGATA	300
GTTCAGCTTG	AATGTCTCTT	AGAGGGTGGG	CTTTTGTTGA	TGAGGGAGGG	GAAACTTTTT	360
TTTTTTCTAT	AGACTTTTTT	CAGATAACAT	CTTCTGAGTC	ATAACCAGCC	TGGCAGTATG	420
ATGGCCTAGA	TGCAGAGAAA	ACAGCTCCTT	GGTGAATTGA	TAAGTAAAGG	CAGAAAAGAT	480
TATATGTCAT	ACCTCCATTG	GGGAATAAGC	ATAACCCTGA	GATTCTTACT	ACTGATGAGA	540
ACATTATCTG	CATATGCCAA	AAAAATTTTA	AGCAAATGAA	AGCTACCAAT	TTAAAGTTAC	600
GGAATCACCT	CGAG					614

- (2) INFORMATION FOR SEQ ID NO:607:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GCGAAGACCA	TCAAATGAAT	TGTCACAATA	CTCGAATAAT	GCAAGACACA	GAAAAGGATG	60
ATAACAATAA	TGACGAATAT	GACAATTACG	ATGAACTGGT	GGCCAAGTCA	TTGTTAAACC	120
TCGGCAAAAT	CGCTGAGGAT	GCAGCCTACC	GGGCCAGGAC	TGAGTCAGAA	ATGAACAGCA	180
ATACCTCCAA	TAGTCTGGAA	GACGATAGTG	ACAAAAACGA	AAACCTGGGT	CGGAAAAGTG	240
AGTTGAGTTT	AGACTTAGAC	AGTGATGTTG	TTAGAGAAAC	AGTGGGGCTC	GAG	293

- (2) INFORMATION FOR SEQ ID NO:608:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GAATTCGGCC	TTCATGCTTA	CTCAGAAAGC	CACTGCCCCA	AACAAGCCAC	CTGCATTATC	60
AAACACAGAG	AAGAGGAATC	ATTCCGCCTT	TTGGGGACCA	GAGAGTCAAA	TCATTCCTGT	120
GATGCCAGAT	AGTAGTTCCT	CAGGGAAGAA	CAGAAAAGAG	GAAAGTTATA	TATTTGAGTC	180
AAAGGGTGAT	GGAGGAGGAG	GGGAACACCC	AGCCCCAGAA	ACAGGTGCAG	TGCTACCCCT	240
GGCGCTGGGT	TTGGCTATCA	CTGCTCTGCT	GCTTCTCATG	GTTGCATGCC	GACTACGACT	300
GGTGATCCTC	GAG					313

- (2) INFORMATION FOR SEQ ID NO:609:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GCCCATTCCG	GCCCCCATCT	CACCCAAGAT	CCCCCAGAGT	CCAGGAGCTG	GACGGGGACA	60
CCCTCAGCCC	TCATAACAGA	TTCCAAGGAG	AGGGCACCCT	CTTGTCCTTA	TCTTTGCCCC	120
TTGTGTCTGT	CTCACACACA	TCTGCTCCTC	AGCACGTCGG	TGTGGGGAGG	GGATTGCTCC	180
TTAAACCCCA	GGTGGCTGAC	CCTCCCCACC	CAGTCCAGGA	CATTTTAGGA	ТАААААААА	240
GAAATGTGGG	GGGCTTCTCA	TCTCCCCAAG	ATCCTCTTCC	GTTCAGCCAG	ATGTTTCCTG	300
TATAAATGTT	TGGATCTGCC	TGTTTATTTT	GGTGGGTGGT	CTTTCCTCCC	TCCCCTACCA	360
CCCGTCCTCG	AG					372

- (2) INFORMATION FOR SEQ ID NO:610:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

GGAGCTAAAT TTAAGAAATG CAACTAGCCA GGTGCTAAGA AGCTCAGTTA CACGTTTCTC AAAAGTTGGC TGTTAGTTCC ATGACTCAGA GTGCACTCAA ATCATTTTAA TTACTCGAG	60 119
(2) INFORMATION FOR SEQ ID NO:611:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 474 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:	
GAATTCGGCC TTCATGGCCT AGGTCCTGTT TGCCTATTTG AGCTGCTATT AGTGTGAGAA GAAACTCAGA TGATAGTAGC AGAAACAGAA AGAGGAAGAG GCTACAAGAG ATGGTAGATG CTGAACTTAA GGCATTTGAT AACCAATGGA TATAGAAAGA AAAGGAAATG AAAGGACAAA AATGGCTCTA AGTTTCAAA CTTGACTGAT GAGGAAAATA TTCACATCAA GAATGGACTG AAGAAATAAG GAGGAGATG TGGGTTAGGG TGAAAGGAGA TGAGCCCCAT TTTACATTGG AAAGCTCTAT GGAACAACGG AAGTAGTAGT AGCTTTATAT TCCAGTATGC CAAATTCTCA GCTCCAAGAC TCCAGCACTG TGTGCTCTAC AGTATGTTTT GTGATGTGCC TGAGTTTTGG TTTCTTTATT TCAATTAGGG ACTCTTCATA CCAGGGTCAG GGGTTATGCT CGAG	60 120 180 240 300 360 420 474
(2) INFORMATION FOR SEQ ID NO:612:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 283 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:	
GAATTCGGCC TTCATGGCCT AGTTCCTGTG CTCTTGAAAG AACAAGTTGA TGCTTGTAAA GCTGTTTTGA TTATTTTTAG GCGCATGATA ATGGAGCTTA CAATGAATAA AAAGACATGG GAACAGATGT TGCAAATACT ACTCAGGATA ACAGAAGCTG TCATGCAGAA GCCAAAGGAT AAACAAATAA AGGACTTGTT TGCCCAGAGC TTGGCAGGGT TACTATTTAG GACGCTCATG GTAGCTTGGA TCCGAGCAAA CCTCTGTGTG TACATTTCTC GAG	60 120 180 240 283
(2) INFORMATION FOR SEQ ID NO:613:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 280 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:	
GAATTCGGCA CGAGGGGCCG CCGTTTTTT TTTTTTTTT TTTTCAGGTG CACATAAAGT TAGTTTATTA ATGACTATAT TTTGAAGCCA GCCATTTTGT CCAATATTTA AATAACAAGC TGTTTAATAT TAAAGCAGAA AGTACTGCCA CATTGTGACA GAAGTACAGC TTTATCCATA AACCCTTCAC ACAATTATAC ATTAAATGCT ATTTTTATTT AAGCAAGGCA CCCCTACTTG	60 120 180 240

280

TTCTAAAATA TGGGATGTAC TACACCATGT ATTACTCGAG

- (2) INFORMATION FOR SEQ ID NO:614:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

GAATTCGGCC	AAAGAGGCCG	GAATTTGGCC	CTCGAAACCA	AGAATTCGGC	ACGAGGGAAT	60
GAAATTAGCT	AACAGCCTTC	AGCTACAGAA	ACTTTGGGAT	CCAGACAGCA	TTTGAGCTGA	120
CGCCACGCCC	TTCTCAGGCA	GCCCCCACAG	TGAAGGAGGA	GGATCTAGAA	GGGCCTGGCC	180
ATTTTTCCTC	AATGTAGGGT	CCCTCTGATG	GGAATTCTTT	GTCTGGAGAC	CCGAGCTGAG	240
ACTTTGTCAG	ATTGGCATCT	CTGTCCCTGC	TCAATGCTGC	TTTCCATGCT	CCCTTTTCTA	300
TCACAGACAT	CATAGCCTGA	AATCTTTCCA	CACCCAATAC	TGCTTCCTAT	ACCCCTTAGC	360
CTTTCCTGAT	CTCATTGAGG	TTACCATTTT	TCCTCCGTCG	CTCGAG		406

- (2) INFORMATION FOR SEQ ID NO:615:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

GAATTCGGCC	AAAGAGGCCG	GAATTTGGCC	CTCGAAGCCA	AGAATTCGGC	ACGAGGCTTT	60
TTTAGGTAAT	TCTTTGTACT	CCTGCTGTCT	ACCTCTCCTC	ACACCCCAGC	ACCCCCATT	120
TTTTCAAACC	TTGGTATCTG	TTGGGTGAAC	AGTATAATCT	TTTCATCTGC	TTTTAGAATG	180
TGGGATATTT	CCAGTACCTA	CTTTTTTTT	TTTTTTTTGC	TGAATCCAAA	GATATATAAA	240
TAAAATATAT	ATATTTTATA	AAGATCAGAA	TGATATAAAG	GAGATACATG	TTTCTTCCTT	300
AATAAAAAT	ACGGAAGTTA	CATTGTTAAT	GTTCATATTA	TGATGCGAAT	TCTCTGGTTC	360
CTCCTCGAG						369

- (2) INFORMATION FOR SEQ ID NO:616:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GAATTCGGCC	TTCATGGCCT	AGGATGTCTG	AGGTCTTAAC	CTGCCCAGTC	CTGAATTCCT	60
GGGACTTCAA	CGACTCTCTC	TCTGCCAAAT	GATGTGAGTC	TTTAGGTAGA	GTTATAGCGC	120
AAAGGGCTAC	TATCAATGTT	ATTAAGCATA	AATTATGACT	AGAGCCACAG	AATGATTTCC	180
TCATTAATCC	AAAAAAAAA	AAAAAGCAAA	CCACTCTTTT	ACTTTATGAT	GAGCACATAA	240
ACAGTTTTTT	TTTCTTTTTA	TTTATCTACT	TTTACTTACT	TAAATTTTAG	AGATGGGGTC	300
TTGCTATGTT	GCCCAGACTA	GACTCAAACT	CCTGGGCTCA	AGTGATCCTC	TAGCCTCAGC	360
CTCCCAAGTA	GCTGGGACTA	CAGGAAGGAG	CTACTGCACC	TGACTCAATT	TTTTTTTTT	420

461

CTGAGATGGA GTCTCACTCT GTGACCCAGG CTTGTCTCGA G

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 391 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:	
GAATTCGGCC TTCATGGCCT ACATCAATAA CAGCCAAACT GAGACACATA ATGTTTTCTA CGTCCAAGAG GCTAAATGTG AGAATCCAGA ATTTGAGAGA AATGTGGAGA ATACATCTTG TTTCATGGTC CCTGGTGTTC TTCCTGATAC TTTGAACACA GTCAGAATAA GAGTCAAAAC AAATAAGTTA TGCTATGAGG ATGACAAACT CTGGAGTAAT TGGAGCCAAG AAATGAGTAT AGGTAAGAAG CGCAATTCCA CACTCTACAT AACCATGTTA CTCATTGTTC CAGTCATCGT CGCAGGTGCA ATCATAGTAC TCCTGCTTTA CCTAAAAAGG CTCAAGATTA TTATATTCCC TCCAATTCCT GATCCTGGCA AGAATCTCGA G	120 180
(2) INFORMATION FOR SEQ ID NO:618:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 306 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:	
GAATTCGGCC TTCATGGCCT ACGTGAAGAC AAGATGAAGT TCACAATTGT CTTTGCTGGA CTTCTTGGAG TCTTTCTAGC TCCTGCCCTA GCTAACTATA ATATCAACGT CAATGATGAC AACAACAATG CTGGAAGTGG GCAGCAGTCA GTGAGTGTCA ACAATGAACA CAATGTGGCC AATGTTGACA ATAACAACGG ATGGGACTCC TGGAATTCCA TCTGGGATTA TGGAAATGGC TTTGCTGCAA CCAGACTCTT TCAAAAGAAG ACATGCATTG TGCACAAAAT GAGCAAGGAA CTCGAG	60 120 180 240 300 306
(2) INFORMATION FOR SEQ ID NO:619:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 370 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:	
GAATTCAAGG CCACGCCGGA GCTGTACCTT GGAAGGAGGA GCCAAAAATT ATGCTGAGAG TGATCACAGT GAAGACGAGG ACAATGACAA CAATAGCCCC ACCGCAGAGG AGTCCACGAA GAAGAATAAG AAGAAACCAC CGAAAAAAAA GTCTCGTTAT GAAANGACAG ATACCGGTGA GATAACATCC TACATCACTG AAGATGATGT GGTCTACAGA CCAGGAGACT GTGTGTATAT CGAGAGTCGG AGGCCAAACA CACCGTATTT CATCTGTAGC ATTCAAGACT TCAAACTGGT AAGCGTTTTT AATGTGCTGT TCACTCTGCT CTGTATTCTC TCTTTTTCCA GTTCCATTGG	60 120 180 240 300 360
288	

> CGCTCTCGAG 370 (2) INFORMATION FOR SEQ ID NO:620: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 183 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:620: GAATTCGGCC TTCATGGCCT AAAAACCTTA CAACTAAAGC AAATAGACTT TTCAAGAATT 60 TAAATAGGAT TCCTTCCCTT TAATCAATTA ATTATCCACT TTGTCATGGT GTCAACCTGT 120 AATTTCATGG TTTTGTGTGT GTGTGTGTGT GTGACAGAAA TTTACAAACA ATGTGATCTC 180 183 (2) INFORMATION FOR SEQ ID NO:621: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 565 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:621: GAATTCGGCC TTCATGGCCT ACAACTAATT TGATCATATT AACAAGAGGT TGGTTTTTAA 60 ACCAAGCAGT ATAAATATAA ATACAGCCTT GGGTAGATCA TAGTCAAACT ATCCAAATGC 120 AACCTCAGCT TCAAAGATTG TAAAGTCTTT TCTTTCCCCT TTTCTCCTTT CCTTTTTTT TCCTCCAAAT ATTTATTTAC TACCTACCAT GTGCCAGGCA CTGTGATGGG CTATGAGGAT 240 GCAGTGGGGG ATAGGACAGA TGCCATCCCT GCCCTGAGGA GACTTGCAGT TTATTGGAAA 300 AGATGGACAT CGTAAAATAT ACAATCATAC AAATAAAAAT TACATAAATA ATTCAGTACT 360 TCAACTTGTG GGAGGTACAG CAGTTTATAA TAATAACATC CCTCCCACCT TCTTGAGAGA 420 GTCATTGGTT GCCCCACTTC TCTTCATGAA TGAGAGGACA TGATTAAACC TATCATTTCA 480 GGTAGGAGTT TACTGTGGGA TGGATATCAA TCTTCTATTA ATATGTTTGT GCTCATGCTC 540 TCCATTTTGC AATGGACGTC TCGAG 565 (2) INFORMATION FOR SEQ ID NO:622: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 294 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:622: GAATTCGGCC TTCATGGCCT AAAATGAAAG CTATGTCTTA GAACCAATGA AAAGTGCAAC 60 CAACAGATAC AAACTCTTCC CAGCGAAGAA GCTGAAAAGC GTCCGGGGAT CATGTGGATC

ACATCACAAC ACACCAAACC TCGCTGCAAA GAATGTGTTT CCACCACCCT CTCAGACATG

GGCAAGAAGG CATAAAAGAG AGACCCTCAA GGCAACTAAG TATGTGGAGC TGGTGATCGT

GGCAGACAAC CGAGAGTTTC AGAGGCAAGG AAAAGATCTG GAAAAAGTCT CGAG

120

180

240

294

- (2) INFORMATION FOR SEQ ID NO:623:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GAATTCGGCC	TTCATGGCCT	AGCTTCTGGT	AATGGCGGAC	TAGATGATTT	AGAGCAACCC	60
ACCCATTGAA	AAGAACTACA	AAACGTCAGA	TCTCTAAAAG	GCTACAAAAT	TAATACAATT	120
GTGAGGAATT	GCTAGGTTAT	ACTACAAGAG	AACAGAAGCA	TCCAGAGAGG	TAAGCCTAGG	180
ACTTAAAACT	ATATTTTTAT	TGAAGGTATC	TGTGGTTGAG	TAATAAGCCT	GTGCTAAACT	240
GCGTGGAACT	TATGGCACAT	TCAAGGCACT	ATAGTAACAG	AAGTCAGAGC	CCAAGGCCCA	300
TCAAAAGGGG	TGGAGTGTTT	CCTGACAAAC	CATCACCCAT	AGTATGCTGG	GAACCGCAAA	360
TGTTTATACC	TTCAGGGTAA	TTGTAATCAA	AAAATATACT	AGCCCTTACA	AAGTCTTGTA	420
GCTTGGCTTT	GCATCATCTG	GGTGGACTAG	TGAACTGTAA	GTTCTGAACA	AATATTATGG	480
AGGCAACTCG	AG					492

- (2) INFORMATION FOR SEQ ID NO:624:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GAATTCGGCC	TTCATGGCCT	ACTTCCCTGA	GCTGGGGTTT	CCCTGCTTGT	CCAGTTGTGA	60
GCTGTCCTCG	GTGTTACCGA	GGCTGTGCCT	AGAGAGTGGA	GATTTTTGAT	GAAAGGTGTG	120
CTCGCTCTCT	GCGTTCTATC	TTCTCTCTCC	TCCTTGTTCC	TGCAAACCAC	AAGATAAAGG	180
TAGTGGTGTG	TCTCGACCCC	ATCAGCCTCT	CACCCACTCC	CAGACACACA	CAAGTCCTCA	240
AAAGTTTCAG	CTCCGTGTGT	GAGATGTGCA	GGTTTTTTCT	AGGGGGTAGG	GGGAGACTAA	300
AATCGAATAT	AACTTAAAAT	GAAAGTATAC	TTTTTTATAAT	TTTTCTTTTT	AAAACTTGGT	360
GAAATTATTT	CAGATACATA	TTTTAGTGTC	AAGGCAGATT	AGTTATTTAG	CCACCAAAAA	420
AAAGTATTGT	GTACAATTTG	GGGCCTCAAA	TTTGACTCTG	CCTCAAAAAA	AAGAAATATA	480
TCCTATGCAT	CTCGAG					496

- (2) INFORMATION FOR SEQ ID NO:625:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

GAATTCGGCC	TTCATGGCCT	ACAAAATTGA	TTATGACAAG	ATTGTCTACT	ATGAAGCAGG	60
GATTATTCTA	TGCTGTGTCC	TGGGGCTGCT	GTTTATTATT	CTGATGCCTC	TGGTGGGGTA	120
TTTCTTTTGT	ATGTGTCGTT	GCTGTAACAA	ATGTGGTGGA	GAAATGCACC	AGCGACAGAA	180

GGAAAATGGG	CCCTTCCTGA	GGAAATGCTT	TGCAATCTCC	CTGTTGGTGA	TTTGTATAAT	240
AATAAGCATT	GGCATCTTCT	ATGGTTTTGT	GGCAAATCAC	CAGGTAAGAA	CCCGGATCAA	300
AAGGAGTCGG	AAACTGGCAG	ATAGCAATTT	CAAGGACTTG	CGAACTCTCT	TGAATGAAAC	360
TCCAGAGCAA	ATCAAATATA	TATTGGCCCA	GTACAACACT	ACCAAGCTCG	AG	412

- (2) INFORMATION FOR SEQ ID NO:626:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

GAATTCGGCC	TTCATGGCCT	AGTTAGGTGG	CTTTTAGTGT	ATTGACAAAG	TTGTGAACCC	60
ATTATCACAA	TCTAATTTTA	GAACATTTTT	ATCAGCCTCC	TTGCCCCCTA	AAAAAACCCA	120
GTACTTTTTA	CCAATCCAGT	CATTTAAAAC	TTACTACATA	TTTAATAGAT	GGATAGATAG	180
ACAGGAGGAT	GGACAGACTG	AAGGAAGAAT	GGATGATTAT	GTATAAATAA	ATGAAAAAAC	240
AAAAACTATC	CCCAAATCAT	AAGGGTATAC	GCAATGCTTT	CCTGTGGCAA	AAGATTCGGA	300
ACATGTACAG	CAGATTTTTT	TTCAAATGTT	CATAATTCTA	AATTCCCAAA	ATGGTCTACA	360
CAACTTCTCG	AG					372

- (2) INFORMATION FOR SEQ ID NO:627:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 575 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GAATTCGGCC	TTCATGGCCT	AGGAGAAAGG	AAGGGAAGCA	TTACTGGGTT	ACTATGCACT	60
TGCGACTGAT	TTCTTGGCTT	TTTATCATTT	TGAACTTTAT	GGAATACATC	GGCAGCCAAA	120
ACGCCTCCCG	GGGAAGGCGC	CAGCGAAGAA	TGCATCCTAA	CGTTAGTCAA	GGCTGCCAAG	180
GAGGCTGTGC	AACATGCTCA	GATTACAATG	GATGTTTGTC	ATGTAAGCCC	AGACTATTTT	240
TTGCTCTGGA	AAGAATTGGC	ATGAAGCAGA	TTGGAGTATG	TCTCTCTTCA	TGTCCAAGTG	300
GATATTATGG	AACTCGATAT	CCAGATATAA	ATAAGTGTAC	AAAATGCAAA	GCTGACTGTG	360
ATACCTGTTT	CAACAAAAAT	TTCTGCACAA	AATGTAAAAG	TGGATTTTAC	TTACACCTTG	420
GAAAGTGCCT	TGACAATTGC	CCAGAAGGGT	TGGAAGCCAA	CAACCATACT	ATGGAGTGTG	480
TCAGTATTGT	GCACTGTGAG	GTCAGTGAAT	GGAATCCTTG	GAGTCCATGC	ACGAAGAAGG	540
GAAAAACATG	TGGCTTCAAA	AGAGGGGATC	TCGAG			575

- (2) INFORMATION FOR SEQ ID NO:628:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

GAATTCGGCC	TTCATGGCCT	AACAGGGTCT	TGCTCTGTCA	CCCGGGATGG	AGTGTAGTGG	60
CGCAATCACA	GCTCACTGCA	GACTCAGCCT	CCCAGGATCA	AGCAATTCTC	CCACCTCAGC	120
CTCCCAAGTA	GCTGGGACCA	CAGGTGCACA	CCATCATGCC	CAGCTAATTT	TTGTATTTTT	180
TTGTAAAGAC	AGGTTTCACT	GTGTTACCCA	GGCTGATCTC	GAACTCCCGT	ACTCAAGCAA	240
CTCCCCACCT	CAGCCTCCCA	AAGTGCTGGG	ATTACAGACG	TGAGCCACAG	CGCCGGGCCC	300
CAAAATCTAT	TTTAAATGTA	AAGAAACCCA	AAAGTAACAG	TTTTGTAAAA	GAAAATTCAC	360
GTACTGTTTT	GTAGTAAATT	CTAAACACTG	TGTATCTTTG	TGTCTAGTTA	AATCCTAGGC	420
TTACAGCTAA	AATTCAATGA	GAAGGCAAGT	ACTCGAG			457

- (2) INFORMATION FOR SEQ ID NO:629:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

GAATTCGGCC	TTCATGGCCT	AGAAAGCTAT	CATTTATTGA	GAGTTAATTG	TATATTAAGT	60
ACCATGCTAA	GTGCTTTGTA	TGTATTATTT	ATCTTTATAA	AAATCCTATG	AAATGAATAC	120
TGTTATTTTC	CCCCATTATA	CAGATGAAGA	TAGAGAAAGG	AAGAAAAGGG	AGGGAAAGAG	180
GAATACCATT	TCACTGAGCA	ATTTTACTGA	AATATTTTAT	GGAGCATTTG	TGGGTTTTGT	240
TTGTTTGCTT	GTTTTGTTTT	TTTGTTTGTT	TTTTTTTTG	AGACAGAGTC	TCACTTTGTC	300
GCCCAGGCTG	GATCTCGAG					319

- (2) INFORMATION FOR SEQ ID NO:630:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 557 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

ACGGTGAAAC	CCTGTCTGTA	CTAAAAATAC	AAAAAATTAG	CGGGGCATGG	TGGTGGGCAA	60
CTGTAGTCCC	AGCTACTCGG	GAGGCTGAGG	CAGGAGAATG	GCATGAACCC	AGGAGGCGGA	120
GCTTGCAGTG	AGCCGAGATC	ACGTCACTAC	ACTCCAGCCT	GGGCGACAGA	GCGAGACTCC	180
GTCTCAAAAA	AAGAAAAAC	CAAGACAAAA	CCAAAAATAA	CTTTGTCTGT	TAAGTACAAT	240
ATCTGTGTTC	CTCAGGGACA	GTTTCTATTG	ACCATTGTTT	TTCTTGTGCA	TAGACTATCC	300
TTTCCTTTTT	TTGTACATCT	TGTAATTTTT	GTTTTATTAA	AACTGGAATT	TTAAAAATAA	360
TGCAGTGTGG	CAACTCTACT	GCTTGATTTG	GCTCAAAGGT	ATATTATTTA	TTTTTTAATA	420
TAACAAACCA	ATATTTGGGT	TCTCTATTCT	ATAGTTTTAG	CATTTTGAAT	GCAACAACTG	480
TCTTATTCAC	CATTTAATTC	TCAGTACTAC	CGTTTCTAGT	ACACAATATG	CACTTAATGA	540
ATATGAGGGT	CCTCGAG					557

- (2) INFORMATION FOR SEQ ID NO:631:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

GAATTCGGCC	TTCATGGCCT	AGACCGTGCC	AGGTATTGAG	AGCGACCCTC	ACATTCCTAC	60
AGTGCTCTGT	GTGGCATCTT	AATGAAACTT	TATTCTCTCC	CCTTAAATGA	GAAAGAATAG	120
CTAGTTGTCA	TCCTTTCTGA	ACCGATTTTG	TCTTTCAAAG	GTAGTAGTGT	ACCAGGCCTG	180
CTATTTTGCA	AAACGGTCTC	CACCAAAATC	GAATTACCTG	CCTCGCGGGG	CAGGCGTGTT	240
GACCAGGTGG	ACTCTAGAAG	TAGGTGGTTT	GCTTGGTTTC	TTTTCCTTTT	AAGGTTTCCC	300
TTTCTTCTTC	TTCTTTTCTG	TGTTTTTTT	TTTTTTTTT	TTTTTTCAAT	ATAGAAACTG	360
TCCCTAAGAG	AGGAAACCTT	TCTGGCCATG	TTATTCCAGG	AATCTTTTGT	CCCCTAAGTT	420
TGACCTTGTT	CTTTCGTTCA	CCCTTTACTC	TTGCATCTCG	AG		462

(2) INFORMATION FOR SEQ ID NO:632:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) "OFOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

GAATTCGGCC	TTCATGGCCT	ACATAAAATC	AGTTGACTAT	TGTGCAACAT	AGAATTATTG	60
TTTGTGTGAA	ATTACCGCTG	AAGGACCTTG	CCTACATTCA	AGGGTCTATT	TTTATTTTTC	120
CAGGTATTCT	TTCACATTAG	TGACATTATA	GTCTAGTACA	ACTGCTTGAT	AATTTGGAGA	180
AACTAACATT	AATTTTAGAT	AGTGATTGAT	AAAATTTGGC	CTGCCAAATG	CATTTTAAAA	240
ATAATTCTAG	GATTTATCTA	TGCTCATTTC	TAGTATACCT	CATGATATAT	AAGACATCTT	300
TCTTTTGTCA	TATCAGTTCT	TCAGATACTA	AGACAGAGGT	CCTCGAG		347

(2) INFORMATION FOR SEQ ID NO:633:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

GAATTCGGCC TTCAT	GGCCT AGGTGGTGCA .	AATATTAATA	ATGTTGCCAG	TCAATGCCAA	60
CCAGTGTCTG ATTGG	CTTCC TGTGCATGTC	CAATTTCCTC	TGTGACACTG	TGTTGGTGCC	120
AGAGCTTCTG AATCT	TCTTG AATCGCTCTT	TGCATAAATG	TAAAGGATTT	CCCCGTCTGA	180
GTCCCTGGTC GGTCT	CCCCA TAATCATCAA	GGTAAGGAGG	AGAATAAAAA	CAGCCTTTGG	240
TTTTGCCAGC TAAAA	ATAGC ACCTGACATT	CCCGTACTCT	CAGGAAGATG	CCCACTCCAG	300
AGCCACAGGA GTAGG	TGTGA GCTGTGCAGG	CTCCTACATC	CTCCCCTTCC	AGTTCAGTCT	360
GGCAGCAGTA ACTCT	GGGAG CACAGCAGAG	ATCCGCACAC	AAGGCACAGA	GTTGGGGCTC	420
TGCTCTTATC ACCAC	CTGAT TTCGGGCACC	TCGAG			455

(2) INFORMATION FOR SEQ ID NO:634:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

GCATGAAGGC	CGGCCTTCAT	GGCCTACAGG	CTATGTACTG	TATGATTCCA	AATATGACAT	60
TCTGGAAAAG	GCAAAACCAG	GGACACAGTG	AAAAGATCAG	GGGTTGAGAG	GGGAAAAAAG	120
GAGGGATGAG	TAATCAGAAC	ATACAAGATT	TTTTTAAGGC	AGTGGAACCG	CTCTGTATAA	180
TACCATAATA	GTGGATACGT	GTCATTATGC	ATTCATCCAA	ACTCCTAGAA	TGTACAGCAC	240
AAATAGTGAA	CTGTAATGTA	AATGCAGTGT	GTAGGTGTTT	ATACAAAAAA	ACAGATGGAA	300
AGATTTTGTA	CATAGCTCTA	TGTGAAAATG	TATTTATTTA	TTAAGAGCAA	AAATATGCTT	360
ATTTCAAATT	TCCACGTACG	ACTTTTTCAA	AAAGACACGA	TCCACTGAAA	TAACCCTCCA	420
AAAGAATTTC	TATAATCTAT	AGCAGGTGTA	CATGTTGTTA	ATCAAGTGCT	TAATGTTACT	480
CGAG						484

- (2) INFORMATION FOR SEQ ID NO:635:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GAATTCGGCC	TTCATGGCCT	ACCCCACCAG	AGGACAGACG	TTGAAAGATA	CCACGTCCAG	60
TTCTTCAGCA	GACTCAACTA	TCATGGACAT	TCAGGTCCCG	ACACGAGCCC	CAGATGCAGT	120
CTACACAGAA	CTCCAGCCCA	CCTCTCCAAC	CCCAACCTGG	CCTGCTGATG	AAACACCACA	180
ACCCCAGACC	CAGACCCAGC	AACTGGAAGG	AACGGATGGG	CCTCTAGTGA	CAGATCCAGA	240
GACACACAAG	AGCACCAAAG	CAGCTCATCC	CACTGATGAC	ACCACGACGC	TCTCTGAGAG	300
ACCATCCCCA	AGCACAGACG	TCCAGACAGA	CCCCCAGACC	CTCAAGCCAT	CTGGTTTTCA	360
TGAGGATGAC	CCCTTCTTCT	ATGATGAACA	CACCCTCCGG	AAACGGGGGC	TGTTGGTCGC	420
AGCTGTGCTG	TTCATCACAG	GCATCATCAT	CCTCACCAGT	GGCAAGTGCA	GGCAGCAGTC	480
TCTCGAG						487

- (2) INFORMATION FOR SEQ ID NO:636:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

GAATTCGGCC	TTCATGGCCT	AATTTTATTT	TATTTTTAAA	TATATATTA	TTTATTTAAA	60
ATTTTCATGA	AATGGCCAAG	CAGGGTTTAA	TATAAAATGG	AAACAGGGTT	TATCTCAGAA	120
ATTTGGTGGC	TAAATTCCTT	GTATCCCGTC	TTATCTAGGG	ATGTTGTTTG	TTTCAAGGTT	180
CTACCTTGAG	AGGAGCCTGT	CATTTTCTTT	TTTGTGTGCT	GCTTTGCCTA	GTTGACATCT	240
TGGCTTTATG	TGCTCCTGTT	GAATGCATTG	GGAAATTTTC	TTTCTTCTTT	CTATGTCCTG	300
AAATAGCTTA	TATAAGAGGG	AAACTCTCGA	G			331

- (2) INFORMATION FOR SEQ ID NO:637:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 625 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

GAATTCGGCC TTCATGGCCT ACAAAAATAC TTTCATTTGT TTTGCTATTA CTAGTTTCTC 60 ATTTTTTATT GCACTTGCAA TCATTTTAGG AATATCCTCA AAATATGCTC CAGATGAAAA 120 TTGCCCAGAT CAAAATCCTC GTCTCAGGAA TTGGGATCCA GGACAAGATT CTGCAAAGCA 180 AGTTGTTATC AAGGAGGGG ATATGCTCCG TCTGACCTCA GACGCCACCG TGCATTCTAT 240 AGTCATTCAG GATGGAGGAC TGCTTGTATT TGGGGACAAT AAAGATGGAT CCAGAAATAT TACTTTGAGG ACTCATTACA TCCTGATCCA GGATGGTGGG GCGCTTCATA TTGGAGCAGA AAAATGCCGC TATAAATCCA AAGCGACAAT TACCTTGTAT GGCAAGTCAG ATGAAGGTGA 420 AAGTATGCCA ACATTTGGCA AAAAGTTTAT TGGTGTGGAA GCTGGCGGGA CACTGGAGTT 480 ACATGGGGCA CGGAAGGCAT CGTGGACGTT GTTGGCAAGG ACCCTGAATT CCTCAGGCTT 540 GCCGTTTGGG TCCTATACCT TTGAAAAGGA CTTTTCCCGG GGCCTCAATG TGAGGGTCAT 600 TGACCAAGAC ACGGACGCTC TCGAG 625

- (2) INFORMATION FOR SEQ ID NO:638:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

GAATTCGGCC TTCATGGCCT AGAGAACTTT TTGAGGGCTT TTTTTTTTCC CCTTTTAAGC 60 TATTTTGTAT GTAGACTTAA TTTTTCTAAT TTTGCCACTT CTGGCAATCT GAAATCATTA AAAAGGACAC AATTCAAATT TATGTTAAAG GTCATAAATT TTGCCCAGGA CTCAATATTT 180 TCTCATTTTT CCAAAAATAA AATCTTATTT ATGCATTATA GCGACTTGGT TTTCACTTTA 240 TCTTGAATTA TAGCTTTTAA GAGGCAGAAA GAATCCTTTT TATAAGGACA GTCTCAAGTG 300 TACACAGA TTAAATATTA CAAATATAGG TTGCAAATAA AACTTTCAAA ATGTGGGATT 360 ATAGGAAGCA AAAGAGAACC AACCAAAGCA TCAACAAATT TACCTTTTTG TTTTTTTTTAA 420 AGATTTTTCT TATTTCCTTA GCTGCTTTTG CATTAGCATT AAATAACATT CTTATTGGAG 480 TGGTATGTGC ATGGCCCAAG CTCGAG 506

- (2) INFORMATION FOR SEQ ID NO:639:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

GAATTCGGCC	TTCATGGCCT	ACTCCAGCTT	TATTATCTCA	GCTACCATCA	AACTATATTA	60
CATCAAATTA	TCATCATTAC	TCTCCTGCAC	AGTAACTTTC	TTTCTGCTCC	ACTAAGAAGC	120
TTACTCCCAT	CCTGTTTATT	CTCTATATCG	TAGCTGGACT	AATCTTTTCA	AAGTGCAAAG	180
CCAATCACAA	TACCACCTGC	TTAAAATCCA	TCAGTGGCTA	ACTTTTCATT	CTAGGACGAA	240
AAGAAAATTC	TATAACATGA	CTTCAAAGGC	TCTGCATGTC	CTTCTATTTC	TCTTGTCCTC	300

TCTAGTCTTT TCTTTGATGG TCTCCACTCC AGCCCTACTG GCTTCTTTCT GGAATCAATG

360

TCACCCACAA CCCGTCACGC CACTCGAG	388
(2) INFORMATION FOR SEQ ID NO:640:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 305 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:	
GAATTCGGCC TTCATGGCCT ACTCCGCTCT GGCCCAGAAG GAGGCCAAGA AGGACGAGCC CAAGAGCGC GAGGAGGCC TCATCATCCC CCCCGACGCC GTCGCGGTGG ACTGCAAGGA CCCAGATGAT GTGGTACCAG TTGGCCAAAG AAGAGCCTGG TGTTGGTGCA TGTGCTTTGG ACTAGCATTT ATGCTTGCAG GTGTTATTCT AGGAGGAGCA TACTTGTACA AATATTTTGC ACTTCAACCA GATGACGTGT ACTACTGTGG AATAAAGTAC ATCAAAGATG ATGTCATCTT AAATGAGCCC TCTGCAGATG CCCCAGCTGC TCTCTACCAG ACAATTGAAG AAAATATTAA AATCTTTGAA GAAGAAGAGC TCGAG	60 120 180 240 300 360 385
(2) INFORMATION FOR SEQ ID NO:641:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 392 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:	
GAATTCGGCC TTCATGGCCT AGCAAGGAGA ACTATTGTCT TATGATCACG TTTGCCATCT TTCTGTCTCT TATCATGTTG GTGGAGGTGG CCGCAGCCAT TGCTGGCTAT GTGTTTAGAG ATAAGGTGAT GTCAGAGTTT AATAACAACT TCCGGCAGCA GATGGAGAAT TACCCGAAAA ACAACCACAC TGCTTCGATC CTGGACAGGA TGCAGGCAGA TTTTAAGTGC TGTGGGGCTG CTAACTACAC AGATTGGGAG AAAATCCCTT CCATGTCGAA GAACCGAGTC CCCGACTCCT GCTGCATTAA TGTTACTGTG GGCTGTGGGA TTAATTTCAA CGAGAAGGCG ATCCATAAGG AGGGCTGTCT GGAGAAGATT GGGGGGCTCG AG	60 120 180 240 300 360 392
(2) INFORMATION FOR SEQ ID NO:642:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:	
GAGTTGAAGT GGCCAAAAA TTATAACACT CTCCTACTTT CATATCTTGA TTTTAATTTT TTCCCTTACT TGTATTTTAT TTCTGAGTGG CTAATGGATC TTAGTCTAAG AACTGGAGGT GGAGAACTCG AG	60 120 132

- (2) INFORMATION FOR SEQ ID NO:643:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

GCACAAAGAC	GCATTTCATC	TGAGTTTCCC	TGAAAGCTAG	AATAAGTTTG	CTGGTGTCAG	60
CTGGGATCCT	GTCTTCTATA	GCTTTGTATC	AAGCAAACTC	AGCATTGTGT	CTTGAATGCA	120
TGTCATGTGC	AGCCTGCGTT	TATGTGCGAC	TGAGCACTTG	GGTGGGGACA	TCTTAAGGCT	180
GTTTATATTT	CTTTTTCATG	TGTTGTTGTT	GTTGTTGTTG	TTGTTGTTTT	GGAGAGAGTC	240
TCGCCCAAAG	CTCGAG					256

- (2) INFORMATION FOR SEQ ID NO:644:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

GTGCTCGCAG	CCNTGGTGGC	CTGGCGCTCG	GCGTNCCTTG	TCTGCCTCGC	TTTCTCCTTG	60
GCCACCCTGG	TCCAGCGAGG	ATCTGGGGAC	TTTGATGATT	TTAACCTGGA	GGATGCAGTG	120
AAAGAAACTT	CCTCAGTAAA	GCAGCCATGG	GACCACACCA	CCACCACCAC	AACCAATAGG	180
CCAGGAACCA	CCAGAGCTCC	GGCAAAACCT	CCAGGTAGTG	GATTGGACTT	GGCTGATGCT	240
TTGGATGATC	AAGATGATGG	CCGCAGGAAA	CCGGGTATAG	GAGGAAGAGA	GAGATGGAAC	300
CATGTAACCA	CCACGACCAA	GAGGCCAGTA	ACCACCAGAG	CTCCAGCAAA	TACTTTAGGA	360
AATGATTTTG	ACTTGGCTGA	TGCCCTGGAT	GATCGAAATG	ATCGAGATGA	TGGCCGCAGG	420
AAACCAATTG	CTGGAGGATG	GCTCGAG				447

- (2) INFORMATION FOR SEQ ID NO:645:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

GCTCAGCAAC	ATTTTAGGAA	CAACATTGGT	GAGTATATGA	GAATAGCCGT	GACCTCCATA	60
TTTCATCAGC	CGGGTTTTCG	TATGTATGTC	ATGTGCTACC	AGAATTCGAT	CTTCACAGCC	120
CTCTTCCACC	AGGAGACGCA	CCCTGTGAAA	AATGTTAACT	CATTAGATGT	CATTTGTCTT	180
TCATTTTCGC	TTTTCAGGAT	GCTTTCAACT	TTTTACTCAT	TAACCTATTG	TGCTTGTCGT	240
AAAGATACTG	ACTTCTACTG	TGGCGTGTGT	ACTGAGAGAC	TCGAG		285

(2) INFORMATION FOR SEQ ID NO:646:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEO ID NO:646:

GGAGATTTGA	AGAAGAATTG	AATGAAAGGA	TGATTCAAGC	AATTGATGGG	ATTAATGCAC	60
AGAAGCAATG	GCTCAAGTCT	GAAGACATTC	AGAGAATCTC	ACTGCTTTTC	TATAACAAAG	120
TACTAGAAAA	AGAGTACCGG	GCCACGGCAC	TGCCAGCGTT	CAAGTATTAT	GTGACTTGTG	180
CCTGTCTCAT	ATTCTTCTGC	ATCTTCATTG	TGCAGATTCT	CGTGCTGCCA	AAAACGTCTG	240
TCCCGGGCTA	TCTCGAG					257

- (2) INFORMATION FOR SEQ ID NO:647:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

GGGGCAGCAG	TAAAATCCAG	GCCCGAATGG	AACAGCAGCC	CACTCGTCCT	CCACAGACGT	60
CACAGCCACC	ACCACCTCCA	CCACCTATGC	CATTCAGAGC	TCCAACGAAG	CCTCCAGTTG	120
GACCCAAAAC	TTCTCCCTTG	AAAGATAACC	CGTCACCTGA	ACCTCAGTTG	GATGACATCA	180
AAAGAGAGCT	GAGGGCTGAA	GTTGACATTA	TTGAACAAAT	GAGCAGCAGC	AGTGGGAGCA	240
GCTCTTCAGA	CTCTGAGAGC	TCTTCGGGAA	GTGATGACGA	TAGCTCCAGA	CTCGAG	296

- (2) INFORMATION FOR SEQ ID NO:648:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

GTGCANATGT	ACGGTGACCA	CCTGGCCCTT	GACCGGGCGG	CTCGAACCTG	GCGGCCCTGG	60
GACCAGCGTC	TTCTTCCTCA	ACAGCCCGTT	CCCCAGAATG	TCCAGCCACT	CTTCTGGGGC	120
CGGGGCTGGG	GCGGGCTCGG	GCTCCATGGC	AGCAAGGAAC	TCTCGGGCCA	GGGCCCCAGG	180
CTGCTCANCC	TCCTCCGCCG	GGGGTTGTCC	CATGTCCTCC	AGCGGTGGCA	GCTCACTCAG	240
GTCATCCTCT	TCCTCCTCTT	CCTCCTCCTC	TTCCTCCTCA	CCCTCTGCAT	CCTCAACCCC	300
ATCCAGTACC	TCGAAGTCCT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:649:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

GAATTCGGCC T	TCATGGCCT	ACTTCCTGAT	ACAGATACAT	TTACTACAGA	AAATTTCCTT	60
TATAGGTGTA A	ATTTCTGTT	TACAACAGGC	GAGTCGAAAA	ATAATAAGAA	CAAAAGGAAA	120
AAAAGCAGTC A	TACTTTATT	TTAGGCAGTT	GAGGGGTAGC	TGAATAAGTT	ATCCTGTGTT	180
GTTTGGTTCT G	TTACTTATA	GCTCAAAGTC	ATCAATATGC	CAGGGTGGCA	TGTTTGGGGA	240
TGGTGCATTC T	TGTCTTTTG	CAGTCATTTA	TCAGGGTGGC	GTTTCCTAAA	TTCTAACACA	300
GACCTCGAG						309

- (2) INFORMATION FOR SEQ ID NO:650:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

GGTGACGCCT	GCTTCACATC	TCTAATGAAC	ACCCTCATGA	CGTCGCTACC	AGCACTAGTG	60
CAGCAACAGG	GAAGGCTGCT	TCTGGCTGCT	AATGTGGCCA	CCCTGGGGCT	CCTCATGGCC	120
			GGAACACCAG			180
			GTGGCGCGGG			240
GCAGTGCTAG	CCCTGTCCCC	TGAGTATGAG	GGCATCTGGG	CCGACCTGCA	GGAGCTCTGG	300
TTCCTCGAG						309

- (2) INFORMATION FOR SEQ ID NO:651:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

GCAAGGGCAG	GCGGGTCCCC	CAGTCCCGCC	ATTACGGGTT	GTCAGACCGT	CTGCGTGTGG	60
CAGGGCTCCC	AAGGGCAGGC	GGGTCCCCCA	GTCCCGCCAT	TACGGGTTGT	CAGACCGTCT	120
	TTTTTTGGCT					180
CCCCCTGCCG	GCAGCCCCTC	AACCTAAGAA	GGCCAGAGCA	TATTTATTTT	CGGAGGGAGC	240
AGATTACTTC	TCCCAGAGAA	AGGAAAATCT	TGGAAAAGAT	TTAAAAACAC	AAATCTAAGC	300
CTTGACGGTT	TTTTTTTCCC	TTTTGACCCC	CTTCCCATCT	CTTCAGAATT	TATTCCCATG	360
GCTTTTTTTT	TTCTTGTGCG	TGTTCTCGAG				390

- (2) INFORMATION FOR SEQ ID NO:652:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

GAATTCGGCC	TTCATGGCCT	ACCAAATTCC	CTGCCTGTGC	CTGCTGGGAC	CAGACTCCGC	60
TGTCATGAGG	GTGACATCCG	CCACCTGTGC	TCTTCTGCTG	GCTCTGATCT	GCAGCGTCCA	120
GCTGGGGGAT	GCCTGCCTGG	ATATCGATAA	ACTGCTTGCG	AATGTTGTGT	TTGATGTGTC	180
CCAAGACCTC	CTGAAGGAGG	AGCTTGCTCG	TTACAACCCC	AGTCCCCTGA	CAGAGGAGTC	240
CTTCCTCAAT	GTCCAGCAAT	GCTTTGCCAA	TGTCCTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:653:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

GGTGTTTGGC	CACAGTTCGG	GACCTATGGT	AGAAAAATAC	TCAGTAGCTA	CCCAGATTGT	60
AATGGGTGGC	GTTACTGGCT	GGTGTGCAGG	ATTTCTGTTC	CAGAAAGTTG	GAAAACTTGC	120
AGCAACTGCA	GTAGGTGGTG	GCTTTCTTCT	TCTTCAGATT	GCTAGTCATA	GTGGCTATGT	180
GCAGATTGAC	TGGAAGAGAG	TTGAAAAAGA	TGTAAATAAA	GCAAAAAGAC	AGATTAAGAA	240
ACGAGCTCTC	GAG					253

- (2) INFORMATION FOR SEQ ID NO:654:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

GAATTCGGCC	TTCATGGCCT	AATTGAATTC	TAGACCTGCC	TCGGCCTCCC	AAAGTGCTGG	60
GATTACAGGG	GTGAGCCACC	GCACCCAGCC	TGTGAAATAC	TATTTTTATG	GTAAGCTAGA	120
ATTTTAAAAC	TATTTCTTGC	AAGTTTAGGA	TTAAATGAAT	TACATTATGT	AAAATTACAT	180
CTTTGTCTGT	ATTACGTATT	TGTATACAGT	TGAATAGTTT	TGGTAACACG	TACCTTAGTG	240
CTTTACATTG	ATTGGCTCAT	TAATTTTATA	TTTTGAGTAA	TAATCATCTA	TATTATTTA	300
TGTACAATTC	AGTCTTAAAT	TATGTTATGA	TGTGAAAATG	GTAGCTTTCT	TGAGTGTATT	360
TATTTTTGTA	GTAGTGGGCA	ATGTAATTAT	CACACATAAA	ATGAACTGTG	AGACTTTTGA	420
GCCTGAAATA	TTATTCATAT	TATAATGCTC	CTCGAG			456

- (2) INFORMATION FOR SEQ ID NO:655:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

```
GAATTCGGCC TTCATGGCCT AGTATATACA TGCATTTAAT TGTGATTTTA TCACCTTTCC
CATTTCTTTC CCCACAGCT GGCATTTCAG TAGTTGCTTT TGAATAATGG TTTTGGTTAC
                                                                     120
CTGGGAAGGC AGGCCCAGAA CCCATTTCCT TGACTTGCAG TTCCGGGCTG TGTTCACATG
                                                                     180
ACTGCTGTCT AGCTGATGCA TTTTTCACAT TTGTCAACTC TGGTTAGAAA CAGGTCCTCA
                                                                      240
GGAGTATTCT CTAACCTGAT ATTTTCTAAA AAGATATGTT GATTCAACTT TGTTTAGCAT
                                                                     300
CCTACTTTCT AGATTGTGGG GCTCATTTTG CCAGGGCCAA GCTACCAGAA AAGTAGAAGT
                                                                     360
GGAGATTACC TGGTATGTAT CTCTCTGGGT GCCCCAGTTA GAGCTGCCAC AGCTCAGGAA
                                                                     420
AAAGATGAGG CATAACGACC TTGAATGTAA TTGGAGTAAG TGACAAAATA AGAACTACCC
                                                                     480
                                                                      493
TGGGAAACTC GAG
```

- (2) INFORMATION FOR SEQ ID NO:656:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

GAATTCGGCC	TTCATGGCCT	ACTTGGCCTT	TGTTTGTGTT	TGCCTTTGTC	AGTCTCCTGC	60
CTCTGGATGG	GTTTCTGTTT	GTTTCCAAAC	TGTCTGGGGC	TGTGCACCAT	GGAGACAGTG	120
TCCTGGGCTG	CCTCTAGCCT	GATCTGGTTA	GAATAAGCCC	CTCTCCTTTG	CATGCGTCTC	180
CAACCTGACA	TTTGGAGCAT	CCAAAACAAA	TCATGACATT	CCCAAGTAAA	GATAGAAACC	240
ACCGTCTCCA	CTCCACTCGA	G				261

- (2) INFORMATION FOR SEQ ID NO:657:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 621 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

GAATTCGGCC	TTCATGGCCT	AGATGGTCTC	TGCTGCTCTT	GCCTCTAGTT	CATGGAGATG	60
TGTCTCTGTT	CAGGCCAAGA	TACAGCCAGC	CAGGCCTGTC	GTCTGGGACC	CAGGAGGCCT	120
CTGATGACCA	AGGGCTTTCA	CATCCTAAGT	CATTTGGAAG	GAGGCCTTGA	GAACAAAGTC	180
ACCTTTGTCA	CTCCCAGTGA	ACTGAATGAG	GAACATGCTG	TCTCCTGTCT	TGGCCTCCCC	240
TTTCATGAGA	TACTGGGGAG	AAGAGAACAT	TCCTCCTGGC	TTAGTTGTAG	CAGACCCAGA	300
CCTGTGCCCA	GCTTTGGTCC	CCCTTCCCAA	CTTCTGAAGC	ACGTGCTGCA	GAGCCACCTT	360
GGTCTGAGCA	CCTGAGGACC	AGCCCCTCCT	CCCTCAGTGC	GGGTCATCTC	TTGGGGGATT	420
TTCTTAAAGT	GAAGAAAGGG	GGTGGGGAAC	CATATTGCCC	CTCCCTCCCC	CATCAAACTT	480
CCTTCATTTA	ACTTGCTATA	AAATGAGTCA	TATAAAGAAA	CTCTATATGG	GTGAGGTATA	540
TCCCACTTCT	GTGAAAACAT	TACAAATCAA	ACCGCTTCTC	TCAGTTTATT	TAAGATGCTT	600
TTGTTGCAAG	CGGTACTCGA	G				621

- (2) INFORMATION FOR SEQ ID NO:658:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 567 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

GAAGTCTTGG	AGATTTCTAG	TTTATTCATT	AACAGCAGAA	GGATGGAAGA	AAATTCCTCT	60
GGCAATACCA	TGTCAGCCTC	TTCGATGTTT	AATACAGAAG	AAAGAAAATG	TTTGCAGACT	120
CACAGAGTCA	CGGTGCATGG	GGTCCCAGGG	CCAGAGCCCT	TTACCGTTTT	CACTATTAAT	180
GGAGGCACCA	AGGCAAAGCA	GCTTCTGCAG	CAAATTCTGA	CAAATGAACA	AGACATCAAA	240
CCTGTTACCA	CAGACTATTT	TTTGATGGAA	GAAAAATATT	TTATATCTAA	AGAAAAGAAT	300
GAATGTAGGA	AACAACCATT	CCAGAGAGCC	ATTGGTCCAG	AAGAGGAGAT	CATGCAAATT	360
TTAAGCAGCT	GGTTTCCAGA	AGAGGGATAC	ATGGGCAGGA	TTGTCTTAAA	AACCCAGCAG	420
GAAAACCTAG	AAGAGAAAAA	CATTGTTCAA	GATGACAAAG	AGGTGATCTT	GAGCTCAGAG	480
GAGGAGAGTT	TCTTTGTCCA	AGTGCATGAT	GTTTCTCCAG	AGCAACCTCG	AACAGTCATC	540
AAAGCACCCC	GCGCCAGCAC	ACTCGAG				567

- (2) INFORMATION FOR SEQ ID NO:659:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

GAATTCGGCC	TTCATGGCCT	AGGCCCTTTG	GCCCTGGGGT	GGGGGTGCTT	ACTACATCCC	60
TGGAAGGTGC	AGGGAGGCTG	ATGGCCTTGA	TCTCTAACAC	AAACAGGAAC	CAGCTTCCTC	120
CCTCCCCCAC	CCTGGGTTCC	CAGGGCCTCC	GGGTGTGAGA	TCCTCCCCCA	CTGCAGTGCC	180
CCACCCGCTC	CCCACAGAAG	CCCGGAGAGT	GGCTCTGTCA	CCAGAGGTGT	CATTTCCCAG	240
CTGTCTGTGG	GAGGTGAGTG	AGCAGGGAAT	GTGTGTGCTG	GGTGTGGGAA	CTCAGCCCAA	300
TCTAAGAGAA	GATACTCTTG	GCTTCCTCCC	CCTCAGAGGA	GCAGCCGCGT	CCCTGGTCCT	360
TGTGCACTGA	CAGTCCCGGA	GTCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:660:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

GAATTCGGCC	TTCATGGCCT	AGCCAGGAGT	TGAGGTGGAA	GTCACCATTG	CAGATGCTTA	60
AGTCAACTAT	TAAATAATT	TGATGACCAG	TTGTTAACTT	CTGTTGGTTT	TTATTCAGAA	120
TACTGGCAGA	TTTTAGGAAT	ATAAAGGTGT	ACTATGAGAC	TTCCACTTTT	CAGGTGGAAT	180
ATATGGGTAT	CTTAGAGTGG	TCTATCCTGT	TTTCGTTGTC	GTTTGAGTCA	TTTGAAAACT	240
GGATTCCGTT	AACTACATAA	TATGTGAGAC	CTGACTGGTT	TTATTGGACA	CTGGCAGTTT	300
ATAACTTTGG	CATACTCTAG	ATAAATTCTG	ATTGGTATGG	GGTGTTAAGG	TTTCTGGGGC	360
GTTTGTAATG	CACACCCATG	GTTGAGAACC	TAGTGCGCTA	GTAGGCACGT	GTTAAAAAGC	420
TAGTAACTAA	TATTTTTAAA	TTAACCAAGT	TTAACGTCCT	TAAAAAAGGA	TTAAGTGGCA	480
AGGACCTCGA	G					491

- (2) INFORMATION FOR SEQ ID NO:661:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

GAATTCGGCC	TTCATGGCCT	ACCTCAATAT	GCTATCAGAT	TCTGAAAATT	CCCAGCATCT	60
GGAACTTCAT	GAGCCACCAA	AAGCTGTGGA	TAAGGCGAAA	TCCCCAGGGG	TTGATCCTAA	120
GCAGTTGGCA	GCAGAACTCC	AGAAGGTTTC	ACTACAGCAG	TCACCGCTGG	TTCTGTCATC	180
AGTTGTTGAA	AAAGGATCTC	ATGTTCATTC	AGGTCCTACA	TCAGCAGGAT	CCAGTTCCGT	240
TCCCAGCCCT	GGGCAACCAG	GGTCCCCCTC	AGTGAGCAAA	AAGAAGCACG	GCAGCAGCAA	300
GCCACTCGAG						310

- (2) INFORMATION FOR SEQ ID NO:662:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 404 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

GAATTCCTAT	GGCCTACTTC	CGGCGCAAGT	GGCTTCTGAT	AATCATGGCG	CCCCTCGGAA	60
CAACTGTATT	GCTGTGGAGC	CTCTTGAGGA	GTTCTCCGGG	CGTGGAACGG	GTCTGTTTCC	120
GGGCTCGAAT	CCAGCCCTGG	CACGGTGGCC	TGCTCCAACC	GCTACCTTGC	TCTTTCGAGA	180
TGGGGCTGCC	ACGCCGCCGG	TTCAGCTCCG	AGGCCGCAGA	ATCTGGTAGC	CCAGAGACCA	240
AGAAACCTAC	ATTTATGGAT	GAGGAAGTTC	AAAGCATACT	CACGAAAATG	ACAGGCTTGA	300
ACTTGCAGAA	GACTTTTAAG	CCAGCTATAC	AAGAACTGAA	GCCACCAACC	TATAAGCTAA	360
TGACTCAGGC	ACAGTTGGAA	GAGGCTACAA	TACAGGCTCT	CGAG		404

- (2) INFORMATION FOR SEQ ID NO:663:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

GAATTCGGCC	TTCATGCCTA	ATTTGTGTGA	TGGCCAAAGA	GTTCTTATCA	GAAGTGGCAA	60
AAACTACATA	CAGGTTGGCT	TCCAATAACA	TGAGCCAGGT	ATTTTTCAGT	AATATTTTGA	120
AGTGTCTTTT	CTTTCTAGAC	ATGCACATGA	TGGTGTCCAA	GCCAGAACAG	TGGGTAAAGC	180
CAATGGCTGT	AGCAGGAGCC	AATCAGTACA	CCTTTCATCT	CGAG		224

- (2) INFORMATION FOR SEQ ID NO:664:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

GAATTCGGCC	TTCATGGCCT	AGGTCTACCA	AAGTGAGGAC	ATTACTGCAG	ATATTCTTCT	60
CCTTTTCTCC	TACATTATCA	TTTCTCTTTT	ATAACATCAT	TTCTGCAGAT	ATGTAAAAAT	120
ACATCCCATC	TTCAAAAAGA	AAAACAAAAA	TCTGACTGTA	CTTCATATCC	CCTTCTAGAC	180
ATTGCCACAT	TTCTCTACTT	CTGTTTACAA	CAAAACTCCT	GGAAAGATTT	GTCTATACTG	240
GCTTTCTCTA	CTTCTTTTAC	TTCCATTCCT	TTCCTAACCA	CTCTAAACAT	GCTTGGGTCC	300
CCACCACTGT	AACAAATATA	ATTTGTGTCC	AATAACCAGT	GATCTCTGTA	TCACCGGTTC	360
CAAGGGTGAG	ATCTCAGACT	TCACCTTTCT	GGATTGATTG	ACACATTGGA	CTCAGTTGGT	420
TACTCCTCAC	TTCTTGAAAC	TGTCTTCACT	GGGCTTTTTG	GACTCCATAT	CTCGAG	476

- (2) INFORMATION FOR SEQ ID NO:665:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

GAATTCGGCC	TTCATGGCCT	ACTCTCTACT	CCTTTGTGCT	CAATTTCCAT	TGTGGAATTC	60
TGCATATATG	ATCTTGTGGC	ACATTTCTAC	ATTTCCTCAG	CCCAGAAGGC	CTTCCCTGTT	120
CACTATCTCC	TTCTTTTTAC	TAACTCTTAC	TATATTTCCA	GGCACAGTTC	AGGCATCAGA	180
TAGCCCTATT	TGTTCCAACT	TTCACCGTAG	GTCAGATTAT	AAGCCTTGCA	ATCTCGAG	238

- (2) INFORMATION FOR SEQ ID NO:666:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

GAATTCGGCC	TTCATGGCCT	AGACCATTTT	CATTGTTTAT	AGTTTATTTC	TTATAAATAG	60
TGCTTTCTGG	AATATCCTTA	AATACCTCTA	TCTTTTTAAC	ATCCTTGTGT	ATACATCTTT	120
TCTCACACTT	GGCTTCCTCT	TGGAATAGAA	TCTCCTGGAA	ATTAGATAGC	TGAGGTAAAA	180
GTCCCTGAAC	CTTTTACAAA	TTGCTACACA	ATAAATACCA	AACTGATTTT	CAGGAATGTA	240
GTCCCATCAA	CAGTGTGCTT	GTTTATCCAT	ATCGTTGCTG	ATCTGAGTTT	TGTCAGTCTA	300
TTGATTCCTA	CCAATCTGCC	AGTATCATAG	ATTTTAAAAT	ATTTTTTGTG	TGCATCTCGA	360
G						361

- (2) INFORMATION FOR SEQ ID NO:667:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

GAATTCGGCC	TTCATGGCCT	ACTCATACAC	AATGAATACA	AAAACTGGAA	CTCTGCAATT	60
						120
						180
						240
						300
						343
	TAATACTGTT ATATCGCAGG AGCAGCCGTA TCAGAGGAAA	TAATACTGTT TCCAAACTGG ATATCGCAGG TGTCCTGGGA AGCAGCCGTA GTAGTTGTGG TCAGAGGAAA GGCTACTTTT	TAATACTGTT TCCAAACTGG ACACTGGAGA ATATCGCAGG TGTCCTGGGA AACGAATGCA AGCAGCCGTA GTAGTTGTGG CCTTAGTGAT TCAGAGGAAA GGCTACTTTT CAAAAGAAAC	TAATACTGTT TCCAAACTGG ACACTGGAGA ATATTCCTGT ATATCGCAGG TGTCCTGGGA AACGAATGCA AGTAGATGAT AGCAGCCGTA GTAGTTGTG CCTTAGTGAT TTCCGTTTGT TCAGAGGAAA GGCTACTTTT CAAAAGAAAC CTCCTTCCAG	TAATACTGTT TCCAAACTGG ACACTGGAGA ATATTCCTGT GAAGCCCGCA ATATCGCAGG TGTCCTGGGA AACGAATGCA AGTAGATGAT CTCAACATAA AGCAGCCGTA GTAGTTGTGG CCTTAGTGAT TTCCGTTTGT GGCCTTGGTG	GAATTCGGCC TTCATGGCCT ACTCATACAC AATGAATACA AAAACTGGAA CTCTGCAATT TAATACTGTT TCCAAACTGG ACACTGGAGA ATATTCCTGT GAAGCCCGCA ATTCTGTTGG ATATCGCAGG TGTCCTGGGA AACGAATGCA AGTAGATGAT CTCAACATAA GTGGCATCAT AGCAGCCGTA GTAGTTGTGG CCTTAGTGAT TTCCGTTTGT GGCCTTGGTG TATGCTATGC

- (2) INFORMATION FOR SEQ ID NO:668:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

GAATTCGGCC TTATCCTACA ACTTTGAATA GACATAAGAG TGCCTGTCTG CATAAACCTT	60
CATCAACATT GGTATTATCT TTCTTTTTCA TCTTTGCTAA TTGGATAAGT TTTAAAAAGT	120
GTAACACATT TTAGTTTGCA TAGCTTTGAT TATAAGTGAG GTTCGACATT TTTTTTCATT	
TCTTTACACT TTAAAAAATC TAACCGTGGC AACGTTTGCA GGTGTGTGTT CTTCTTATGT	
TGCTGAGTGT TATTTACTCC TGGACG	266

- (2) INFORMATION FOR SEQ ID NO:669:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

CAATTCCCCT	TCATGGCCTA	CAAAAAAGAA	ATTAAGAAGC	TCCTAAAGAC	GCAAAGAAAT	60
	TCTGTCTGAA					120
						180
AGGAAGAGTC	TGTCAAGAAA	GATTCTGTTG	CTGCCGGAAA	GCCAAAGGAG	AAGGGGAAAA	
TAAAAGTCAT	TAAGAAGGAA	GGCAAGGCCG	CAGAGGCTGT	CGCTGCAGCT	GTCGGCACTG	240
	AGCAGCTGTC					300
	TGAGAGGTCC					360
AGTTAAAGGC	TGAAGAGGTC	GATGTAACAA	AGGACATCAA	GCCTCAGCTG	GAGCTAATCG	420
	GAAACTGAAG					452

- (2) INFORMATION FOR SEQ ID NO:670:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

GAATAATTGA	CTGAAAGTGT	AGTGTCGAGT	GGTAGAATAA	GTGCTGATCC	TGGGGTCTTA	60
TACCAATGTT	GCTAACTGTG	AGCAGCCTTT	GTCAAATCAC	TTGGCTTCAT	TTTCAGTGGC	120
CTAAGAGTAA	TAGGTTTAAT	TATTTCCATA	ATTCCTTTAA	GTTTTTACAT	TTTCTGAGTT	180
CATCTTTTGT	GTTTTTCCTG	GCATTTTACT	ATTCCTCTTT	CCTGCTTTTG	GCTATTTTCT	240
CAACAGGTCC	ACGACTGGAA	TTTGAAAGCA	AGAAACATCT	CGAG		284

- (2) INFORMATION FOR SEQ ID NO:671:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

GAATTCTGGA	AGCAGCCTAT	CATCGCTCCG	TCTGCCCTCC	ATACACAGCG	TTTGTGTGTG	60
TTATGCCAAA	CTGCTTGGTG	TTTTCCAACC	GTGGACCATG	ATATCTCACT	TCCTTAACCT	120
TACCTTCATA	TGCTTTTCCT	TTGTGTCTTC	TTCTGAAATG	CTTCTTCCTT	TTGTCCAGGC	180
TGACTCCTGT	TTGTCTGAGA	CATGTGTCTC	AGGAAGCCTT	TCCGTTCCCC	TCGAG	235

- (2) INFORMATION FOR SEQ ID NO:672:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

GAATTCGGCC '	TTCATGGCCT	AGCATTGATG	GCCCATGTAG	AAGACCTGAT	CATTAAGACT	60
ATAATCTCTG	CTGAACTAGC	TATTGCTACT	GCCTGTAAAA	CCTTTGTTCC	TCATCGCAGC	120
AGTTGTTTTG .	AACTCTATGG	CTTTGACGTG	CTCATAGATT	CTACTCTGAA	GCCATGGTTG	180
TTGGAAGTGA	ATCTCTCTCC	TTCTTTGGCC	TGTGATGCGC	CTCTGGACCT	AAAGATTAAA	240
GCCAGTATGA	TTTCAGATAT	GTTCACTGTT	GTAGGATTTG	TGTGCCAAGA	TCCTGCCCAG	300
CGGGCATCAA	CTCGGCCAAT	TTATCCCACC	TTTGAGTCTT	CCAGGCGAAA	CCCTTTCCAG	360
AAACCTCGAG						370

- (2) INFORMATION FOR SEQ ID NO:673:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:673:
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60	TTTCCAACAT	AAGATGACCA	CATCATGCAG	ACACAGACAT	TTCATGGCCT	GAATTCGGCC
120	GACGAGAGAA	CTCACAAAAA	ACGGGAGGAA	TCCTCAAGCA	ATGAATAGAC	GGAGGCAGAT
180	AAAATGTGGC	GAGGGAGATA	GGAGAATGGA	AGATAGTCAA	AGAAGGGAGA	ACTTTCAAAA
240	ATGACAGTAT	GATTACATCA	TGCTAATATC	AGTCACTGAC	GAAGAGATGG	TAATATCAAT
295	TCGAG	AACCAACTAC	GGAAGAAGCA	TAATGCAGAT	CAGGCCAACA	TTCTCATTCT

- (2) INFORMATION FOR SEQ ID NO:674:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

GAATTCGGCT	TCATGGCCTA	CCTGCCTCGA	GTGATGGGTA	TCGGGATGGG	TATCGGGATG	60
GCCCACGCCG	GGATATGGAT	CGATATGGTG	GCCGGGATCG	CTATGATGAC	CGAGGCAGCA	120
GAGACTATGA	TAGAGGCTAT	GACTCCCAGA	CTCGAG			156

- (2) INFORMATION FOR SEQ ID NO:675:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

GAATTCGGCC	TTCATGGCCT	AATAATTTGT	AAGTTAAAAT	AAGTAATACA	AATTAAATGC	60
AAATCAAATG	CCTGAAGAAG	AAGCACGAAT	ACCTATTTTG	AAATCTGCTG	TAGCCGAGAC	120
AGCTTCTAAA	TCTCCCACTT	GGGTTCTGTT	TCTGGAAGGT	GTGGGTCCTG	TGGTAGCTGG	180
AGTGTTGGTG	GCCATCTTGG	TGCTGGCGGT	CCTCATGCTG	ATGTACTACT	GCTGCAGACA	240
GAACAACAAA	CTTGGCCAAC	TCGAG				26 5

- (2) INFORMATION FOR SEQ ID NO:676:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

GAATTCTGGA TCAAAA	CAGA GGAAAATGGT GGG	AATTCTT GTATAGATAC	AGTCTAACAT 60
AGAAACCCAT GCCCAT	CAGC AGTAATTTCC AGT	CCCCAG TCCTCCAAGC	CCTGGTACTC 120
GAG			123

WO 00/45436

WO 98/45436	PCT/US98/06955	
	(2) INFORMATION FOR SEQ ID NO:677:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 243 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:	
	GAATTCAGAG ATAAAGCTAA AGTTCCATTT GAGCACCAGC CCAAATCCTG GACTTCTTTC TGCTCCTCCT CAGAGGTTCT CTGGTTATAA GTTTTATGTG TATCTTGCCA GAATTTTTCC TATGTTATTA ATACAAATAT ATGTAGCCAC AGAAATTATA GCGTGTCATT CAGCCTTTGG TTTTATTTGC ATTGATAGTA TTATGTCCAT ATCACTCTAC AACTTCTTAG GCCATGAAGG CCG	60 120 180 240 243
	(2) INFORMATION FOR SEQ ID NO:678:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 121 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:	
	GCGATTGAAT TCTAGACCTG CCTCGAGACC ACCTATGGAA GCCAAGTGTT CCCGGGCCAT GAGACCTGCC CAATCAAGCA GAAACACATT TGGAGAGACA AACAATCACG ACACGCTCGA G	60 120 121
	(2) INFORMATION FOR SEQ ID NO:679:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 283 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:	
	GAATTCTAGA CCTGCCTCGA GTACCTGATC TTTTACTGTC TCTATAGGTT CATCTTTTC TTCCCTTTGT TAATTCTACT TTTTAGTTTT TTTGCTAGAT TTTTCTTGCA ATTGGATAGG CCCATTTAAC CTATTTTGCC TCCACTCTAA ATTCAGTACT CCAAGAATTG GTTTCACTCT TCCAAATTTT GTATATAAGC CAGAGTTCTG CATAAAGGAA AATACTTAAA TTCTTTCTAA	60 120 180 240

- (2) INFORMATION FOR SEQ ID NO:680:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 373 base pairs

 - (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

TCTAATGTGG TTTCCTGCAT CTTTCAGGAA ACTTTTCCTC GAG

283

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

GAATTCGGCC	TTCATGGCCT	AGGGTTTGTG	GCTAAAAATT	ATGCTTAAGA	ACACATCTAA	60
CAAACCTAAA	GCTGCAAAGA	CATAATGTTA	ATGTAGGTGA	AAATTTCACT	TGTGTTTATT	120
CTGATAGACA	AAATTGTATT	TTAGATGAGA	AGCAACAATT	TTCATGTTGT	ACTGAGATTG	180
TTAGTAATGA	AATACTTCCA	AATATTAGTG	ATGGTAGAAA	TCTAGTGTAG	GGCTCTTTGC	240
TGAGAAGGGA	AAAAAGTCAC	ATAAGAAATC	TACTTTTCAG	TAAACTGCAA	ATATGTGTGC	300
TTCAACCTAT	AACATATTCT	GTCACTTTGA	GCTTGTCATA	TTGACAGAGA	ATGAAAACTT	360
GATAAGACTC	GAG					373

- (2) INFORMATION FOR SEQ ID NO:681:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

GAATTCGGCC	TTCATGGCCT	AGAGCGACTT	CGACACCATG	CCAGACATTG	AGAGTGATAA	60
AAACATCATC	CGGACCAAGA	TGTTCCTTTA	CCTGTCAGAT	TTGTCCAGGA	AGGACCGGAG	120
AATTGTCAGC	AAAAAATATA	TTTATTTAAA	TTGGAACATC	ATCACCATTG	CTGTGTTTTA	180
CGCGCTGCCC	GTGATCCAGC	TGGTCATTAC	CTATCAGACA	GTAAGTGCTA	AACCTAGCCC	240
CAAACCCCTC	GAG					253

- (2) INFORMATION FOR SEQ ID NO:682:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOFOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

GAATTCGGCC	TTCATGGCCT	AATCGAGGAG	AATGGAGACC	AAACCTGTGA	TAACCTGTCT	60
CAAAACCCTC	CTCATCATCT	ACTCCTTCGT	CTTCTGGATC	ACTGGGGTGA	TCCTGCTGGC	120
TGTTGGAGTC	TGGGGCAAAC	TTACTCTGGG	CACCTATATC	TCCCTTATTG	CCGAGAACTC	180
CACAAATGCT	CCCTATGTGC	TCATCGGAAC	TGGCACCACT	ATTGTTGTCT	TTGGCCTGTT	240
TGGATGCTTT	GCTACATGTC	GTGGTAGCCC	ATGGATGCTG	AAACTGTATG	CCATGTTTCT	300
GTCCCTGGTG	TTCCTGGCTG	AGCTCGTAGC	TGGCATTTCA	GGGTTTGTGT	TTCGTCATGA	360
GATCAAGGAC	ACCTTCCTGA	GGACTTACAC	GGACGCTATG	CAGACTTACA	ATGGCAATGA	420
TGAGAGAATG	CTCGAG					436

- (2) INFORMATION FOR SEQ ID NO:683:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

GAATTCGGCC	TTCATGGCCT	AGTCCCCACT	TTATCTCTTT	AAACGGTTTC	TTTTTTCTTT	60
TTTTTTTTA	GACCTCTCAG	GGATGAAACA	TTTTATTTT	TAAACTAGTT	AATTTTTTTT	120
ATAACATTAA	CACATGCTGA	ATGCTTAAAT	CTTTTTAGAA	TTCAGAAAGG	TAAAATGAAA	180
GTCACCATTC	TCATTCTCAT	CATCTTACTC	CCAGAGATGA	TTGTTATTAA	TATTTCCAGA	240
AATTTTGCTT	GTATATGCAA	ACAGCAATAT	ATTGTAGCTG	CTCGAG		286

- (2) INFORMATION FOR SEQ ID NO:684:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

GAATTCGGCC	TTCATGGCCT	ACCCTTACCA	GATACTGAAT	CTGCCAGTGC	CTTATTTTGG	60
ACTTCTCAGC	CTCCTGGGCT	GGGTGAGGTG	GTTCACTACC	AGCCTTGGCA	CCATAGTGAG	120
ACTCCCATCT	CTACAAAAAA	ааааааааа	AAACTTTCTG	TTGTTTGTAA	GCTACCCAGT	180
TTATGGTATT	TTGTTACAGC	AACCCAAACA	GTCTGAGACG	TTTAGCTTAA	CTCCTGTATG	240
CACTAGATAC	AGTCTGCACT	TTGACATCAA	TCTCGA			276

- (2) INFORMATION FOR SEQ ID NO:685:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

GAATTCGGCC	TTCATGGCCT	ACTAAGAATA	GGAAAAAAAA	TAACACTATG	ATACCACAAC	60
CTTATTACAT	CAAACTGCTT	TGGGCTTTAT	CCTCTTTAAA	GTGTGCTCAG	GTGTTCAGCC	120
ACGAGGTTTC	TGACAGCCCT	CATAAGACCT	TCGAG			155

- (2) INFORMATION FOR SEQ ID NO:686:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

GAATTCGGCC TTCATGGCCT ACTTTGAAGA GTACGATTTC AAAACCAGCA ATTGGTGTGA 60 ATGCAAAAAC ATTTGTTGGC ACCATTTATT TAAAAAAAAA AAAAGCTGTA TGCAGCAGAA 120

AGCCTTATAC	AAGTTGTTTT	TCTTTTTTTC	CTTTTTCTTT	TTTTTGGTAC	CTTCATTTCT	180
GTTACTTTTA	TATAAAATTC	TCTGCAAAGG	AAGGCCTCTC	TTTGGACTAC	AATTTGGAGG	240
CAGCCACTTG	TTGTGCCTGC	TTCTGTTAAA	GAATGTGGAT	ATCAAGCCCC	CCCGACTCGA	300
G						301

- (2) INFORMATION FOR SEQ ID NO:687:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

GAATTCGGCC	TTCATGGCCT	AATTTTTACA	GAAATTATTT	CCACAATCAG	AAGTACTGTA	60
CTGATTGCAT	TTCTTTGTCT	CAAAAAGTTT	TCCTTATGTT	TCTCAAAGCA	GTATTTACAC	120
TAATTATTCA	ATTCTTATCT	TTCTTTCAGT	TTTCTCCAAT	AGACTGTGAG	ATCTTTGAGG	180
GCCAGGTTGA	CATGTCTCTG	ATACCTACAC	CCTATGCAGC	TCCTAGTGCA	GGACCTTGCA	240
GTGACAAGCT	CGAG					254

- (2) INFORMATION FOR SEQ ID NO:688:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

G	AATTCGGCC	TTCATGGCCT	AATATTTATT	TAGATGCTAT	TATTACTGTT	TGGACTTTTA	60
Т	TTTGGCAGG	CTTTGTTCCA	GACTGTAGGG	TTTTCCAATG	TGACTAATGA	CCACTCCTGC	120
С	TCTCCCGTG	GTGTATTTTG	GGCACCCTCC	CACCCGGCTG	CATACCCGGC	CAGGGCTCCC	180
Α	CAGAGACAA	GGAGGGCACA	GGTGTCTGCC	CCCTCTTTGA	AATCGATATA	CACACATCCA	240
_	GCACATGCG	GCCCACTCGA	G				261

- (2) INFORMATION FOR SEQ ID NO:689:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 214 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

GAATTCTAGA	CCTGCCTCGA	GCTTCTGGCT	GTTGTCTTTG	CTGGGCATCC	TTTTTACAAG	60
TGGAAGAACT	AGGATGGCTT	TCCAAAGTCT	TCTAGAAATG	AAGTTCTTTC	TCTGTGCAGC	120
TTTCCCCCTT	GGAGCAGGAG	TGAAGATGTT	TCATTATCTT	GGGCCTGGGA	AACCACTTCC	180
CCAGGCTTCT	CCCTCCCCC	ACCCCGACT	CGAG			214

(2) INFORMATION FOR SEQ ID NO:690:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GAATTCGGCC	TTCATGCCTA	CAAACTTAAA	AGTAAATCTT	TGGAAATCAG	ATAGTAGTCT	60
TGAAACTATG	GAAAACACAG	GAGTGATGGA	TAAGGTTCAG	GCAGAGTCTG	ATGGGGACAT	120
GTCTTCAGAT	AATGACTCAT	ACCACTCTGA	TGAATTCCTT	ACAAATTCTA	AGTCTGATGA	180
AGACAGGCAG	CTAGCTAACT	CATTAGAGAG	TGTAGGGCCA	ATAGATTACG	TTCTTCCTAG	240
TTGTGGTATT	ATTGCCTCAG	CGCCTCGATT	GGGCAGTCGG	TCCCAGTCTC	TTAGCAGCAC	300
ACTCGAG						307

- (2) INFORMATION FOR SEQ ID NO:691:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

GAATTCGGCC	TTCATGGCCT	ACTCCATATT	TATTTAGATG	CTATTATTAC	TGTTTGGACT	60
TTTATTTTGG	CAGGCTTTTT	TCCAGACTCT	AGGGTTTTCC	AATGTGACTA	ATGACCACAC	120
CTGCCTCTCC	CGTCGTCTCT	TCTGGGCACC	CTCCCACCCG	GCTGCATACC	CGGCCAGGGC	180
TCCCACAGAG	ACAAGGAGGG	CACAGGTGTC	TGCCCCCTCT	TTAAAATCGA	TCTACACACA	240
TCCACGCACA	TGCGACCCCG	AGGAAACGAA	ACCCACTCTA	GAAAACGCGA	CCTTGGCCGC	300
ACCTAAAGCA	GCCAGCCGTG	AGTGCAGACC	CCTTGGCCAG	CGTGGCGCAG	TGGCCCTGAG	360
CAGTAGTGGC	GTGTGTGTAG	ATCAAGTCGG	ATCTAGTCCA	GCTCGGTTCA	TTAGCGATCC	420
ATGTAATCTG	ACGTCATCTT	GTCTCGAAGT	CTCTTTTTTT	GGCCCAGGCC	TTGAAGAATA	480
CACTGGACTC	GAG					493

- (2) INFORMATION FOR SEQ ID NO:692:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

GAATTCTAGA	CCTGCCCCTG	CCTCCTGCAT	CCAGCCCCCA	ACATGGTGCC	AAAGCTTCCA	60
GAAGCCAAAA	AGCTTCTGAT	TTTTAAGGTA	GTGGGCATCT	CTCTCCTAAT	GACGAAGCTG	120
CTCAGCAACT	CCACCTGCCC	GCCGCAGGAA	GGAGCAGTCC	CCTGCTATCC	CTGCAGCCAC	180
TCCCAGCACA	CCCGCACACA	GCCAGCACCA	CCGCCCACTC	TCGAG		225

- (2) INFORMATION FOR SEQ ID NO:693:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

GAATTCGGCC TTCATGO	SCCT ACTGGCTCAT	ACAATACATC	AATAAGTATG	CAACTTTTCA	60
TTTGTTATTT CGTTGC	TGGA AGTGGGAAAT	ACCCCATCTT	CCCAGGAGTG	AAATGGTTCT	120
ACTITCTCTC CGTGGT	SCCC TGTATCATTA	CTCAGCTCTG	CTGCTGCTCT	CCGCAGCCCC	180
TAAAAGTAGC ATGGAT					240
GGCAGGTCGA G					251

- (2) INFORMATION FOR SEQ ID NO:694:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

GAATTCGGCC	TTCATGGCCT	AGTGTGTGTG	TGCGTGTGTG	TGTGTTTACA	TATAAAGTTT	60
				TGTTTGCTTA		120
				CTATGTTGTT		180
					TGATGCCCCC	240
TCTTTCATTC	CTGATATGAG	TAATTCTTAT	TCTCTTTTTG	TCTATCAGCT	CGAG	294

- (2) INFORMATION FOR SEQ ID NO:695:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

GAATTGGCCT	TCATGGCCTA	ATTGGGACCA	AATAGAGGCT	CACAGATATT	TGGATTATTT	60
TATGTGCTTA	TTATTAAATA	AGGAAAGCAT	TTTGTGATAT	GTGGAAGACG	CTATGTGAAG	120
TTTTACCTAT						180
AAACAAAGAA						240
GTCGAG		00.10.11.11				246

- (2) INFORMATION FOR SEQ ID NO:696:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

GAATTCGGCC	TTCATGGCCT	ACCCTAATAT	AAAAAGCATT	GTCACCATGT	TGATGCTGAT	60
GCTATTGATG	ATGTTTGCTG	TCCACTGTAC	CTGGGTCACA	AGCAATGCCT	ACTCTAGTCC	120
AAGTGTAGTC	CTGGCCTCAT	ACAATCATGA	TGGCACCAGG	AATATCTTAG	ATGATTTTAG	180
AGAAGCTTAC	TTTTGGCTAA	GGCAAAATAC	AGATGAACAT	GCACGAGTAA	TGTCTTGGTG	240
GGATTATGGC	TATCAGATAG	CTGGAATGGC	TAATAGAACT	ACGTTGGTGG	ATAATAACAC	300
CTGGAATAAC	AGCCACATAG	CACTGGTGGG	AAAAGCTATG	TCTCTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:697:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 220 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

GAATTAAATA	AGTTACTGAC	TTTGTGACTT	ATTTAATTCA	TATTAATATA	TTAGGCTTCC	60
CAACTGACGG	TGTTGCAGTT	GAGCTAGCTT	CCAGTTTTGG	AGAAACACAT	AGTTGATTAG	120
TTCTGTCAGT	AATTTTCAGG	GATATTAATA	TAACTTTGAT	ATTAGTGAGA	AATTTTCTTT	180
CAGTAGTAAA	ATGTTTTCTA	ACTTAGGAGC	TGTTCTCGAG			220

- (2) INFORMATION FOR SEQ ID NO:698:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

GAATTCGGCC	AAAGAGGCCT	AGCAGAGCTT	TCATATCCAC	GATGCGTTTT	CTGGCCGCCA	60
CGATCCTGCT	GCTGGCGCTG	GTCGCTGCCA	GCCAGGCGGA	GCCCCTGCAC	TTCAAGGACT	120
GCGGCTCTAA	GGTGGGAGTT	ATAAAGGAGG	TGAATGTGAG	CCCATGTCCC	ACCGATCCCT	180
GTCAGCTGCA	CAAAGGCCAG	TCCTACAGTG	TCAACATCAC	CTTTACCAGC	GGCACTCAGT	240
CCCAGAACAG	CACGGCCTTG	GTCCACGGCA	TCCTGGAAGG	GATCCGGGTC	CCCTTCCCTA	300
TTCCTGAGCC	TGACGGTTGT	AAGAGTGGAA	TCAACTGCCC	CAGTACAGTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:699:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

GCGATTGAAT	TCTAGACCTG	CCTCGCTTCC	CCACCCTTAC	TAACATTAAC	GAAAATAACC	60
CCACCCTACT	AAACCCCATT	AAACGCCTGG	CAGCCGGAAG	CCTATTCGCA	GGATTTCTCA	120
TTACTAACAA	CATTTCCCCC	GCATCCCCCT	TCCAAACAAC	AATCCCCCTC	TACCTAAAAC	180
TCACAGCCCT	CGCTGTCACT	TTCCTAGGAC	TTCTAACAGC	CCTAGACCTC	AACTACCTAA	240
CCAACAAACT	TAAAATAAAA	TCCCCACTAT	GCACATTTTA	TTTCCCCAAC	TCCTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:700:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

GAATTCGGCC	TTCATGCTTA	GCCTCAGCTC	TTTCTTCTGG	GTTGTTTGTA	TTTTCTTTTC	60
TGTCCCAAAC	AGTTTCCCCC	ACAAAAAGAA	CTTTATGTCT	TTCTCTGTCT	TCCCTCAGTC	120
CTTCCAGTCA	GCAGCCTGTG	ATTGGGCTTT	TCCCCTCAGA	AACGAACAAT	CCAGAACCCA	180
CTGTTTAAAA	CAACTGTATT	TTGCCTTGGG	AAGTCCCATT	GCCTTCCCTG	AAAACATTAA	240
ACATTCCTCC	GATCCCCAGC	CTGAGTCTCT	CTGTCTCTGG	GCCCCATCCT	GCTCCACAGC	300
AGGGCTGGTG	TGTCCAGCAC	AGAGTGACCC	TCCGATGCCC	TTTCCCACCC	GCCGCCCTGC	360
CTCCCTCGAG						370

- (2) INFORMATION FOR SEQ ID NO:701:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

GAATTCGGCC	TTCATGGCCT	AGGAAAGATC	TAATTATCAT	GGACCTGCGA	CAGTTTCTTA	60
TGTGCCTGTC	CCTGTGCACA	GCCTTTGCCT	TGAGCAAACC	CACAGAAAAG	AAGGACCGTG	120
TNCATCATGA	GCCTCAGCTC	AGTGACAAGG	TTCACAATGA	TGCTCAGAGT	TTTGATTATG	180
ACCATGATGC	CTTCTTGGGT	GCTGAAGAAG	CAAAGACCTT	TGATCAGCTG	ACACCAGAAG	240
AGAGCAAGGA	AAGGCTTGGA	AAGATTGTAA	GTAAAATAGA	TGGCGACAAG	GACGGGTTTG	300
TCACTGTGGA	TGAGCTCAAA	GACTGGATTA	AATTTGCACA	AAAGCGCTGG	ATTTACGAGG	360
ATGTAGAGCG	ACAGTGGAAG	GGGCATGACC	TCAATGAGGA	CGGCCTCGTT	TCCTGGGAGG	420
AGTATAAAAA	TGCCACCTAC	GGCTACGTTT	TAGATGATCC	AGATCCTGAT	GATGGATTTA	480
ACTATAAACA	GATGATGGTT	AGAGACGTTC	TCGAG			515

- (2) INFORMATION FOR SEQ ID NO:702:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GAATTCGGCC	TTCATGGCCT	AGGGGACCTG	ACGTTCACTG	TGGCCCAAAA	GATGGCTGAG	60
CCAGAGAAGG	CCCCAGCCCT	CAGCATCCTG	CTGTACGTGC	AGGCCTTCCA	GGTGGGCATG	120
CCACCCCCTG	GGTGCTGCAG	GGGCCCCCTG	CGCCCCAAGA	CACTCCTGCT	CACCAGCTCC	180
GAGATCTTCC	TCCTGGATGA	GGACTGTGTC	CACTACCCAC	TGCCCGAGTT	TGCCAAAGAG	240
CCGCCGCAGA	GAGACAGGTA	CCGGCTGGAC	GATGGCCGCC	GCGTCCGGGA	CCTGGACCGA	300
GTGCTCATGG	GCTACCAGAC	CTACCCGCAG	GCCCTCACCC	TCGTCTTCGA	TGACGTGCAA	360
GGTCATGACC	TCAAGCTCGA	G				381

- (2) INFORMATION FOR SEQ ID NO:703:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GAATTCGGCC	TTCATGGCCT	AGCTCCACTT	TCTCTGAAAA	TTTATTCATA	TTGTTAATTA	60
AATTTGTTTT	TATTATAGAA	ATAATATATT	GCATGATTTG	TAAAAATGCA	GAGGAACAGA	120
ATGGCACAAA	ATTATGTAAC	CCTTTCTATC	TCCCCTTGGT	GTACCTCCTT	AATCATACTT	180
CTCAGAACCA	TTGTCAATAA	TTTGCTGGGA	GTTCTTCTGA	TGGTTACCAT	CGTGACTGAT	240
AGATTTATTT	CCCAGGTTCA	AGCGGTTCCC	CTGCCTCAGC	CTCCCGAGTA	TCTGGGACTA	300
CAGGCATGCA	CCACCACTCA	GCTCGAG				327

- (2) INFORMATION FOR SEQ ID NO:704:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

GAATTC	GCC	TTCATGGCCT	TGCCTTTTTT	CTTTCACCAC	TTTACTACAC	ACAATTACTG	60
GATTAAT	CTC	TTTAATGCCG	AGATCTTTTT	TCCTTAGTGA	CACCTTAATC	ACTCTTAGCT	120
TAACATA	TAT	GGTCATCCAT	TACTGGGTTG	CCTCTGCCTT	TCCAGGATTG	GCTGCCACTG	180
CTCCTCC	ACA	TACCCTGTAT	TCTAGCCAAA	TGGAATCACT	GCTGTGTCCC	AAGCAGATTC	240
TTTATTI	CTC	TTGGCTGTTG	CTCTCTATTT	CTAATGCTAC	CTGCCCTTCA	AAACTCGAG	299

- (2) INFORMATION FOR SEQ ID NO:705:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GAATTCGGCC TTCATGGCCT ACTTGATTTG TGGCTTATCT CAAGTTACCA TTTTTCAGTC 60
AAGTCTGTTT GTTTGCTTCT TCAGAAATGT TTTTTACAAT CTCAAGAAAA AATATGTCCC 120

AGAAATTGAG	TTTACTGTTG	CTTGTATTTG	GACTCATTTG	GGGATTGATG	TTACTGCACT	180
ATACTTTTCA	ACAACCAAGA	CATCAAAGCA	GTGTCAAGTT	ACGTGAGCAA	ATACTAGACT	240
TAAGCAAAAG	ATATGTTAAA	GCTCTAGCAG	AGGAAAATAA	GAACACAGTG	GATGTCGAGA	300
ACGGTGCTTC	TATGGCAGGA	TATGCGGATC	TGAAAAGAAC	AATTGCTGTC	CTTCTGGATG	360
ACATTTTGCA	ACGATTGGTG	AAGCTGGAGA	ACAAAGTTGA	CTATATTGTT	GTGAATGGCT	420
CAGCAGCCAA	CACCACCAAT	GGTACTAGTG	GGAATTTGGT	GCCAGTAACC	ACAAATAAAA	480
GAACTAGTCT	CGAG					494

- (2) INFORMATION FOR SEQ ID NO:706:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

GAATTCGGCC	CTTCATGGCC	TACTCCCGAG	CTCTACTGAC	TCCCAAAAGA	GCGCCCAAGA	60
AGAAAATGGC	CATAAGTGGA	GTCCCTGTGC	TAGGATTTTT	CATCATAGCT	GTGCTGATGA	120
GCGCTCAGGA	ATCATGGGCT	ATCAAAGAAG	AACATGTGAT	CATCCAGGCC	GAGTTCTATC	180
TGAATCCTGA	CCAATCAGGC	GAGTTTATGT	TTGACTTTGA	TGGTGATGAG	ATTTTCCATG	240
TGGATATGGC	AAAGAAGGAG	ACGGTCTGGC	GGCTTGAAGA	ATTTGGACGA	TTTGCCAGCT	300
TTGAGGCTCA	AGGTGCATTG	GCCAACATAG	CTGTGGACAA	AGCCAACCTG	GAAATCATGA	360
CAAAGCGCTC	CAACTATACT	CCGATCACCA	ATGTACCTCC	AGAGGTAACT	GTGCTCACGA	420
ACAGCCCTGT	GGAACTGAGA	GAGCCCAACG	TCCTCATCTG	TTTCATCGAC	AAGTTCACCC	480
CACCACTCGA	G					491

- (2) INFORMATION FOR SEQ ID NO:707:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

GAATTCGGCC	TTCATGGCCT	ACCTTATCTT	CTTAACCTTT	CAAATACTTG	CAGATATTTT	60
GCTTGGTGCT	TCCCATCTAT	TGCAATACCC	CTTTAGATAA	AGTCAATTCT	TATCTAAAAT	120
CAAATTCATT	TTATTTGACA	ATGTTTACAA	ACAACCCCAG	GACGATAACA	ATTACACTCT	180
CAATACTGGC	ATCACACCTT	CACAATTACA	CTAACCCCAA	CCTAGGCCAT	GAAGGCCTCG	240
AG						242

- (2) INFORMATION FOR SEQ ID NO:708:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

WO 98/45436

PCT/US98/06955	
GAATTCGGCC TTCATGGCCT AGACAGAATT ACTGGGAACC ATTTTCCAAG TAGCCCACCA CAAAGGTTGT ATTTTGTCAA ATTGAAGGAG TCATCTGACT TTCCTTAATC ATAAGCTACA AATATAATAA GCTACATTAA TAGATTTTCT AATATTTATT TAACTTTGAA TTTCTGGAAA AAACCCAACT TGGTAATGAT TTATCATCTG AGCTTTGTT TTGGCTTTGG TATGCTAATT TTTGGCTTAG GATTTTATA TCTATTTCAT GAGTGGCACC TCGAG	60 120 180 240 285
(2) INFORMATION FOR SEQ ID NO:709:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 319 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:	
GCACGCCATG GGAGAAAAG AAGAAGCCAA AAAAACAGAA GACAAGTCTT TGGCAAAGCC TGAAACTGAT AAAGAACAGG ACAGTGAAAT GGAGAAGGGT GGAAGAGAG ATATGGATAT AAGTAAATCT GCAGAGGAGC CACAGGAAAA AGTTGACTTG ACTCTAGATT GGTTAACTGA AACCTCTGAA GAGGCAAAAG GAGGAGCAGC ACCAGAAGGA CCGAATGAAG CTGAGGTCAC TTCTGGGAAG CCAGAACAGG AAGTACCAGA TGCTGAGGAA GAAAAATCAG TTTCTGGAAC TGATGTCCAA GATCTCGAG (2) INFORMATION FOR SEQ ID NO:710:	60 120 180 240 300 319
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 190 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:	
GAATTCGGCC TTCATGGCCT AGACACATAC AAAGATAAGG CTTTGATAAA ATTCAAGAGT TATTTGTATT TTGAGGAAAA AGACTTTGTG GATAAAGCAG AGAAGAGCCT GAAGCAGACT CCCCATAGTG AGATAATATT TTATAAAAAAT GGTGTCAATC AAGGTGTGGC TTACAAAGAC ATTTCTCGAG	60 120 180 190
(2) INFORMATION FOR SEQ ID NO:711:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 199 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:	

GGATTGAATT CTAGACCTGC CTCGAGTAAG ACCCCTTTTT AAAATGACTC CCACTGTCTA

TTCCACAGCC GGTGTGCGGC ATGCTGATTC AATCCCCACA ACAGCCCAGG AGGTAGGCGC

CGTCCCATCC TCCTTTACAG GAGGGGAAAC TGAGGTTCAG GTGGTCAGAT GGTCAGCTGC

CTCCAAGACC ACGCTCGAG

826

60

120

180

199

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

GAATTCGGCC T	TTCATGGCCT	ACCTGTACCT	GTTTTATACT	TGCTTTTGCT	TCAGCGTTCT	60
GTGGTTGTCA A	ACAGATGCCA	GTGAGAGCAG	GTGCCAGCAG	GGGAAGACAC	AATTTGGAGT	120
TGGCCTGAGA	TCTGGGGGAG	AAAATCACCT	CTGGCTTCTT	GAAGGAACCC	CCTCTCTCCA	180
GTCATGTTGG (GCTGCCTGCT	GCCAGGACTC	TGCCTGCCAT	GTCTTTTGGT	GGCTAGAAGG	240
GATGTGCATT (CAGGCAGACT	GCAGCAGGCC	CCAGAGCTGC	CGGGCTTTTA	GAACACTCCT	300
CGAG						304

- (2) INFORMATION FOR SEQ ID NO:713:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

GAATTCGCCC	TTCATGGCCT	ACCCAATTCA	GTTTCCAGAG	GAGGTGGAAC	CTTCTGCAAC	60
CCAACAGGAG	GCCCCAATTG	AGCCTCCAGT	TTCTCCTATG	GAGCATGAAC	TTTCCATCAG	120
TGAGCAGCAG	CAGCCAGTTC	AGCCTTCTGA	GTCTTCTAGG	GAGGTCGAAT	CTTCTCTGAC	180
CCAGCAGGAG	ACCCCAGGTC	AGCCTCCAGA	ACATCATGAA	GTCACAGTTT	CACCTCCAGG	240
TCACCATCAA	ACTCATCATT	TAGATTCACC	CAGTGTCTCT	GTGAAGCCTC	CAGACGTGCA	300
GCTCACCATA	GCAGCAGAGC	CTAGTGCAGA	GGTGGGAACT	TCTCTAGTCC	GACCCCTCGA	360
G						361

- (2) INFORMATION FOR SEQ ID NO:714:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

GAATTCGGCC	TTCATGGCCT	ACCGAGATGG	AAATAACCTA	AGAAAAAGAG	GGCATCCAGC	60
TCCATCTCCC	ATTTGGCGTC	ATGCTGCTCT	GGGTCTGGTA	ACTCTTTGCC	TGATGTTGCT	120
GATTGGGCTG	GTGACGTTGG	GGATGATGTT	TTTGCAGATA	TCTAATGACA	TTAACTCAGA	180
TTCAGAGAAA	TTGAGTCAAC	TTCAGAAAAC	CATCCAACAG	CAGCAGGATA	ACTTATCCCA	240
GCAACTGGGC	AACTCCAACA	ACTTGTCCAT	GGAGGAGGAA	TTTCTCAAGT	CACAGATCTC	300
CAGTCTTAAC	CTCGAG					316

(2) INFORMATION FOR SEQ ID NO:715:

- (i) SEOUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

GAATTCGGCC	TTCATGGCCT	AGGCAATATC	AAGGTTTTAA	ATCTCGGAGA	AATGGCTTTC	60
GTTTGCTTGG	CTATCGGATG	CTTATATACC	TTTCTGATAA	GCACAACATT	TGGCTGTACT	120
TCATCTTCAG	ACACCGAGAT	AAAAGTTAAC	CCTCCTCAGG	ATTTTGAGAT	AGTGGATCCC	180
GGATACTTAG	GTTATCTCTA	TTTGCAATGG	CAACCCCCAC	TGTCTCTGGA	TCATTTTAAG	240
GAATGCACAG	TGGAATATGA	ACTAAAATAC	CGAAACATTG	GTAGTGAAAC	ATGGAAGACC	300
ATCATTACTA	AGAATCTACA	TTACAAAGAT	GGGTTTGATC	TTAACAAGGG	CATTGAAGCG	360
AAGATACACA	CGCTTTTACC	ATGGCAATGC	ACAAATGGAT	CAGAAGTTCA	AAGTTCCTGG	420
GCAGAAACTA	CTTATTGGAT	ATCACCACAT	CTCGAG			456

- (2) INFORMATION FOR SEQ ID NO:716:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

GAATTCGGCC	TTCATGGCCT	AGATCATTCA	GTGGCTCACC	TAATATCACA	GAACAAGTGG	60
TGGAGTCAGA	ATCTTTTATC	TAAAGGAGAT	ATTTTCATCC	TTAGATTAAT	GTCCTCTTCA	120
			ATTGCTGTTC			180
AACTTCATTT	GTAACGGAAG	AATCAAAATT	AGAGCCCGGG	TCTCATCCTA	CGGTATCTCG	240
TCCTGAACCT	CTGGTCTCCC	TCAAGAATGA	CTCAGAAGGA	CGGACTCGAG		290

- (2) INFORMATION FOR SEQ ID NO:717:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

GAATTCGGCC	TTCATGGCCT	ААААААААА	GCCTTTTAAA	CTTGTAGGAA	TTAAGAAATA	60
AGAATAACCT	ACAAAATGCT	AGCAAAATTT	ATCTCATTTT	TTTTCATTGT	ATTTTCAGGT	120
			CTAGAACTTG			180
			CCAACTTCTC			240
			AATCGCTGGG			300
CTCGAG						306

- (2) INFORMATION FOR SEQ ID NO:718:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

GAATTCGGCC TTCATGGCCT	AATATTTATT	AAATGACTTG	GTAGATAGAG	CAACTGACTG	60
AATATATTAT TTTTTAGGAA	GAAGAAGAAC	ATTTTTGCTT	TTAAATTAAA	TCTTATTTTA	120
TTTCTCTTTC CCCTTTTATC	CAGGGTAGGT	CCAGGTAAAG	CCAAAGGCCT	TATCCTTATC	180
TACACTGCTG GGGGACACAA	CACAAGAATT	TCAAGTTCAA	GTATTATTTC	TCATTTTGAG	240
TAATTTTGTT CTCATTTTGT	TCCAGTTCTC	ACTCTCAGAA	AAAGATTACT	CGAG	294

- (2) INFORMATION FOR SEQ ID NO:719:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

GAAACAATAG AAACACTGAG	AGAAAATTCA	GAGAGACAGA	TTAAGATACT	GGAACAGGAA	60
AATGAACATC TGAATCAAAC	AGTGTCTTCC	TTAAGGCAGC	GGTCCCAGAT	AAGTGCAGAA	120
GCAAGAGTGA AAGACATTGA	AAAAGAAAAC	AAAATTCTTC	ATGAATCTAT	CAAAGAAACA	180
AGTAGCAAGC TAAGCAAGAT	TGAATTTGAA	AAAAGACAAA	TTAAAAAAGA	ATTGGAACAT	240
TATAAAGAAA AAGGAAGCTO	GAG				263

- (2) INFORMATION FOR SEQ ID NO:720:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

GAATTCGGCC	TTCATGGCCT	ACCTGCCCTT	CTGCGGTCAC	AGCTGCCTGC	TGGGTGGGAG	60
TCCGGGGGAA	TGGTATGTGT	GGTCACCAGA	GGGCACTGAG	TGGGCTTCAG	TGGCATGTGA	120
ATCCTGGCAG	AGTCTCGGAT	CCCCGATGGG	GAGAGGAGAA	AGCACAAGCC	AAGACAACGA	180
GTGGGGGAAG	GAGGCAGGGG	CTAAGTGACG	GGTGGGGGGT	GGGGGTGGGA	ACTCCAGTGT	240
ACACATTGAC	AGTCTCTATG	TTGGCTTCAC	CAGCGCTTCT	CTGTTTGTCT	CGTCCCTGGA	300
TTTCTAACAG	TTGCCTCGAG					320

- (2) INFORMATION FOR SEQ ID NO:721:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

GAATTCGGCC	TTCATGGCCT	AGTCGGGAGT	GTCTTAAGCT	TTTCATTTAA	CCTAAAGTAC	60
AGAGTCTGCT	CTGTAGAAAT	ATGTCATTAA	GAAAATATTT	GAGTCCCAGC	TCCTCCTTGT	120
TGTGTAATGT	CTGATAATTT	CACTCATTAA	ATTACCCAGA	CAGACCATAA	AGTCCTCTCA	180
GTTTGCATCA	CCTGAAAGTC	AGTCAGCCTG	GGCTGTGAGG	ATTGTGAGGT	AGAACTCACT	240
GTGGAAGGAC	GGCATTAGGG	AAGACTTTAG	GAAAATGGAG	CGGAACCTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:722:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 371 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

CTCGAGACCT	GTGTGCGCAG	GCAACGGGGA	AACTGGAAAT	GCGTTGACAA	ACTGACGCAA	60
AACTGGGCCC	AACAGCCACA	AGGCACTGGT	CGTTTTCCAC	TGGGCAAAGT	TCAGTCGCAT	120
TTCTTTCTGT	TCTCTTTCTT	TCTTTCTTTT	CTTTTTTCTC	TTTCTTTCTT	TCTTTCTTTC	180
TTTCTTTTTT	CTTTCTCTCT	CTCTTTCTGT	CTGTCTCTCT	CTTTCTTTCC	TTCTTTCCTT	240
CCTTCCTTCT	TTCTTTCCTT	CCTTTCCTTT	CTTTCTTTTT	TTTTTCTTTT	AAGAGACGGA	300
GTCTCGCTCT	GTTACCCAGG	CCGGAGTGCA	ATGGCACAAT	CTCGGCTCAC	TAGGCCATGA	360
AGGCCGAATT	С					371

- (2) INFORMATION FOR SEQ ID NO:723:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

GAATTCGGCC	TTCATGGCCT	AGTTCCTTGG	TGGTTTGAAA	GTTAGAGAGA	TCCTGATAAG	60
CATAATGACC	AACATAGAAG	AGATTAAGTA	CCTTTACTCA	TAAATGTGAG	TTCACAGACT	120
TCAGGTCTAA	ATTCGTAACA	ATATTTAAGA	TGTATATGGC	TTAAAGTGCT	GGTAGTTTTG	180
ATTAGAATCC	ATAGGTTTCT	AGTCACTGCT	CTTTTCATTA	TTTGAGTTTT	TATGTATTTT	240
TTAACTAGAA	ATAAGAGGGT	CTCGAG				266

- (2) INFORMATION FOR SEQ ID NO:724:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

GAATTCGCCT	TCATGGCCTA	GAAAGTTTTT	CAAAAATTCT	TCAATTGTCT	CTGGTTGATG	50
CAACTTAATT	TTTTGCTGAG	AGAGACCTTA	AATGTAATTA	GTATTGTATA	ATTAGCCTGA	120
TTAATCTGAC	CTGTACATCA	CGAGTCACTT	GTCTTTAGCC	CAAGAGGAAT	GCTTCCTTTC	180
TGATTTGAGG	CAGTGGCCCA	TCATTGCTTC	TAGCAACCTT	CCTACTTACT	AGATGACCTT	240
GAGTCAAGGT	TTCTGTATAT	ATGATTTCAG	ATTTGTCCCC	TAGAACTGAA	AAAGGGTAGG	300
AGAGGCAAAG	ATAGGAAAAA	TATTTTTTAA	AATTTTTAA	GTATTTTATT	TTTATTGGGA	360
AAATATTTAT	TGTAAGTCTT	CCATTTGTTA	TCCTTCTGCC	ACTAGCATTA	CGTAAAAAGT	420
AAAAAGAGCT	TTACATCAAA	AAGCACAATG	AAACTTTGTA	TCCTTAAGTC	CGTACTCGAG	480

- (2) INFORMATION FOR SEQ ID NO:725:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

GAATTCGGCC	TTCATGGCCT	AGTCGGAGGT	GTAGGAGGG	CCGTGGAGGT	CCAGGTGACT	60
GCTTAGAAAA	CTGCACAGCA	TCTGATGAAA	TTAGCGAATA	AGAACATCAA	CCATGTCTTA	120
CACTCCAGGA	GTTGGTGGTG	ACCCCGCCCA	GTTGGCCCAG	AGGATCTCTT	CTAACATCCA	180
GAAGATCACA	CAGTGTTCTG	TGGAAATACA	AAGAACTCTG	AATCAACTTG	GAACACCTCA	240
AGATTCACCT	GAATTGAGGC	AACAGTTGCA	ACAGAAGCAG	CAGTATACTA	ACCAGCTTGC	300
CAAAGAAACA	GATAAGTACA	TTAAAGAGTT	TGGATCTCTG	CCCACCACCC	CCAGTGAACA	360
GCGTCAAAGG	AAAATACAGA	AGGATCGCTT	AGTGGCAGAG	TTCACAACAT	CACTGACAAA	420
CTTCCGCAAG	GACTCGAG					438

- (2) INFORMATION FOR SEQ ID NO:726:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

GAATTCGGCC	TTCATGGCCT	AGCTACCTAT	CTACAAAAAC	TCCTGGATCC	TTTATTACGA	60
ATTGTGATCA	CATCCTCTGA	TTGGCAACAT	GTTAGCTTTG	AAGTGGATCC	TACCAGGTTT	120
GTCATCTTTT	CACATAGAAC	CGCTGTTTTT	TGTTTTTTT	TTTTGTTTGT	TTGTTTTACT	180
AACACTGCAT	GAAGCAAGGC	ACCTTCTCCC	CTTGATCATT	AAAATTAGTT	TTTAATTA	240
AAAGTTATAT	ACAAATACAC	GTTTCTTTAA	TGATATCTGT	AATTTTTTTT	TAAGGTATCC	300
TTTTATTTGC	CTTAGATCCA	GGGACAAACT	AGAGAAAGGT	GTCTTTGACT	TCCACCTCCA	360
GAGACTGTTA	CTAGTTAAGT	CTGTTCCCCT	GTCCTTTTTC	CATGCACCGC	CTCGAG	416

- (2) INFORMATION FOR SEQ ID NO:727:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

GAATTCGGCC	TTCATGGCCT	AAGGAGGTCC	ATGAGGAAGT	GTCCCAGCCT	GTCAGTGCAT	60
CTCATGAGTT	CGCTGAGTGA	TCAGCAGACA	GTTCCAGGAA	GTGAACAAGT	CCAAGAGGAC	120
TTCTGATTAG	TCCACAGTCT	CCTCTATAGG	CTCAGTAGAT	GAAGGCGTTT	CTGAGGGCTT	180
GCCTACACTT	CAAAGCACGT	CTAGCACTAA	TGCTCCTCCG	GATGATGATG	ATCGATTGGA	240
AAATGTTCAG	TATCCCTACC	AACTCTACAT	TGCTCCTTCC	ACCAGCAGTA	CAGAGCGACC	300
AAGTCCAAAT	GGTCCCGACA	GACCTTTTCA	GTGTCCAACC	TGCGGGGTGC	GATTCACCCG	360
TATTCAGAAC	CTAAAGCAGC	ACATGCTCAT	CCACTCAGGA	ATTAAACCAT	TTCAGTGTGA	420
CCGCTGTGGG	TCTCGAG					437

- (2) INFORMATION FOR SEQ ID NO:728:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 451 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

GAATTCGGCC TTCATGGCCT	AGATCACTGC	CCTTTCAATA	ACACTCTTGC	CTCTAGAATC	60
ATATGTTCAA AGTATGAATA	CACACCTAGC	ACATAGTAGG	TGCTCAAATA	TTAATTTCCT	120
CCTTGCCTTC CTTATCTACC	CTGTGTCCTC	CATTTCCCCG	TATGATTCCA	ACCCAATATA	180
GCAAATGACA TTTACATGTT .	ATGAAAACAT	CTATTGGGTA	AAATCAGATC	TTGGATAAAG	240
AAATTCTGAC TTTTATATAA	GCTTTTGGTA	GACAGAAAAA	ACAGAAAGGT	ATTCGTTGGT	300
AGAACATTTT TAAGTTCAGG	AAAGAAAGCT	GGAATAATAC	TACGTAACTT	TGTCCAGGTT	360
ACTTTGACTG AAACACGTTT	TTGGTGGATT	TCTTTTCCTC	AAAGAACTCT	CTAAATGCAA	420
CTCCTTGCTG GATTCCTCAC	CCGATCTCGA	G			451

- (2) INFORMATION FOR SEQ ID NO:729:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

GAATTCAACC	ATTAAAGATA	ATTTATATTA	GTGTTTCTAT	AACTTCTAAA	ACATCTTTTG	60
ATAAGGATAA	TAATCTCATT	GTCATTCTGT	ACTGATATTT	GGATATAATC	CTAGCAGGGC	120
ATAGCTCTGA	TTAAGAACAA	TTGAACCATT	CAATTTTTTA	TTAGCCTCTA	TTTTCACTAG	180
CCAGGATATT	TTCATGAAAC	TTTTTTAGTTT	CAAAGCAAGT	TTTTTCTTTC	CAATAGAAAG	240
TGTTATATTA	GTAAACAATT	TTGTCTTCTG	CCAAGACCAG	CTCAGTCGGG	AAGATCCTAA	300
CCCAGTGGCA	AAACTCGAG					319

- (2) INFORMATION FOR SEQ ID NO:730:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

GAATTCGGCC	TTCATGGCCT	AGGGAAGAAT	AAAGAACAAA	ACCCAAAACT	TTGGACCTTA	60
AAAAACCCAG	GCTGGCATTT	TAGTAGCAAT	TGGGTGTGTT	CGGTTTTGAA	TATATTTGTA	120
TATACATGCC	TCCATGTGCT	TTGGCCTTCT	GGTATCTTCA	CCAGATGCTG	CCTTTTTTTT	180
TTTTTTTAAC	AAGTTCCTGT	TTCACTTTTC	CAGCTAGCTG	CTGGGTATCT	CCAACAAAAT	240
ATCTCATAGA	TCTCCCAACT	GTAATGTATT	CAAGCCAAAA	ATCAGCTCTG	CCCATTCTCC	300
ATCCCAAAGC	CCCTCCTCTT	GGTTACCAGA	CAACCTTAAC	CAAACCACTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:731:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 base pairs
 - (B) TYPE: nucleic acid
 - (C, STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

TTCATGGCCT	AGAGGAGGAA	GGCCTTCGTA	AAGGTTGCAT	CTCCGTCCCT	60
GGACCCGCGG	GAAAAAAAAA	AATCCAACAC	CCAGGCCCCG	CGGCTAGCCC	120
GCTCTCTCCG	CTCGATTTTG	TCACCGTTAT	GTGGGAAGCG	AATCCATGTA	180
CGAGTCTTTG	AGCCGTGCTA	TACCAGTTTG	TCCAGATTGT	TTATACTAGC	240
ACGGTGAAGA	CCTGCCTTCC	CTCTGGGAAT	CTGGAGCTTC	AGTAACAGGA	. 300
AAAGCAGAAG	AATTATTTTC	TAAAACAACA	AACAATGAAG	TGGATGACAT	360
GATACCCAGC	TCGAG				. 385
	GGACCCGCGG GCTCTCTCCG CGAGTCTTTG ACGGTGAAGA AAAGCAGAAG	GGACCCGCGG GAAAAAAAAA GCTCTCTCCG CTCGATTTTG CGAGTCTTTG AGCCGTGCTA ACGGTGAAGA CCTGCCTTCC	GGACCCGCGG GAAAAAAAA AATCCAACAC GCTCTCTCCG CTCGATTTTG TCACCGTTAT CGAGTCTTTG AGCCGTGCTA TACCAGTTTG ACGGTGAAGA CCTGCCTTCC CTCTGGGAAT AAAGCAGAAG AATTATTTTC TAAAACAACA	GGACCCGCGG GAAAAAAAAA AATCCAACAC CCAGGCCCCG GCTCTCTCCG CTCGATTTTG TCACCGTTAT GTGGGAAGCG CGAGTCTTTG AGCCGTGCTA TACCAGTTTG TCCAGATTGT ACGGTGAAGA CCTGCCTTCC CTCTGGGAAT CTGGAGCTTC AAAGCAGAAG AATTATTTTC TAAAACAACA AACAATGAAG	TTCATGGCCT AGAGGAGGAA GGCCTTCGTA AAGGTTGCAT CTCCGTCCCT GGACCCGCGG GAAAAAAAAA AATCCAACAC CCAGGCCCCG CGGCTAGCCC GCTCTCTCCG CTCGATTTTG TCACCGTTAT GTGGGAAGCG AATCCATGTA CGAGTCTTTG AGCCGTGCTA TACCAGTTTG TCCAGATTGT TTATACTAGC ACGGTGAAGA CCTGCCTTCC CTCTGGGAAT CTGGAGCTTC AGTAACAGGA AAAGCAGAAG AATTATTTTC TAAAACAACA AACAATGAAG TGGATGACAT GATACCCAGC TCGAG

- (2) INFORMATION FOR SEQ ID NO:732:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

GAATTCGGCC	TTCATGGCCT	ACTCCGTCTC	CAAAAAAAAA	AAAAAATAGT	GTTCAGCAAG	60
GTTGAAGCAT	AAAAGGTTAA	TAGCCAGAAT	CATTTATCAA	TTGTATTTCT	ATACATCTAC	120
AAGACACAAT	CTGAAAATGA	AATTAGAGAA	ACAATTTCAC	TGGGCAACAA	GAGCAAAACT	180
TCATCTCAAA	ATAATAATAA	TAATAATAAT	AATCATCATC	ATCATCATCA	TCTACAATGT	240
CATTTCCCAT	CCAAGTCTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:733:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 503 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

GAATTCGGCC	TTCATGGCCT	AGACCTGCCT	CGAGCTCCTG	GCCTCGGGCA	CTCTACCCGC	60
TTCAGCCTCC	CAAAGTGCTG	CGACTGATTA	CAAGTATGAG	CCACTACGCC	TGACCATAAC	120
ATGTAAAATT	ATGGCAAATG	GTAATTCACA	GCTCAATTCT	AAAATGTGAT	GAAATTTAAA	180
TCAGAAAGGC	CAAATGAGTC	ACTTTTTCTT	AACACTAAGA	ATTATAAACC	TTTAAATTTC	240
TTTTGTACTG	TAATTTTTTA	TGTGACATGT	ATATGCTTTT	TAATATGTGT	GATAGGATGA	300
GGGGCAGGAG	AGGGGGCTCT	AGACATGAGG	GTGCCTGGGG	CCTCTGTAGA	CCTTCAGATG	360
GCCCTGGGTG	TTATAGCAAG	AGCTGGTCTA	CATCTAATAC	TACTGCAGGT	GCTGTCATGA	420
ATTCTTTGTA	TAATTCTTTG	TATATTAAAT	GACATTATTC	TATGTATAAT	GTCATTTAAT	480
ACTTATAACC	TACTTTCCTC	GAG				503

(2) INFORMATION FOR SEQ ID NO:734:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

GAATTCGGCC	TTCATGGCNT	AATGGATTCA	TTTTTTTCA	GCAGCATGGC	ATAGTGGATT	60
ATGAAATCAA	AATTAACTAC	ATGTGGAGTC	NTACATTGAA	ATCCCCCTTC	AACAAAATAG	120
TATACTATGA	GTATTTTTAA	ATTATTTAAC	CCCTCCGAAC	ACCAATTTGT	ACACGAATAA	180
AACTTGACAC	AACAGGATTT	TGTGGGGCGT	GAGTAACACA	ACATATACAA	AAGCACCTTA	240
TAAAGTGTTC	TATATAGCAA	CTTCTCTCTC	AGTTTGAACG	GGTCTCAGGA	TAAATTAGCA	300
AATATGAATT	CTAACCTTTG	TACTTACATT	TTAATTCTGC	TAAGTGTGTG	AACCCCAATT	360
TAGCAATTAA	TTATTTATA	TCCAGAATGT	TTTGACCCTG	AGCATATTTT	TAAAAAGCAC	420
AGTAGCTCGA	G					431

(2) INFORMATION FOR SEQ ID NO:735:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

AAAAGTGACT GAAAGTTTG	TAGTGTTTTT	AGTACCGATA	TTTACTGGTA	GTAAATATAT	60
ACTAAATCCA GTGAAATATC	ACTTCTCTAA	CTGAGCTTGA	CATATCCTGG	TTATATCTCA	120
TGGCAGCTGA AAACTAGAAA	TGACTTATTT	TTACCTTGTA	GCCACAGCAC	ACTTGAGGTT	180
ATTCTTAGGT TTTTGTTAG	GACAAAGCTG	GTTAGTGACT	CCTGGATTAA	GAATTATGAG	240
TGATCCCATA ACCCTCGAG					259

- (2) INFORMATION FOR SEQ ID NO:736:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

GAATTCGGCC	TTCATGGCCT	AAAGGATATT	GGCATGTTCC	TCTTCTCATC	AATATCCTAA	60
			AAAAATTAAC			120
			TTTTGTGAAA			180
			CAGACATATG			240
			TTGATATTGA			300
			GGCAAGCATC			360
GTTGTAGGGG	AGAGACTGTG	TATATATTT	TTAAAAGCAA	TCCAATGGAT	TTGTTTTTGT	420
	GAAACAACTC					443

- (2) INFORMATION FOR SEQ ID NO:737:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

GAATTCGGC	T TCATGGCCTA	CAAAAGATGG	CCCTAAGCCT	GGCCTCTAGC	TTTCACTCGT	60
	T TCAGACCTAA					120
	G GCTACTTTTT					180
	T CCGTATTTGA					240
GTTTTGAAA	A ATTGCCATAA	ATTTGGTGCC	ACTTTCTTTT	ATTTATTTGA	CTGAGTTAAT	300
	TAACATTTTA					360
	A TAACTTGTCT					420
	A ATAGCTAACT					480
AG						482

- (2) INFORMATION FOR SEQ ID NO:738:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

GAATTCGGCC	TTCATGGCCT	AGATTGTCAG	TTTATCTTAG	ATGATGAGGA	AGCAGTACCA	60
AGAAAACACT	TGGGGGTTGA	TACAACAGGC	ACATGAGCCC	TTAAAACTCC	TTCCTGTTTT	120
TTTTTTTT	TTTTTCTCTT	AGGTAGATTA	GTGCATTTAA	AGCCTGAAGT	TAATTTGACC	180
TAAAATTTTT	ATAAGTCTTT	GCAGAAAGTT	CACTTGTTTC	CTGAAATCAT	CTCCTTGATA	240
			GGAATGATAT			300
			ACATGCCTGA			360
			AGGATAAATG			420
			TGACTCAGCA			474
,,0,,,,,,,						

- (2) INFORMATION FOR SEQ ID NO:739:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

GAATTCGGCC	TTCATGGCCT	AGCCTTTGAG	ATCAATACCT	GTGAAAAGTA	GGGAAAGAAA	60
GCAGATGAGG	CATAGGGAAA	AGGTGGACTG	CCACAGGCAA	CCCAGCGAAC	CTCACCAGCA	120
GCTCTGGAGC	TAAAATAGCT	CTTCAGAATT	GTCCAGAGTT	GGGCTGAGGA	GGCCAGAATT	180
TTATTTGTGT	TCCCACGATG	ACGACTTCGA	G			211

- (2) INFORMATION FOR SEQ ID NO:740:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

GAATTCGGCC	TTCATGGCCT	AAATACCTTA	ATGGTGGTAG	AGCCTTTACC	TGTAGCTTGA	60
AAGGGGAAAG	ATTGGAGGTA	AGAGAGAAAA	TGAAAGAACA	CCTCTGGGTC	CTTCTGTCCA	120
GTTTTCAGCA	CTAGTCTTAC	TCAGCTATCC	ATTATAGTTT	TGCCCTTAAG	AAGTCATGAT	180
TAACTTATGA	AAAAATTATT	TGGGGACAGG	AGTGTGATAC	CTTCCTTGGT	TTTTTTTTGC	240
AGCCCTCAAA	TCCTATCTTC	CTGCCCCACA	ATGTGAGCAG	CTACCCCTGA	TACTCCTTTT	300
		ACTTGATAAA	TAACTTATAG	GTGATAGTGA	TAATTCCTGA	360
TTCCAAGAAT	GCTCGAG					3 7 7

- (2) INFORMATION FOR SEQ ID NO:741:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

GAATTCGGCC	TTCATGGCCT	AAGGCGTTTG	GGGTTTCCTA	GTTGTGCTGC	TGCTCTTGCC	60
TAGGGAATCT	GCTCTTGCTT	TGGCCTCTTT	CCTTGGGGCA	AGAGTGAGGG	GGACAGGGAG	120
						180
						240
CCCTACTGAC	TAACCACCTT	CTTAGCCAGG	CCATAGCCAT	TCAGCAGTGC	CTCCTTCCTC	300
TGGGTAGACA	AACAGCCTTG	AACAGAAAGG	TGGAACACTC	GAG		343
	TAGGGAATCT CTTCAAGTCA ACCCAGCCAT CCCTACTGAC	TAGGGAATCT GCTCTTGCTT CTTCAAGTCA GCCCTCCATG ACCCAGCCAT GCCAATCCCC CCCTACTGAC TAACCACCTT	TAGGGAATCT GCTCTTGCTT TGGCCTCTTT CTTCAAGTCA GCCCTCCATG TTGAAGTTTG ACCCAGCCAT GCCAATCCCC ATGATCACCA CCCTACTGAC TAACCACCTT CTTAGCCAGG	TAGGGAATCT GCTCTTGCTT TGGCCTCTTT CCTTGGGGCA CTTCAAGTCA GCCCTCCATG TTGAAGTTTG GTAGAAGCTC ACCCAGCCAT GCCAATCCCC ATGATCACCA ATCCGAACCC CCCTACTGAC TAACCACCTT CTTAGCCAGG CCATAGCCAT	TAGGGAATCT GCTCTTGCTT TGGCCTCTTT CCTTGGGGCA AGAGTGAGGG CTTCAAGTCA GCCCTCCATG TTGAAGTTTG GTAGAAGCTC TGCCCACACC ACCCAGCCAT GCCAATCCCC ATGATCACCA ATCCGAACCC CTTGAAGTAG CCCTACTGAC TAACCACCTT CTTAGCCAGG CCATAGCCAT TCAGCAGTGC	GAATTCGGCC TTCATGGCCT AAGGCGTTTG GGGTTTCCTA GTTGTGCTGC TGCTCTTGCC TAGGGAATCT GCTCTTGCTT TGGCCTCTTT CCTTGGGGCA AGAGTGAGGG GGACAGGGAG CTTCAAGTCA GCCCTCCATG TTGAAGTTTG GTAGAAGCTC TGCCCACACC TTGGACTGGA ACCCAGCCAT GCCAATCCCC ATGATCACCA ATCCGAACCC CTTGAAGTAG AATTTTCATA CCCTACTGAC TAACCACCTT CTTAGCCAGG CCATAGCCAT TCAGCAGTGC CTCCTTCCTC TGGGTAGACA AACAGCCTTG AACAGAAAGG TGGAACACTC GAG

- (2) INFORMATION FOR SEQ ID NO:742:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

GAATTCGGCC	TTCTGGCCTA	GAGTCCTTGT	TGTCCTTTGC	AAAGGTTGCT	CATCACCTCT	60
CCCCTCCCTC	TGGCTCTTTT	CCGTGGTGAT	GCATAGTTCA	ATGCGCCCAG	GAAGCTTCAT	120
GATGAGGCCG	TCACCCAAAC	TAGCAGCCCT	CCTTTCCTTC	TTTCTTTGCC	AAGTGTCCTG	180
GACATCAGCT	CTTCCTCAGT	CTTTGACTCT	AAATAAAGAA	CTTGAATTTC	ACCATTCAAC	240
TGAAATCCCT	CTAACCTCG					259

- (2) INFORMATION FOR SEQ ID NO:743:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

GAATTCGGCC	TTCATGGCCT	ACACCGTCGC	CATTGCCAGA	AAGAGCGATT	TATGGCTTTG	60
TTCTTTTCTT	AAGCTCCCAA	TTTGGCTTCA	TACTTTACCT	CGTGTGGGCC	TTTATTCCTG	120
AATCTTGGCT	AAACTCTTTA	GGTTTAACCT	ATTGGCCTCA	AAAATATTGG	GCAGTTGCAT	180
TACCTGTCTA	CCTCCTTATT	GCTATAGTAA	TTGGCTACGT	GCTCTTGTTT	GGGATTAACA	240
TGATGAGTAC	CTCTCCACTC	GACTCCATCC	ATACAATCAC	AGATAACTAT	GCAAAAATC	300
	GAAATACCAA					360
	AATGTTCTTT					420
	TAACACCAAG					450

- (2) INFORMATION FOR SEQ ID NO:744:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

GAATTCGGCC TTCATGGCC	T AAATCTTCAG	GGTCTTAACT	TAGTTTTTGA	TCCCTAAAAT	60
TAGTGCTGCA TATGTAGAC	T CAGAAACCTC	ACGTAAAAAT	TTAAATTGGC	CTCAGGTTGG	120
CAATGTTCCA AGGCAATGO					180
TACAGATAAA ATCCCAAGO					240
GAG					243

- (2) INFORMATION FOR SEQ ID NO:745:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi)	SECUENCE	DESCRIPTION:	SEO	TD	NO: 745

AAGCGAGGCC	CTGGGGGACA	ACGTGAAACA	ATACTGGGCT	AACCTAAAGC	TGTGGTTCAA	60
GCAGAAGATC	AGCAAAGAGG	AGTTTGACCT	TGAAGCTCAT	AGACTTCTCA	CACAGGATAA	120
TGTCCATTCT	CACAATGATT	TCCTCCTGGC	CATTCTCACG	CGTTGTCAGA	TTTTGGTTTC	180
TACACCAGAT	GGTGCTGGAT	CTTTGCCTTG	GCCAGGGGGT	TCCGCAGCTT	CTCGAG	236

- (2) INFORMATION FOR SEQ ID NO:746:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 215 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

GAATTCTAGA	CCTGCCTCGA	GCCTGCAGAC	ATCTCCTCCT	TCTTTGTGGT	TCTGGGAGCC	60
ATTCTGTGCC	TCTAAGGTCC	TCTTTCTTTT	TTCTCACCAA	TACACATATT	TTCTGTCCTT	120
CGCAATTCTA	TTAAACCTCA	CATTTGATGG	TTGTTTTCTT	AAAATTCCTT	TACTTGGTTC	180
CTGCATTCCT	CATTCCTTCC	CAGCACAATC	TCGAG			215

- (2) INFORMATION FOR SEQ ID NO:747:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double .
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

GAATTCGGCC	TTCATGGCCT	AGAAGAAAAC	CCATCAGATA	TTATAATAAG	ACAATAACTC	60
AATTTCAGAC	TTGTAAACAA	AGGTGACATT	AATCTATTGA	AATGTGGGAA	AATAGTCAAC	120
CTGTATCCTT	CTCATACCAT	AAATCAGCAT	GTTTGATCAC	TGGAAGCTTC	ATTTTGATGA	180
TTAGCAGTCA	TGTATTGAGG	CTAAATGATA	TGTTTGTCGC	ACAGCATCTC	GAG	233

- (2) INFORMATION FOR SEQ ID NO:748:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

GAATTCGCCT	TCATGGCCTA	CACAGGAGAA	AAACCCTATG	AATGTAGTGA	ATGTGGGAAA	60
ACTTTTGTTC	AGAAGTCCAC	CCTCAGAGAT	CATCACAGAA	TTCACACAGG	GGAGAAATCC	120
TTTCAATGCA	ATCAATGTGG	AAAAACATTT	GGCCAGAAGT	CAAACCTCAG	AATACATCAG	180

PCT/US98/06955 WO 98/45436

AGAACTCACA CTGGGGAGAA AACTTACCAG TGTAATGAAT GTGAAAAATC CTTCTGGCGA AAAGATCATC TCATTCAACA TCAACTCGAG	240 270
(2) INFORMATION FOR SEQ ID NO:749:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 309 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:	
GAATTCTAGT TTAATTACAT ATACCTCTCT GTTGGCTTAG TAGTAATAAA AATATTTTCT	60
GTAGGTGTAG AATATCCTTA CAGTCCAAAA GGAGAGTACA TGTTCACAAT TAAAGTTTGA	120
AATTTGTGCT TTGATAACAG CATGTTTTAT TCATTCATTT TTATAATAAT ATTACTGAGC	180
CTGTATCATA TAGTGATGAA CTTTTCAGCT GTTTTGAGGG TTTGTGTTAG CCACATTCAC ATTTGTATAA CCTGTGTTTC TTTTTTATTT TCTTTATTT TCATTTTAGA TTCAGGGGGT	240 300
CGGCTCGAG	309
(2) INFORMATION FOR SEQ ID NO:750:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 328 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:	
GAATTCGGCC TTCATGGCCT AAGCTCTTTT AGTGAAGGAT TGTTTTAAAT AAGAGCTCTC	60
AGTTCAAGAC AACTACTGTT AGGAGCTTAA ATCGGAACCA CAATCAGCAT ATAAAGGTCC	120
TAATCCTGAC CTTAATCCCT TTGGAATATT GGTTTTATAA ATCATCAATC AACAGTGTTC	180
CACTATGAAA GCATATTCTG TCTTCTTCTT TTCATGTATT CCTTCACTGC TGGTGCTTAA TGTCTTTCCT TCCTCTTCTG CCATTTCTCT TTCCATGAAT TATAATTGCC TTTTGAATTC	240 300
AGAAATTAAA ACCACTCCAC AGCTCGAG	328
(2) INFORMATION FOR SEQ ID NO:751:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 239 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:	
GAATTCGGCC TTCATGGCCT AATAAGGAAG AAATTGTCTC ACTTTATTGA ATAGTTGATT	60
TAAATTTTCT GGTATTTAGA GGTAATATAG TATAAGTTTT TTGTATATTT ATCTAAGATT	120
TTCCTTTTGA AAATTTTCTT CCCTTTTCAT ATTATTTTCA TTAAACGATT TTCCTTTAAA	180
ATTTGTTACT AACAAGAACT ATCTAATATG CAATGAGATT TTTGCAGGGC ATTCTCGAG	239

(2) INFORMATION FOR SEQ ID NO:752:

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 231 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:	
GAATTCGGCC TTCATGGCCT AAGGAAAGTA CTTTAGACAA AAAAAAAAAA	60 120 180 231
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 308 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:	
GAATTCGGCC TTCATGGCCT ACAATAGAGC TCTTAAACTT ATTTAACTGA AATTTTGTAT CTTTTCACCA ACATTTCCC AACTCCCCTT TACCCCAACT ACTCCAGCCA CTGATAACCA CCATTCTGTT CTCTATTTCT TTTTCTTTTT TTTTTTAAGAG ATGGCGTCTT GCTGTGTCGC CCAGGCTGAA GGGCAGTGGC ATGATCTCGG CTTACTGCAA CCTCTGCCTC CCCGGTTTAA GCAATTCTCT ACCTCAGCCT CCCGAGTAGC TGGGATTACA AGCACCCATC CACTCGAG	60 120 180 240 300 308
(2) INFORMATION FOR SEQ ID NO:754:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:	
GAATTCTAGA CCTGCCTCGA GCCCTTTGTG GTTTTTAAGA AAAAAATTCT GTGCAGATCT GTTCCTCCTC CTGCTCCTTC CCTTTTCTCT ACATACAGTG CTCATTGGAG GCTCCCCACT CGAG	60 120 124
(2) INFORMATION FOR SEQ ID NO:755:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 369 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

GAATTCGGCC	TTCATGGCCT	AATCGGTGTC	TTTGGTAAAA	ATTCTATGAG	GATGACATAT	60
TCCATCATGT	TATTCGTTTC	ACATTTCCTT	TTGCTCAGTC	TCCAATGCAA	GCACAGCTTG	120
TGGTATAACC	TATTGTTTTC	CCATTCTAAT	AACTTCTCAA	TCGATCTTCG	TGTTCTTTTA	180
CTGAGGCAAA	TAACTGGCCA	CATACTGCAA	CCTAATGTGC	AGCAGCAACA	AAGGCAGCCA	240
CAAAGTAGCC	AACGTACATT	AACAGGAAGG	TTCTTCTTAA	GACAACTGTT	AACTCTGTTG	300
ATGCTGGCTT	TAAATTCTTC	AGGAGCTACT	TTTTCAGTTA	ATGAAGAAGG	GAATTCAGAT	360
TCAAATTTG						369

- (2) INFORMATION FOR SEQ ID NO:756:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

GAATTCGGCC	TTCATGGCCT	ACCGGCGAGG	AATAGGAATC	ATGGCGGCTG	CGCTGTTCGT	60
GCTGCTGGGA	TTCGCGCTGC	TGGGCACCCA	CGGAGCCTCC	GGGGCTGCCG	GCACAGTCTT	120
CACTACCGTA	GAAGACCTTG	GCTCCAAGAT	ACTCCTCACC	TGCTCCTTGA	ATGACAGCGC	180
CACAGAGGTC	ACAGGGCACC	GCTGGCTGAA	GGGGGGCGTG	GTGCTGAAGG	AGGATGCGCT	240
GCCCGGCCAG	AAAACGGAGT	TCAAGGTGGA	CTCGGACGAC	CAGTGGGGAG	AGTACTCCTG	300
CGTCTTCCTC	CCCGAGCCCA	TGGGCACGGC	CAACATCCAG	CTCCACGGGC	CTCCCAGAGT	360
GAAGGCTGTG	AAGTCGTCAG	AACGCATCCT	CGAG			394

- (2) INFORMATION FOR SEQ ID NO:757:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 497 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

GAATTCGGCC	TTCATGGCCT	ACTGATGTTG	AAGACGACAC	CACGGCTTTG	ATGGAATATC	60
AGATATTGAA	AATGTCTCTC	TGCCTGTTCA	TCCTTCTGTT	TCTCACACCT	GGTATTTTAT	120
GCATTTGTCC	TCTCCAATGT	ATATGCACAG	AGAGGCACAG	GCATGTGGAC	TGTTCAGGCA	180
GAAACTTGTC	TACATTACCA	TCTGGACTGC	AAGAGAATAT	TATACATTTA	AACCTGTCTT	240
ATAACCACTT	TACTGATCTG	CATAACCAGT	TAACCCAATA	TACCAATCTG	AGGACCCTGG	300
ACATTTCAAA	CAACAGGCTT	GAAAGCCTGC	CTGCTCACTT	ACCTCGGTCT	CTGTGGAACA	360
TGTCTGCTGC	TAACAACAAC	ATTAAACTTC	TTGACAAATC	TGATACTGCT	TATCAGTGGA	420
ATCTTAAATA	TCTGGATGTT	TCTAAGAACA	TGCTGGAAAA	GGTTGTCCTC	ATTAAAAATTA	480
CACTAAGAAG	TCTCGAG		•			497

- (2) INFORMATION FOR SEQ ID NO:758:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

GAATTCGGCC	TTCATGGCCT	AACCAAATCA	ACAACAACCT	ATTTAGCTGT	TCCCCAACCT	60
TTTCCTCCGA	CCCCCTAACA	ACCCCCTCC	TAATACTAAC	TACCTGACTC	CTACCCCTCA	120
CAATCATGGC	AAGCCAACGC	CACTTATCCA	GTGAACCACT	ATCACGAAAA	AAACTCTACC	180
TCTCTATACT	AATCTCCCTA	CAAATCTCCT	TAATTATAAC	ATTCACAGCC	ACAAAACTCG	240
AG						242

- (2) INFORMATION FOR SEQ ID NO:759:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 221 base pairs
 - (B) TYPE: nucleic acid
 - (^) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

GAATTCGGCC	TTCATAGCCT	ACCTAAATTA	ATAATAATGT	ATAGTTCAGA	ATTGCTAAGA	60
GTACTTTTTT	TTTTTTTTTT	TNGAGACAGG	TTCTCGCTCT	GCCCTCCAGC	CTGGTGACAG	120
AGCAAGATTC	CATCTCAAAA	AAGAAAAAA	ACACACAGCT	AATAGAATTG	CCATTGTTTT	180
TCATAATAGA	ATCTAGCTGC	TTACTCCAAC	CTCACCTCGA	G		221

- (2) INFORMATION FOR SEQ ID NO:760:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

GAATTCGGCC	TTCATGGCCT	AAAATCAAAG	ACTTTGCCAA	TACCATTCCT	GGCCATGGAG	60
GCATCATGGA	TCGCTTTGAC	TGCCAGTATC	TGATGGCCAC	CTTTGTCAAT	GTATACATCG	120
CCAGTTTTAT	CAGAGGCCCT	AACCCAAGCA	AACTGATTCA	GCAGTTCCTG	ACTTTACGGC	180
CAGATCAGCA	GCTCCACATC	TTCAACACGC	TGCGGTCTCA	TCTGATCGAC	AAAGGGATGC	240
TGACATCCAC	CACAGAGGAC	GAGTAGGGGC	CACCCAGGGC	CAGGAGAACA	GGAACAGAAC	300
TGAGCAGGGG	CAGGTCTCCA	AGGCAAGCCC	AGCTGGTGTG	ACTTAGACAA	TGACGAGGCT	360
TCAACTCACT	GTCTTTTTT	TTTTTTTTTG	GAGGGTATTT	TTTATTTGTG	GGTTCAAAAA	420
ATCTGTATAT	ACAGTCTATG	TGTTTAGAAT	TTGTGTTGTA	AGTAAACTAC	AGCTTTGAGT	480
TGGAAAGAAG	TCACGGGTTG	TAAAACCATT	TGGATTTTTT	TAAAACAAAA	GTATTAATAA	540
TCTGGAAGAC	TCGAG					555

- (2) INFORMATION FOR SEQ ID NO:761:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

GGCCGATCAG	GTTATTTTTT	GAAAGTTTTA	CTTACAGAGC	ATAAAATTA	CCCTTGGTTA	60
TTCTCAGCTG	TGATTGAGTT	CTGTGAAAGC	ATAGTACCCT	AGTACCCTGG	GATATCTCTA	120
CATGTGAAAT	TATTCAAATG	TCTCCCTTAC	TTTTTTTTT	TTTTTTTTG	AGACAGGCTC	180
TGTTGCCCAT	GCTGCAGTGC	AGTGGCACAA	CTATGGCTCA	TCTCAGCCTC	GACCTCCTGG	240
GCTCAAGCGA	TCCTCCCACC	TCAGCCCCCC	AGGCAGCTGG	GACCACAGGC	ACACACCACC	300
ATGTCCAGCC	AATTCCTGTA	TTTT				324

- (2) INFORMATION FOR SEQ ID NO:762:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

GAATTCGGCC	TTCATGGCCT	AGTGCCGGGG	AGAAAGGGCT	TCCTCCCCCA	CACATCAGAC	60
AGGGCACCAA	TGAGTGGGGC	ACTCAAAAAA	GAGAGCAGGC	CCTGGAGAGG	AAACCAAAGC	120
AAAGGTTAGT	TTTATAATCT	GATCCCTCAA	TTACCTGTAA	TTCATATTTT	CTAAATGCAT	180
TAGCTCTAAT	TCATTGTACT	GCCCCCAAAA	CAGAATAATA	CTTTGAAACA	TTAAATACAA	240
ACTACAACTA	AAAAAATAAA	ATTAGGCCTG	GCGTGGTGGC	TCATGCCTGT	AATCCCAGCA	300
CTTTGGAAGG	CCGAGGCGGG	TGGATCACTC	GAG			333

- (2) INFORMATION FOR SEQ ID NO:763:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

GAATTCGGCC	TTCATGGCCT	AATTTGAATC	AACACAACCA	CCCACAGCCT	AATTATTAGC	60
ATCATCCCTC	TACTATTTTT	TAACCAAATC	AACAACAACC	TATTTAGCTG	TTCCCCAACC	120
TTTTCCTCCG	ACCCCCTAAC	AACCCCCCTC	CTAATACTAA	CTACCTGACT	CCTACCCCTC	180
ACAATCATGG	CAAGCCAACG	CCACTTATCC	AGTGAACCAC	TATCACGAAA	AAAACTCTAC	240
CTCTCTATAC	TAATCTCCCT	ACAAATCTCC	TTAATTATAA	CATTCACAAC	CACAGAACTC	300
GAG						303

- (2) INFORMATION FOR SEQ ID NO:764:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

WO 98/45436 PCT/HS08/06055

_	PC 1/US98/06955	
	GAATTCGGCC TTCATGGCCT AGGGATTTAA AGAGTTTTTC TTGGGTGTTT GTCAAACTTT TATTCCCTGT CTGTGTGCAG AGGGGATTCA ACTTCAATTT TTCTGCAGTG GCTCTGGGTC CAGCCCCTTA CTTAAAGATC TGGAAAGCAT GAAGACTGGG CTTTTTTTCC TATGTCTCTT	60 120 180
	GGGAACTGCA GCTGCAATCC CGACAAATGC AAGATTATTA TCTGATCATT CCAAACCAAC TGCTGAAACG GTAGCACCTC TCGAG	240 265
	(2) INFORMATION FOR SEQ ID NO:765:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 427 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:	
	GAATTCGGCC TTCATGGCCT ACCAACAGCA AGCTCCAATA TCACACATCC AGACTCCTAT GCTTTCCCAA GAACAGGCAC AACCCCCGCA GCAGGGTTTA TTTCAGCCTC AGGTGGCCCT GGGCTCCCTT CCACCTAATC CAATGCCTCA AAGCCAACAA GGAACCATGT TCCAGTCACA GCACTCAATA GTTGCCATGC AGAGTAACTC TCCATCCCAG GAACAGCAGC AGCAGCAGCA ACAGCAGCAG CAACAGCAGC AGCAACAACA ACAGAGCATT TTATTCAGTA ATCAGAATAC CATGGCTACA ATGGCGTCTC CAAAGCAACC ACCACCAAAC ATGATATTCA ACCCAAATCA AAATCCAATG GCTAATCAGG AGCAACAGAA CCAGTCAATT TTTCACCAAC AAAGTAACAG TCTCGAG	60 120 180 240 300 360 420 427
	(2) INFORMATION FOR SEQ ID NO:766:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 275 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SECUENCE DESCRIPTION, SEC ID NO. 766.	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

CGATTGAATT	CTTGTCTGTT	CTGCCTCACT	CCCGAGCTCT	ACTGACTCCC	AACAGAGCGC	60
CCAAGAAGAA	AATGGCCATA	AGTGGAGTCC	CTGTGCTAGG	ATTTTTCATC	ATAGCTGTGC	120
TGATGAGCGC	TCAGGAATCA	TGGGCTATCA	AAGAAGAACA	TGTGATCATC	CAGGCCGAGT	180
TCTATCTGAA	TCCTGACCAA	TCAGGCGAGT	TTATGTTTGA	CTTTGATGGT	GATGAGATTT	240
TCCATGTGGA	TATGGCAAAG	AAGGAGGGTC	TCGAG			275

- (2) INFORMATION FOR SEQ ID NO:767:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

GAATTCGGCC	TTCATGGCCT	ACGTAATTCT	GGAAAAGTGA	ATACTTGTGA	AGAGTCGTCT	60
TGAATGATTT	GTAAAAAATC	CTGTTCTTAT	ATTCAACGAG	TTTCGAATCT	TTGTCAGAGG	120

AGTATTACCA	TTAGATTGAA	AAAAAGGAAA	ATAAATAATA	AACACTTTTA	AAAAAACTCC	180
CCATTCTCTT	ATTCTCACTT	TTAGGAAAAG	AGACTGACTA	ATATCTTCTG	CCACAAATAC	240
CGATGTTCTT	TTTATAAAAA	ATGGGÄCTGC	TTTTGGCAAC	CAGCCCTATT	TTGTTTTCAT	300
ATCCCTTTTT	GCTCCCATCT	TTCCAAACTC	ATAAACTCGA	G		341

- (2) INFORMATION FOR SEQ ID NO:768:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

GAATTCGGCC	TTCATGGCCT	ACAGAAAGAG	TTTGAGACCT	GAATAGCTCC	CAGATTTCAG	60
TCTTTTCCTG	TTTTTGTTAA	CTTTGGGTTA	ААААААААА	AAGTCTGATT	GGTTTTAATT	120
GAAGGAAAGA	TTTGTACTAC	AGTTCTTTTG	TTGTAAAGAG	TTGTGTTGTT	CTTTTCCCCC	180
AAAGTGGTTT	CAGCAATATT	TAAGGAGATG	TAAGAGCTTT	ACAAAAAGAC	ACTTGATACT	240
TGTTTTCAAA	CCAGTATACA	AGATAAGCTT	CCAGGCTCGA	G		281

- (2) INFORMATION FOR SEQ ID NO:769:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

GAATTCGGCC	TTCATGGCCT	ACTAACGAGG	AAAGGGATTT	AAAGAGTTTT	TCTTGGGTGT	60
TTGTCAAACT	TTTATTCCCT	GTCTGTGTGC	AGAGGGGATT	CAACTTCAAT	TTTTCTGCAG	120
TGGCTCTGGG	TCCAGCCCCT	TACTTAAAGA	TCTGGAAAGC	ATGAAGACTG	GGCTTTTTTT	180
CCTATGTCTC	TTGGGAACTG	CAGCTGCAAT	CCCGACAAAT	GCAAGATTAT	TATCTGATCA	240
TTCCAAACCA	ACTGCTGAAA	CGGTAGCACC	TGACAACACT	GCAATCCCCA	GTTTAAGGGC	300
TGAAGCTGAA	GAAAATGAAA	AAGAAACAGC	AGTATCCACA	GAGAGACTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:770:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

GAGCGTGGTG	GATATAAAAC	AGGTAAGAGA	CTTTCATGGT	ATACCTTTAT	ATTGTTGGAT	60
TAAAGGCACT	GCCAACTCAA	AAAACTTAAC	CGAAAATTTT	TTTTAATCAG	TTAAAATT	120
ACTGATATGA	AAATGACATG	AAACTAACTT	TTTGTGTTTT	ACTTAAAGGG	TGCTCTGTTT	180
GAAACTTCCT	CAGACAACTG	AATGGGAGAA	CCAGATGAAT	TTAGTAAAAG	TATTAACGTC	240
הבדדד מיי א א א	ACTGCTTTTT	TTTGTTTGTT	TGTTTTTGAG	ACAGAATCTT	GCTCTGTTGC	300

1	CCAGGCTGGT CTCGAG	316
	(2) INFORMATION FOR SEQ ID NO:771:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 473 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:	
	GAATTCGGCC TTCATGGCCT ACTTTGATGG AATATCAGAT ATTGAAAATG TCTCTCTGCC TGTTCATCCT TCTGTTTCTC ACACCTGGTA TTTTATGCAT TTGTCCTCTC CAATGTATAT GCACAGAGAG GCACAGGCAT GTGGACTGTT CAGGCAGAAA CTTGTCTACA TTACCATCTG GACTGCAAGA GAATATTATA CATTTAAACC TGTCTTATAA CCACTTTACT GATCTGCATA ACCAGTTAAC CCAATATACC AATCTGAGGA CCCTGGACAT TTCAAACAAC AGGCTTGAAA GCCTGCCTGC TCACTTACCT CGGTCTCTGT GGAACATGTC TGCTGCTAAC AACAACATTA AACTTCTTGA CAAATCTGAT ACTGCTTATC AGTGGAATCT TAAATATCTG GATGTTTCTA AGAACATGCT GGAAAAGGGTT GTCCTCATTA AAAATACACT AAGAAGTCTC GAG	60 120 180 240 300 360 420 473
	(2) INFORMATION FOR SEQ ID NO:772:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 253 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:	
	ATACAGTAAT CAAAGTAAGT AATATTCAA TCCAATATTT TTAAAAATCA GAATTAATGC AAAAAAAAACC ATGATGAACA AAATATTAAA ATTTAAAATA AAGACAGGAT TAGTATTACT GAGTTTTCCT TTTGTCCCAG GCTCTAATAT GGCTTGGCAT GGGGCAGAAC ATTACAACAT ACCAGTCGTG TCATGGTGCC CAAGGCTCCA CAGACCTCAG TGGCTCCCTG CTGCCTGCCA CAGCAATCTC GAG	60 120 180 240 253
	(2) INFORMATION FOR SEQ ID NO:773:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 286 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:	
	GAATTCGGCC TTCATGGCCT AGTGAGAATT GACTGTTGCT TTTGTTTGCC TGCTTACTGT TTTCTTTTAT TTATTTGTTT TTGGACCTGT GGCACAAAGG ATCTGTTTAC TGACCATCCT TATTGTGAGG CACACAGTCA CCATGGCACC CTGCGCGTTA CTCCTGTTCC ACTTGTTAT TCTCTGTATC CCCATACTAG TTATTATCGA AACCATCAGC CTACTCATTC AACCAATAGC CCTGGCCGTA CGCCTAACCG CTAACATTAC TACAGGCCAC CTCGAG	60 120 180 240 286

- (2) INFORMATION FOR SEQ ID NO:774:.
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

GAGGCTGACA	AAATACTCAC	CTTTACCTTT	ATTTTTGCAT	TTTATACTCA	CAACCATATT	60
TTTTTTGGCC	CCCTTCCCTT	TATTTTAACT	CATAACTGAT	ACTTAAAGGT	GCTCTGCCTT	120
ATTAAATCAG	CTCCTAGGCT	GCAAGTGCAT	AATATTTAAA	AATTTGCAAC	TTTGACTTTT	180
TAAAAATCTG	GTCTTGGTAT	GGAGCAACTT	TGCCTTTTTT	TTTTTTTTT	TTGAGACAGA	240
GTCTCGCTTT	NTCGCCCAGG	CTGGAGTGCA	GTGGTCCCAT	CTCAGCTCAC	TGCAACCTCC	300
TCCTCCCGGG	TTCAAGAGAT	TCTCCTGCCT	CAGCCTCCCG	AGTAGCTGGG	ATTACAGGTG	360
CCTGCCCCAA	CACCCTCGAG					380

- (2) INFORMATION FOR SEQ ID NO:775:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

GGCCTGGTAG	GATAAGAATA	TAAACTTCAG	GGTGACCGAA	AAATCAGAAT	AGGTGTTGGT	60
ATAGAATGGG	GTCTCCTCCT	CCGGCGGGT	CGAAGAAGGT	GGTGTTGAGG	TTGCGGTCTG	120
TTAGTAGTAT	AGTGATGCCA	GCAGCTAGGA	CTGGGAGAGA	TAGGAGAAGT	AGGACTGCTG	180
TGATTAGGAC	GGATCAGACG	AAGAGGGGCG	TTTGGTATTG	GGTTATGGCA	GGGGGTTTTA	240
TATTGATAAT	TGTTGTGATG	AAATTGATGG	CCCCTAAGAT	AGAGGAGACA	CCTGCTAGGT	300
GTAAGGAGAA	GATGGTTAGG	TCTACGGAGG	CTCCAGGGAA	GCTCGAG		347

- (2) INFORMATION FOR SEQ ID NO:776:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

GAATTCGGCC	TTCATGGCCT	AAGAGGATAA	GGGAAGAAAA	AGAAGAAAGT	ATTCCATTCC	60
CACATCCCTT	TAGGTTGGCT	TCTTATTTTA	TGTTTTTGTT	GGTGTGTTTA	TTTTGCTTTG	120
TTAACATTTT	CAACTAGCTA	TAGAAACGTT	TGCAATTCTT	ATTACTGATT	AGCATTCCAA	180
AACTTTGTAA	TGAACATTTT	TCTCTCTTTC	TTTTTTTTT	TTTTTTNGAG	ACAGGGTCTC	240
GCTCTGTCAC	CAAGCTGGAG	TGCAGTGAGC	CAAGATCCTA	CTGCTGTCCA	TTCCAGCCTG	300
GGTGACAGAA	CAAGACCTTG	TCCGCCCACC	TTCCACCCCC	CCCTCGAG		348

(2) INFORMATION FOR SEQ ID NO:777:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

GAATTCGGCC						60
TTGATGCTAA	GGATATAGCA	GTGAACAAAA	CAATCCTTGT	GGACTTACAT	CATAGTAGGG	120
			TCAGTTGATA			180
CAAAGCAGGA						240
TTGGGATGGT						300
TGTCTGCTGT	GTGTAGAACA	TTCTGGGAAA	GGGCAGAGAA	GGGAACAAGA	CTATTCCAGA	360
AAAAGAGGGC	ACTCGAG					377

- (2) INFORMATION FOR SEQ ID NO:778:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

GAATTCGGCC TTCATGGCCT	AGCACAGCTA	GACGGTTCCA	GCTCAGGGTC	TCTCATGAAG	60
TTGCAATCAA AATATTGGCA	GGAGAGAAAA	ACATATTTTC	AGAAGCTGCA	GGCATAGGAA	120
GACTTGGCTG GGGTTGAAGG	ATCCACTTCC	AAGATGGCGC	ACTCAGTGGC	TCTTGGCTGG	180
AGGCCTCAGT TCCCTGCTGC	GTGGAGCTCT	CCCTCCAGCT	GCTTGAGTGG	ACTCATGACA	240
TGCAGCTGGC CTCCCCTGGA	GCAGTCGATC	CAACAATGAG	CATGGCCATG	AACTAGAGCT	300
CGAG					304

- (2) INFORMATION FOR SEQ ID NO:779:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

GAATTCGGCC	TTCATGGCCT	AGCCAAAACC	ACAGAATATA	TAATATAGAT	CTTGGGGATA	60
CAGCAGAGAA	AAAAGACAAA	AATCCCTGTT	ACAATCCGTT	CTAGAATTGA	TGTTCCTTTG	120
			CTTACCTCTT			180
			GGAAATGGGG			240
GAGTAGGTTG	ATTAACTTGT	CTGCTGTCAG	AGTGGAAGCA	GGGGTAGTTT	CCCTTTCCGA	300
CCAGAGGCAT	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:780:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

GAATTCGGCC	TTCATGGCCT	ACAGAAGATT	TGGACAATTC	CATTGATAAA	ACAGAAGCTG	60
GAATTAAGGA	GCTTCAGAAG	AGTATGGAGC	GCTGGAAAAA	TATGGAAAAA	GAACATATGG	120
ATGCTATAAA	TCATGATACT	AAAGAACTGG	AAAAGATGAC	AAATCGGCAA	GGCATGCTAT	180
TNAAGAAGAA	AGAAGAGTGT	ATGAAGAAAA	TTCGAGAACT	TGGATCACTT	CCCCAGGAAG	240
CATTTGAAAA	GCACCAGGCT	CGAG				264

- (2) INFORMATION FOR SEQ ID NO:781:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 580 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

GAATTCGGCC	AAAGAGGCCT	AGCGATTGGG	TCTTTGATAT	CTGTAAGCCG	TTGAATTAGC	60
CCTGCCCTCT	GTTCTTAGTT	TAGGAGACCA	TAGATGTGCC	CTTATTATTG	AAACTGATTT	120
TATTCAGTTA	CTGAAGTTAT	CTTACCTGAT	ACATAATTTT	ACCCATAGAA	AATAATATGA	180
AAATAGCAAA	ATCACTCAGG	TAAGATAGAT	GAGTGCCTGC	TGTGTTCAAG	AGACTGTTAA	240
TATGAGGCTC	TGGGGCTGCA	AAAAATCAAG	TTGCTAAGAA	ATATGAGGTC	AGAGCAGCAG	300
AAGTTCTGAG	TAACCACTGA	TTACTGGACT	TGGGGTGATC	AGAAGTGACT	GTGTGGGAGA	360
GGTGAAATTG	AGCAGACTCT	GAAGGAACCT	CTGGGTTTTG	GTAAATAGGG	AGCTGGGGAT	420
GAGGATGCCC	CAGGTTTTAG	AAAGAACACA	GGCTGTTGAA	TCACACCTGG	GTTCAAACCC	480
TGGCTTGCTA	CTCCCTAGTT	TGTGACCTTG	TCAAATTCCT	TGATTTCTTT	TTTCTTTTTC	540
TAATTTTTTT	TTTGGAGACA	ACAGTCTCGC	TCTGTCACCC			580

- (2) INFORMATION FOR SEQ ID NO:782:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

GAATTCGGCC	AAAGAGGCCT	AGAATGGTAG	AGTAAAAAGA	ACCCTCTGCT	GAGTAACCAA	60
GCCTTTAATT	TCCTGTTCCT	GCTGTAGGGC	TTTCACAAAT	GCATTTTTCA	GCCGGTTGGT	120
GTGTCCTCGA	G					131

- (2) INFORMATION FOR SEQ ID NO:783:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

GAATTCGGCC	AAAGAGGCCT	AGATTGAGGT	TGTGGTAGAT	TAGGCGTAGG	TAGAAGTAGA	60
GGTTAAGGAG	GGTGATGGTG	GCTATGATGG	TGCGGCTCGA	GGCAGGTCTA	GAATTCAATC	120
G						121

- (2) INFORMATION FOR SEQ ID NO:784:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

GAATTCGGCC	AAAGAGGCCT	AAGCAAGATG	AAGCCCAACA	TCATCTTTGT	ACTTTCCCTG	60
CTCCTCATCT	TGGAGAAGCA	AGCAGCTGTG	ATGGGACAAA	AAGGTGGATC	AAAAGGCCGA	120
TTACCAAGTG	AATTTTCCCA	ATTTCCACAC	GGACAAAAGG	GCCAGCACTA	TTCTGGACAA	180
AAAGGCAAGC	AACAAACTGA	ATCCAAAGGC	AGTTTTTCTA	TTCAATACAC	ATATCATGTA	240
GATGCCAATG	ATCATGACCA	GACCCGAAAA	AGTCAGCAAT	ATGATTTGAA	TGCCCTACAT	300
AAGACGACAA	AATCACAACG	ACATCTAGGT	GGAAGTCAAC	AACTGCTCCA	TAATAAACAA	360
GAAGGCAGAG	ACCATGATAA	ATCAAAAGGT	CATTTTCACA	GGGTA		405

- (2) INFORMATION FOR SEQ ID NO:785:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 642 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

GAATTCGGCC	AAAGAGGCCT	ACTACTCACC	TCTTGCTCTC	TCCCAACCAT	AGAAACAGCC	60
ACGACTCCTA	CCACAAACTT	GGGAAACACC	ACCACTGAGA	CCACCTCCCA	CAGTACTCCC	120
AGCTTCACTT	CTTCAGCCAT	CTACTCCACC	GTCAACATAT	CCACAACTAC	CATCTCCTCA	180
TTTCCCCCTT	CCTCAGGTAC	CATGGTGACA	TTCACAACCA	TGAACCCATC	CTCTCTGAGT	240
ACAGACATAT	CTACCACCAC	ACTGAAAAAT	ATCACCCAGC	CTTCTGTGGG	CTCTACTGGT	300
TTCCTGACTG	CAGCTACAGA	CCTCACCTCA	ACATTCACTG	TTTCCACTTC	CTCAGCAATG	360
TCCACAAGTG	TCACTCCATC	TGCCCCCAGC	ATCCAGAATA	AAGAAATCTC	AACACTTGTG	420
AGTACAACCA	CTACCACCAG	TCCCACTGAG	AGAATGACTC	TCACAAGTAC	AGAGAATACC	480
CCGACAAGTT	ACATCCTGAC	CACCAGTCCA	GTGACATATT	CATTTTCCCC	TTCCATGTCT	540
GCCAGCAGTG	ACTGGACCAC	TGACACAGAG	AGCATCTCCT	CAGCTCCAGC	CATCACCAGT	600
ACACTCCACA	CAACAGCTGA	ATCCACCCTG	GCAGGTCTAG	AA		642

- (2) INFORMATION FOR SEQ ID NO:786:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 469 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

GAATTCGGCC	AAAGAGGCCT	ATGGCCTTGG	AAGGGATGAG	CAAACGGAAG	AGAAAGAGAA	60
GTGTCCAGGA	GGGAGAGAAT	CCTGACGACG	GCGTTCGCGG	GAGTCCGCCG	GAAGACTACA	120
GGCTTGGACA	GGTCGCCAGT	AGCTTATTTC	GCGGCGAACA	CCATTCCAGA	GGTGGCACCG	180
GTCGGCTGGC	GTCCCTCTTC	AGTTCTCTGG	AGCCCCAGAT	TCAACCCGTG	TACGTGCCTG	240
TGCCTAAACA	AACCATCAAA	AAAACGAAAC	GGAATGAGGA	GGAAGAAAGT	ACATCCCAGA	300
TTGAAAGACC	ACTTTCGCAA	GAACCTGCCA	AAAAAGTGAA	AGCGAAGAAG	AAACACACTA	360
ACGCAGAAAA	AAAGTTGGCA	GACAGGGAAA	GCGCTCTAGC	GAGTGCTGAT	TTAGAAGAAG	420
AAATTCACCA	GAAACAAGGG	CTTAGCTCGA	GCAGGTCTAG	AATTCAATG		469

- (2) INFORMATION FOR SEQ ID NO:787:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

GAATTCGGCC	AAAGAGGCCT	AAGAAAAGAT	ATAAATCAGA	GAAAAAGCAT	GAAGCGTATC	60
ATATTGATTT	TAACAGTATT	GCTTGCCATG	TTAGGGCAGG	TTGCCTATGC	GCAGAAAACG	120
TGTGTCATCG	CATCGGCAGA	AAATCATGTG	CCTATTCGTG	AAGCACTTAT	TCATACCAAT	180
AACAATCATT	GGGCAAGAAC	AGATTATCGG	GGCTATTGGA	CGATGCGCTA	TCAGTTTGAT	240
TCAGCAACCG	TATCGAAACC	TGGTTTTATG	AAGGCAACTA	TCCGGTACAA	GGAACTGCCG	300
GATACTCTGT	TTCTCTTGCC	GGATGCCAAA	CAGTTAGGCG	AAGTGACAGT	TTGGGGCAAG	360
AATCAGGAAG	GCATCAAAAA	TATGGAAGAG	GATATTCAGG	AGAAGATAAA	CTCTTTGCCA	420
ACTTCATCTG	CTGGCATTGG	TTTTGATGCT	TTCGGATGGA	TGGATAAACA	GGGAAAACGT	480
GATAAGAAGC	ATCTGCAACA	G				501

- (2) INFORMATION FOR SEQ ID NO:788:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

TGATGATCGA	TATCCAGAAA	GACACTGCGG	TGGAAGGTGA	GGAGATTGAA	GTCAACTGCA	60
CTGCTATGGC	CAGCAAGCCA	GCCACGACTA	TCAGGTGGTT	CAAAGGGAAC	GCAGAACTCG	120
AG						122

- (2) INFORMATION FOR SEQ ID NO:789:
 - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 274 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

GGTGAGCTGA	GATCGCACCA	CTGCACTGCA	AGACCCTGTC	TCAAAACAAA	CAAACAAACA	60
ACAACAACAA	CAACAAACCA	AACCAAACAA	AAAACCTGCA	TAGCCAACTA	GACCAGCATA	120
GAGGGCGAAA	ACCATGCTTT	TTGTCAAATG	GTACTGTTTA	TTCTGTTTTG	CTGTCAGCTG	180
GTTTGCCGCT	TCTGATAAAG	CTAGCCCTTG	CTGTGTGCAT	GCAGGTTATA	GTGCCCAGGC	240
TCATATTTCC	TCTTCTTGCT	GCACCTCACT	CGAG			274

- (2) INFORMATION FOR SEQ ID NO:790:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

GAATTCGGCC	TTCATGGCCT	AGGGAAAGGA	GGCGGCAGCC	AGGCTGTGTC	CCCTGACCGT	60
TGGAGCGTCT	GCGACCCCCG	CATCCCCGCA	CCCTCAAGGC	ACCTCCAAAG	ATGATGATGG	120
GTTGTGGGGA	GTCAGAGCTG	AAGTCGGCGG	ACGGGGAAGA	AGCCGCGGCG	GTCCCGGGGC	180
CACCCCGGA	GCCCCAAGTC	CCGCAACCG				209

- (2) INFORMATION FOR SEQ ID NO:791:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

GAGAGAATTA	AAGAGAACCA	CNAAGCTGAA	CCTCAAAAAG	TTAGCCTGGC	GAGGGGAGGA	60
TGATGAGATT	TCCCCTGTTG	TCACATAAAC	AAGGAAGTAA	AGGGGCCCC	TTGTGCTCTC	120
AGAACTCCAA	GCATGAAACG	ATAGCAAAGG	GAAAAACAGC	TAAGTGTTTC	CTGGCTGAAT	180
TTTATTTTGC	TTTCAGTTTC	TGCCATTTCA	GTTCCTGTTA	TCGTGCTTTG	AGGTGCACTG	240
AACTGCAGCA	AACCCAGGGG	ATCCAAGGCT	ACGTTGAAAA	GCCTTTGACC	ACAGTGCAGG	300
GAGCAGAAGA	CATTAATGAC	GTGATGTCGA	CACAGCCCGC	ACTCAGGATC	CTCCAGGAAA	360
AGAACACAGA	GATAACCCCG	GAACTCGAG				389

- (2) INFORMATION FOR SEQ ID NO:792:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

GTGCTTTGGA	TTTTGCATCC	AGCTTTTTCT	CAACACCCCC	GCTGGAACTC	AGCGGCTCCA	60
TCTCTTCGCC	TTCGGAAGCA	CCTGCGTCTC	TGTCTCTGAT	GCCGAGTGAC	TTGTCCCCCT	120
TCACATCTCA	GTCTTTTTCT	CCCTTGGTTG	AGACATTTAC	ATTGTTTGAC	TCTAGTGATC	180
TGCAGTCATC	TCAGCTGTCT	CTTCCCAGTT	CCACAAATCT	TGAGTTTTCG	CAGCTCCAGC	240
CAAGTTCCGA	GCTGCCTTTA	AACACCATCA	TGTTGCTACC	TANCCGTTCT	GAGGTGTCAC	300
CATGGTCAAG	CTTCCCTTCT	GATTCTCTCG	AG			332

- (2) INFORMATION FOR SEQ ID NO:793:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

GAATTCGGCC	TTCATGGCCT	ACTGGAATTT	CTTTCTTGCC	CTTTCATATT	TTAAGATGGC	60
TGGAATAGCA	CAGGGAGTAT	ATAGCAGATA	TCTTCTGGGA	AATAATTCAT	CTGAGGATAG	120
CTTTTTATTT	GCCAATATTG	TGCAACCTCT	GGCAGAAACT	GGACTACAAC	TCTCCAAACG	180
AACTTTCAGT	ACTGTACTAC	CACAGATTGA	TACTACTGGA	CAGTTGTTTG	TACAGACTCG	240
GAAAGGTCAG	GAAGTTCTCG	AG				 262

- (2) INFORMATION FOR SEQ ID NO:794:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

GAATTCGGCC	TTCATGGCCT	ACTATGCCGT	CATGATAGAG	AAGATGATCC	TGAGAGACCT	60
GTGCCGTTTC	ATGTTTGTCT	ACGTCGTCTT	CTTGTTCGGG	TTTTCCACAG	CGGTGGTGAC	120
GCTGATTGAA	GACGGGAAGA	ATGACTCCCT	GCCGTCTGAG	TCCACGTCGC	ACAGGTGGCG	180
GGGCCTGCC	TGCAGGCCCC	CCGATAGCTC	CTACAACAGC	CTGTACTCCA	CCTGCCTGGA	240
GCTGTTCAAG	TTCACCATCG	GCATGGGCGA	CCTGGAGTTC	ACTGAGAACC	ATGAACTTCT	300
CGAG						304

- (2) INFORMATION FOR SEQ ID NO:795:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

GCGATTGAAT TCTAGACCTG CCTCCAAGCA GCTGCAGTAT CTCGGAAGAA AAAACGAAGA ATGGGAACCT ATAGCCTGGT TCCTAAGAAA AAGACCAAAG TATTAAAACA GAGGACGTG ATTGAGATGT TTAAGAGCAT AACTCATTCC ACTGTGGGTT CCAAGGGGGA GAAGGACCTG GGCGCCAGCA GCCTGCACGT GAATGGGGAG AGCCTGGAGA TGGACTCAGA TGAGGACGAC TCAGAGGAGC TCGAG	60 120 180 240 255
(2) INFORMATION FOR SEQ ID NO:796:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:	
CTAGTCTTCC AACCCTTCTG GACTTTCTTT GCTCTTGTCT TGTTTTGGGT GTACTGGATC ATGACACTTC TTTTTCTTGG CACTACCGGC AGTCCTGTTC AGAATGAGCA AGGCTTTGTG GAGTTCAAAA TTTCTGGGCC TCTGCAGTAC ATGTGGTGGT ACCATGTGGT GGGCCTGATT TGGATCAGTG AATTTATTCT AGCATGTCAG CAGATGACAG TGGCAGGAGC TGTGGTAACA TACTATTTTA CTAGGGAAGT ACTCGAG	60 120 180 240 267
(2) INFORMATION FOR SEQ ID NO:797:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 185 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:	
GAATTCGGCC TTCATGGCCT AGGGGGAGTT TAGCTGAAAC AAGTTTTACA GAAGCAGAGC TGGCAAATAG TTAAAATATT AATTGGTTAC AATAGCAGTT ACAAAACAAA	60 120 180 185
(2) INFORMATION FOR SEQ ID NO:798:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 434 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:	
GGGCGTGTGA CGACTGCTGG GAGAGGAAAG CGAGACATCA TTCCAACCCT CCAGAAGCTA AAGATCCTGG AACTCAAGGG GAAAACTAAC GTAAGTGCGA AAGCGAACAA GCAAACATGT CCTCAACGGG GCAGGCAGGC TGTCGGGGTA CAGAGCTGGG ATCTGGGAAG GAACAGAGAG GGCCGCTCAG GGAGAGGAAG CACAGTGCCA CCGGAGGCAC GCACTCAGCA GGCACTCGCA GGCTGGGCAG AGGTAGAGAA GCAGCGCTGC ACAGGCAGGC AGCTGACCCA GGGCTCTTAG	60 120 180 240 300

AGCCGGGCAG GA	GAGCTGGT GTGG	SACCTG GGAGGAG	GAC AGGAGCCTTC	AAAGCAGCAC 360
CGCCTGATTG CA	GCCAGGAG GGTAG	GCATCA AGGAAGA	TGG AACTGCGGCC	AGGCCACATC 420
CAGGGGTGCT CG	AG			434

- (2) INFORMATION FOR SEQ ID NO:799:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 424 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

GAAAAGTCGG	ATGCTGGCCT	CTGGAAATCA	GCCAGATCAA	GATATTACAC	ATTTCTTCCA	60
ACAGATCCAG	GAGCTCAATT	TGGAAATGGA	AGACCAACAG	GAGAACCTAG	ATACTCTTGA	120
GCACCTGGTC	ACTGAACTGA	GCTCTTGTGG	CTTTGCGCTG	GACTTGTGCC	AGCATCAGGA	180
CAGGGTACAG	AATCTAAGAA	AAGACTTCAC	AGAGCTACAG	AAGACAGTTA	AAGAGAGAGA	240
GAAAGATGCA	TCATCTTGCC	AGGAACAGTT	GGATGAATTC	CGGAAGCTGG	TCAGGACCTT	300
CCAGAAATGG	TTGAAAGAAA	CTGAAGGGAG	TATTCCACCT	ACGGAAACTT	CTATGAGTGC	360
TAAAGAGTTA	GAAAAGCAGA	TTGAACACCT	GAAGAGTCTA	CTAGATGACT	GGGCAAGTCT	420
CGAG						424

- (2) INFORMATION FOR SEQ ID NO:800:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

GAATTCGGCC	TTCATGGCCT	AGGGGTGCTG	TGTGTTTTTC	AGGGCGCCCT	GCGTCCGGCA	60
GAGGAGGCGA	GCATCCCGCT	CAGGTGATGA	GGAACCCCTC	GCGCACCCAG	CGCAGAAGGC	120
TGCTGCCGCC	GGACGCCTCC	ATTGTTTGAC	CACAACAAGG	GCCGGATTCT	CACCCAGCAG	180
GATCCTAAGG	CCTTTGTAGT	CCTTCAGCCA	CTGTGGGCCC	TGCCTCTGCC	TGTTCTTCTG	240
GAATGTCTTG	GGGGTTTTGA	TCCTGTCACT	GTGACCTGCA	AATCCAAGAG	ACAACTCGAG	300

- (2) INFORMATION FOR SEQ ID NO:801:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

GAGAAATCAG	TGAAGGATTT	GCAACGCTGC	ACCGTTTCTC	TAACTAGATA	TCGCGTCATG	60
ATTAAGGAAG	AAGTGGATAG	TTCCGTGAAG	AAGATCAAAG	CTGCCTTTGC	TGAATTACAC	120
AACTGCATCA	TTGACAAAGA	AGTTTCATTA	ATGGCAGAAA	TGGATAAAGT	TAAAGAAGAA	180
GCCATGGAAA	TCCTGACTGC	TCGTCAGAAG	AAAGCAGAAG	AACTAAAGAG	ACTCACTGAC	240

CTTGCCAGTC AGATGCCAGA GATGCAGCTG GCCGAACTCA GGGCAGAAAT TAAGCACGGT

300

CTCGAG	306
(2) INFORMATION FOR SEQ ID NO:802:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 263 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:	
GCTCGCGGCC GTTCAGAATT ATAAGGCTGT CTGCAGAGAT TTGAAAAATG GCAACAAATG AAAGTGTCAG CATCTTTAGT TCAGCATCCT TGGCTGTGGA ATATGTAGAT TCACTTTTAC CTGAGAATCC TCTGCAAGAA CCATTTAAAA ATGCTTGGAA CTATATGTTG AATAATTATA CAAAGTTCCA GATTGCAACA TGGGGATCCC TTATAGTTCA TGAAGCCCTT TATTTCTTAT TCTGTTTACC TGGATGTCTC GAG	60 120 180 240 263
(2) INFORMATION FOR SEQ ID NO:803:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 276 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:	
GAATTCGGCC TTCATGGCCT AAATAGTTAG TCACCTTCTG ACCTTCTCT CTTTCTCAAA GCCTTCTGTC CCTGGTTTTT GCAAGTGCTG CATTTCCGCC GAGAATCCGC GTTGCCTACT GCTGCCACCT CCTGTTCATT TAGAACTATG CAAAGACTCC GCTTCCGTTT TCCTGAGCTC CTCGGGCCCC AGAGTCTCTG TTTGATTATT TATTTATTTA TTTATTTATT TGCCAAAAAT TCTCCTCTTC AACTTATAGA ATGCACCCAA CTCGAG	60 120 180 240 276
(2) INFORMATION FOR SEQ ID NO:804:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 580 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:	
GAATTCGGCC TTCATGCCTA CAGCCATATT AAAACTAAGT AAACTCGTCC CTGGGAACTA CACTTTCAGC TTGACTGTAG TAGACTCTGA TGGAGCTACC AACTCTACTA CTGCAAACCCT GACAGTGAAC AAAGCTGTGG ATTACCCCCC TGTGGCCAAC GCAGGCCCCA ACCAAGTGAT CACCCTGCCC CAAAACTCCA TCACCCTCTT TGGGAACCAG AGCACTGATG ATCATGGCAT CACCAGCTATA GAGTGGTCAC TCAGCCCAAG CAGCAAAGGG AAAGTGGTGG AGATGGAGGG	60 120 180 240 300
TGTTAGAACA CCAACCTTAC AGCTCTCTGC GATGCAAGAA GGAGACTACA CTTACCAGCT CACAGTGACT GACACAATAG GACAGCAGGC CACTGCTCAA GTGACTGTTA TTGTGCAACC	360 420
TGAAAACAAT AAGCCTCCTC AGGCAGATGC AGGCCCAGAT AAAGAGCTGA CCCTTCCTGT	480

GGATAGCACA ACCCTGGATG GCAGCAAGAG CTCAGATGAT CAGAAAATTA TCTCATATCT CTGGGAAAAA ACACAGGGAC CTGATGGGGT GCAGCTCGAG	540 580
(2) INFORMATION FOR SEQ ID NO:805:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 323 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:	
CAAATTGATT TCGGCACAGT TCTGGGAGCT GGGACATTCA AGGTCACCAC GTTGCCACCT GTGAAGGCCT TCTGCTGCAT CCTCATGTTG GGGAAGATCA GAAGTGAGAA CACATGCTGG CCAGTCCTTT CACAGCAGCA TCAATCCGTG CATGGGGCAG GGCCCTCGGC CTGAGCGCCT CCCCCAGGCC CTAACTCCCA GCACTGCCCT GCTGGGGATG GAATTTCCAA CATGAATCTG GGGGATGCTT TCGGACCACA GCCGGGGAGC CTGCCCTGGC TTCCAGCTGC TGGTGGCCCA GGGGCTCCCT GGCTTGCCTC GAG	60 120 180 240 300 323
(2) INFORMATION FOR SEQ ID NO:806:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 304 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:	
GCGATTGAAT TCTAGACCTG CCATTCTCGC TCTGCCGACG TTGACTCTCT CTCTGAATCC AGTCCCAACT CCAGCCCTGG CCCCTGTCCT GAGAAGGCCC CACCACCCCA GAAGCCCAGC CATCTCCCAG GGGGCCCTCA TCGCCATCGT CTGCAACGGT CTCGTGGGCT TCTTGCTGCT CTCTGCATCCT GCTGGATCC CCATCTCTC TCTCGCACG TTGACTCTCT CTCTGAATCC AGTCCCAACT CCAGCCCTGG CCCCTGTCCT GAGAAGGCCC CACCACCACT CGAG	60 120 180 240 300 304
(2) INFORMATION FOR SEQ ID NO:807:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 556 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:	
GAATTCGGCC TTCATGGCCT AGATATGAGA AATGAGTGTT GGACGTCGAA GAATAAAGTT GTTGGGTATC CTGATGATGG CAAATGTCTT CATTTATTTT ATTATGGAAG TCTCCAAAAG	60 120

240

300

CAGTAGCCAA GAAAAAAATG GAAAAGGGGA AGTAATAATA CCCAAAGAGA AGTTCTGGAA GATATCTACC CCTCCCGAGG CATACTGGAA CCGAGAGCAA GAGAAGCTGA ACCGGCAGTA

CAACCCCATC CTGAGCATGC TGACCAACCA GACGGGGGAG GCGGGCAGGC TCTCCAATAT

AAGCCATCTG AACTACTGCG AACCTGACCT GAGGGTCACG TCGGTGGTTA CGGGTTTTAA

GCTTATAGAT CA	ACAGATTTA AAGACTTTCT GCTGTATTTG AGATGCCGG AGCCGGATA AGTGTGCAAA GAAACCTTTC TTGTTGCTG ATTTTGCCA GAAGGCAAGC AATCCGGGAA TCCTGGGGG ICGAG	GG CGATTAAGTC	420 480 540 556
(2) INFORMATI	ION FOR SEQ ID NO:808:		
(i) SE	QUENCE CHARACTERISTICS: (A) LENGTH: 359 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii) M	MOLECULE TYPE: cDNA		
(xi) S	SEQUENCE DESCRIPTION: SEQ ID NO:808:		
TCGCATTTGC TA AAGGAAAGGA GC GCAGCTCCCA TA AGCCCACGTT GC	AACTATTTT GCTCGCAACT TTTACAACAT GAGAATGT ATCAATTTC ATCTTGCTCT TTTATAAGGT CTCCACTTC CTCCCCACG AGAAGTTCAA GTGAAAATGC CAAAGTGA AGAATCATC GCAGTTCACT ATGTACTAGA GGAGAGCAC CGTATCTTA GCTATTCTGC ACACGGTCAT TTCTTTCT TTGAAAGTC CCATTGGTTA TTTTTAAGCG AGAAAAGG	CT TCTGTGGTTG CA AGCCTGGACA GC GGCTACATGG TC TGCATCATTG	60 120 180 240 300 359
(2) INFORMAT	ION FOR SEQ ID NO:809:		
(i) SE	EQUENCE CHARACTERISTICS: (A) LENGTH: 299 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii) N	MOLECULE TYPE: cDNA		
(xi) S	SEQUENCE DESCRIPTION: SEQ ID NO:809:		
TGCAGTCCAA TA ATGCGGTACG TA ACTTTGATAA C	ATGTCCAGG AAACAGAACC AGAAGGATTC ATCAGGAT ACCGTACTG GCCCAGGGAG GAGCTTTTGA GAACATGA GCAATAGTT CCTAATAAGA GCAACAATGA AATTATCC TGTGTGGAC AAAACAGTAC AAGCATTCAT GGAAGGTA TGGACAGTA ACAGNCAAGA AAAAGAACAA AAAGAAGA	AAA GAGAAGATAA CTG GTTTTGCAGC AGT GCCAGTGAAG	60 120 180 240 299
(2) INFORMAT	TION FOR SEQ ID NO:810:		
(i) S	EQUENCE CHARACTERISTICS: (A) LENGTH: 413 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:810:		
TGCATGTGTA A CTGGCTGAAA A GTGGGCTGCC C	TTCATGGCCT AGTAGCTGTT CCAGTACAAT TCAATGT: ATGATATTTC TGTACTTTTG TATCAACTCA GAATTTC AGATGTCCAA GGATCATCTC CGGAATGGAA GAGGTGA CAATCCATCC AACCCTTGGC ATTGGGATCA ATGTTGA	CAG AGAGCTCTTC GGC CTGTTAGCTT TGA GGACAAGACC	120 180 240

ACCAACTCCA ATTATTGTAG AGAAATTTAG GTACTGCAGG ACGCAAGGGA TCATGTCTGC AAGCTGGTCC AGAGATGGGT ACTGATATCC CAAAGGGAAC ACAGGGGCTC GAG	360 413
(2) INFORMATION FOR SEQ ID NO:811:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 324 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:	
TTGGTATTGT CTCTGTACTA GTCTTTCCAA ATTCTGCTGT GAGCTTTTTG CTTAGACTGT AAGCCTTAGA GTCACTCATC ACAGTAATCC TAAAGACAGA T3TTTCTGTT CTATTTGATA AGGCCTTTTT GTGGGTTGTG CCGACTGTCA GTTTCATGTT TGTTTGTTTG TTTTTGGAACT GCAGTTACAT CCAGGAGACC TGTGGTGAGC ATAATGGGCT GTAGTTTGTG CAGTTGTCAG TATAGCTTGT TAGGGAGCTC TTCCTGGGCA GAGTCTTGCA CAGCAGAGCC CAGTGCTGAG CTGAGTTCTT GGCACCATCT CGAG	60 120 180 240 300 324
(2) INFORMATION FOR SEQ ID NO:812:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 352 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:	
ACATTTCTTT GTAAGTTNNN AAAAGCCTAT GAGGGTTTTT TCCACGATTC CGTTCCCAGT TTGGCTTTTG TTGTTGTTG GGCTGTTCTT GGCCCCCCTG GGCCCTGCAG TGGAGTGGGG GGCTGCACCT GGGAGCCTCG AGCTGAGGCC CAGCCCCTCC TGCCCTGCAT TTTCCTGCCA AGCAGCACCT GAGACTCTGA AGCCGATGCC TATACAGGCA GAAACCTGCC AATTCCAGCT TGAACGACTG GAGGGTCCTG AGGATGGGG TCCCTGGGGT GCCATCATGG GCAGGGTGCA TCTGTTTGGG TATGCTGCCC CCCAGCTGGC GGGCACCGG GGACAGCTCG AG	180 240
(2) INFORMATION FOR SEQ ID NO:813:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:	
GAATTCGGCC TTCATGGCCT AGGGAAAGGG AANGTGGGGA GGGTCCGAGG GGAAGGGGAC CCCAGCTTCC CTGTGCCCGC TCACCCCACT CCACCAGTCC CCGGTCGCCA GCCGGAGTCT CCTCTCTACC GCCACTGTCA CACCGTAGCC CANATGGATA NCACNGTTGT CAGACAAGAT TCCTTCAGAT TCCGAGTTGC CTACCGGTTG TTTTCGTTGT TGTTGTTGTT GTNTTTNTTT TTNTTTTNNN TNCGGAAGAC AGCAATAACC ACAGTACATA TTACTGTAGT TCTCNATAGT TNCACATACA TTNATACCAT AACCTCGAG	60 120 180 240 300 329

- (2) INFORMATION FOR SEQ ID NO:814:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

GAATTCGGCC	TTCATGGCCT	ATCCATTTCC	AAATCCACCA	AGGTCCAGTC	GACAGACATT	60
TCCAAAAAGA	ATCCTGTTCT	AGGACCACTT	GCGCTGAGAG	CACACCCGGG	GGTCAAAGGG	120
CAGCCACCGG	${\tt GGGTCAAAGG}$	GCAGCCATCA	GGTACTCCCC	AGGGAAGGGC	TTGCGGCCAC	180
CAGTCACTGC	AACCCCGCCT	CACCTCCGAT	GCCTGCTGTG	CCCAGGGTGG	TCCCGCTCAT	240
AGCGACGGCC	TGNGCGTNCA	TANGACCTCG	AG			272

- (2) INFORMATION FOR SEQ ID NO:815:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 584 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

GATTGAATTC	AATGTTAAGC	ACCAATGCTG	GATTTGGTGG	TGGACTGAAC	ACCAGTGCTG	60
GCTTTGGTGG	TGGCCTAGGC	ACCAGTGCTG	${\tt GCTTCAGTGG}$	TGGCCTAAGC	ACAAGTTCTG	120
GCTTTGATGG	TGGGCTAGGT	ACCAGCGCTG	${\tt GCTTCGGTGG}$	AGGACCAGGC	ACCAGCACTG	180
GTTTTGGTGG	TGGACTGGGC	ACCAGTGCTG	GCTTCAGTGG	CGGACTGGGC	ACCAGTGCTG	240
GCTTTGGTGG	TGGACTGGTC	ACTAGTGATG	GCTTTGGTGG	TGGACTGGGC	ACCAATGCTA	300
GTTTCGGCAG	CACACTTGGC	ACCAGTGCTG	GCTTTAGTGG	TGGCCTCAGC	ACCAGCGATG	360
GCTTTGGCAG	TAGGCCTAAT	GCCAGCTTCG	ACAGAGGACT	GAGTACCATC	ATTGGCTTTG	420
GCAGTGGTTC	CAACACCAGC	ACTGGCTTTA	CTGGCGAACC	CAGCACCAGC	ACGGGCTTCA	480
GTAGTGGACC	CAGTTCTATT	GTTGGCTTCA	GCGGTGGACC	AAGCACTGGT	GTTGGCTTCT	540
GCAGTGGACC	AAGCACCAGT	GGCTTCAGCG	GCGGACCGCT	CGAG		584

- (2) INFORMATION FOR SEQ ID NO:816:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GAGAATGTCC	AGCAAGGAAG	TGAAGACTGC	TCTAAAAAGT	GCTAGAGATG	CAATCAGAAA	60
CAAAGAATAC	AAAGAAGCTT	TGAAACACTG	TAAGACAGTG	TTAAAGCAAG	AGAAAAATAA	120
CTATAATGCC	TGGGTTTTTA	TTGGCGTTGC	TGCAGCTGAA	CTAGAACAAC	CTGATCAGGC	180
CCAGAGTGCC	TATAAAAAAG	CTGCTGAATT	AGAGCCAGAC	CAATTACTAG	CTTGGCAGGG	240
GTTAGCAAAC	TTGTATGAGA	AATATAATCA	CATAAATGCT	AAGGATGACT	TGCCTGGTGT	300
TTACCAAAAG	CTCCTGGATC	TTTATGAGAG	TGTTGACAAG	CAGAAGTGGT	GTGATGTCTG	360

CAAGAAACTT GTGGATCTAT ATTACCAAGA AAAGAAACAC CTAGAGGTGG CTCGAACATG GCACAAGTTG ATAAAAACAC GGCAGGAACA AGGTGCAGAA AATGAAGAGC TTCATCTCGA G	420 480 481
(2) INFORMATION FOR SEQ ID NO:817:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 209 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:	
GAATTCGGCC TTCATGGCCT AGGGGGAGTG GTGGGTATTG CTAAGTTATC AGTTATTTAA CCTTATGGAG TTTTATTTAA CCGTTTTTGT TTGACATGTT TTATATATAT GTAATTTTAT TTATTCTTCA CAAAATCCCT GTGAGGGGGG TGGTACTATT GTCCCCATTT AAAGATGAGA ACACTGAGGC ATGTCTAGAA TTCATCGAG	60 120 180 209
(2) INFORMATION FOR SEQ ID NO:818:	•
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 220 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:	
GGCTCTGTGG AATTCCATGG CATCTTCCCC GCCCCCCCA ACCCCCCCT TTCCCCCTTC TTTTTTTTT TTTCTTTTCT TTTCTCCCCT CCCCCCCTT CACCATTTCC CCTCGGAGGC GCTTTCCCCG GGCAGGGGCA GAGCCGGTCT CACCCCCCGC CTCTCCCCGG CCCCCGCCCC CCTATGGCGA GAGGGAGCCC CCTCCCAACC CGGGCTCGAG	60 120 180 220
(2) INFORMATION FOR SEQ ID NO:819:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 346 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:	
GAATTCGGCC TTCATGGCCT ACACATTCTT TTAGTCAGAA ACATTAAAAT AGTAGAGTAA GTTGGCTTGA AGTGAATTTT TGTGTGAAAT CTTTTCTCTG CCCTAGCCTA GTTTGTCCAT GCACATTTGC ACACAGGAAG AACATTTTTA GACCTGCCAG AATATGCAAT GACAGGGTAA AAAATGCCGG AGGTTGACTG TGTTCATAGA CATTGTGCTA AACACTCAAC ACTCCTGATC ACACTGAATG CTTTTGACAG TCCTGTGAAT TGAGGGCTAT TATTATCCCC ATTTTATATA	60 120 180 240 300
TGAGCGAGCA GAGGCCCAGA CAGATTAACA AAGGTGCTCC CTCGAG	346

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 355 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:	
TGGCACTTCT ATGTTGCCAG GATTTCTCCA CAGATTGCTT GCAGAAATAA GGTATTTGGT AGAAAAACCA AAATATAAAA AAGCACTTGG CACTAAGACA TTTCGAATTC ATACTCCACC TGCAAAAGCT AATTGTGTGG CCTGGTTGGG AGGGGCTATT TTTGGAGCAT TACAAGATAT ACTTGGGAGC CGTTCTGTTT CAAAGGAATA TTATAATCAG ACGGGCCGTA TACCTGATTG 3	60 20 80 40 00 55
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 273 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:	
GCTCGCCAGA TGATGTTCAC GACCACCCTT CTCATTGTGT TCTTCACTGT CTGGATCATT GGAGGAGGCA CGACACCCAT GTTGTCATGG CTTAACATCA GAGTTGGCGT CGAGGAGCCC TCCGAAGAGG ACCAGAATGA ACACCACTGG CAGTACTTCA GAGTTGGTGT TGACCCCGAT	60 .20 .80 .40
(2) INFORMATION FOR SEQ ID NO:822:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 286 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:	
AGGTTCGTGC CGCAGTAACA GACACAGTAT TTAATTGCAC ATACAGATGT TTGCTGGGTA TATTCACTGT AAATTTTATT TAATCTGTTT TTTTGTTTGT TTGGGGGGTTA TTTGGGGGGA	60 120 180 240 286
(2) INFORMATION FOR SEQ ID NO:823:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 297 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

GGTCTGGAGG AGGCCCGGAG	GGGCTGTGGG	TGGACCACTG	CAGTAATCTG	GGTGAAAGAT	60
GATGATAGGC TAGACTAATA	TGGTACCAGA	GACAAAGAAG	AGGGACTTGA	GAGTTATTTA	120
GGAGGAAAAA AACAAAACAA	AACAAAAATC	AACCAGACTT	ACGTTTTGAA	ATAGGACAAG	180
TGAGGAAAAG GAGGGTTTCG	AGAATAGCTT	ATAGTTTTCG	AGAAGATGAG	GTTGGACAAG	240
ATGCCACTGC TTTTCTTAGC	ACTCTTCCCT	CCCCTAAACC	ATCCCGTAGT	GCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:824:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

GAATTCGGCC	TTCATGGCCT	ACCCTCATTA	CCCCAAGTGC	CTCCTAATGG	ATCTGTCCTT	60
ATTCTTCCTT	GTTCTGTCTC	CCTCATGCCC	TGGAGCTCCT	CTCTTTGGGA	CCTTCCTCTC	120
CCAAGTCACC	ACCCTCTCTC	CCCTTCTACC	ACTCAGCCAT	TCCCCAGTTT	CCACAGTTCC	180
TCAAACATTA	CCCCACTCCC	CACTCCCCAG	TTTCCTCCCC	CTCCCCATTT	GTCCCCCTCA	240
CCTGGGGGTC	CCCGAAGTAG	ATCTGCAG				268

- (2) INFORMATION FOR SEQ ID NO:825:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

GAATTCGGCC	AAAGAGGCCT	AGATGTGAGC	TGGGGAAGGG	AGGGTGGCCA	GTAATGGGTT	60
		ATCACTGTGG				120
GGGATCCAGT	GCAGAACATA	TCCCTCGCAG	GAGATGAGGA	ACTGGGGTGT	TCACAGAGTA	180
ATTCCCTCCC	TCACTAGTTG	AGGGCTGCCT	CTGGGGGTGG	CTGAACTACC	TCATGCAGCC	240
AGAGAAAGTC	CTCAGGCAAT	GAAATACAGA	CACTGGCCAG	CCAGCACTGA	GGTGGCGAGA	300
CCTTACTGGC	TGGTCCCCAG	AGTGTCTGCA	GCATTGTGTG	AGATCTTAAA	CTGGCTAGAA	360
GGACGGTAAC	AGCAGCACCT	GTTTCATAGG	ACGTGAAGAT	AGACGAGACA	G	411

- (2) INFORMATION FOR SEQ ID NO:826:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

GAATTCGGCC	AAAGAGGCCT	ACTAAAACCA	TAATTGCTTG	TTTTTGCCTG	TATCTGTCTT	60
			TACATTCCCA			120
			TTGGCCTTCA			180
TTCCTATGGA	AAAGTAAAAT	TGAATTATTC	CAGATATGAT	GACTTTAGGA	TATCCTTTTC	240
CCTCTTGTAC	ATCCTTCATT	GTATTTGTGT	TTTCCCTTTG	GTCTCCAACG	TCCCCACCAC	300
CCCCAATCCC	TCCACGACTT	TTAAGCCCTT	GGAAGCCAAC	TTGATTAGTC	AGG	353

- (2) INFORMATION FOR SEQ ID NO:827:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

			CCCAGGGTGG			60
			CTCCGCTCCC			120
AGGGGCTCAG	CCACTGCTTT	TAGCTGTCTG	CTGGCTTTCC	ACCCTTCCAG	CCTGAACCCT	180
			GACACTCCAG			240
CTGAATTTCT	GTAACGACAT	CTAACTTTTA	TTTAATTAAT	TTATTTATTT	AGAGATGGAG	300
TTTCTCTCTT	GTTGCCCCGG	CTGGAGTGCA	ATGGCACCAT	CTTGGCTCAC	TGCAACCTCC	360
GCCTCCCAGG	TTCAAGTGAT	TCTCCTGCCT	CGGTCTCCTG	AGTGGCTGGG	ATTGCAGGCA	420
CCCATCTG						428

- (2) INFORMATION FOR SEQ ID NO:828:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 base pairs
 - (B). TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

GAATTCGGCC AAAGAGGCCT	AAGCGGTATT	TCAGCCACAG	AGTTGGTGTT	GGGTTTACTT	60
ATCTATTTTG AATTTAAAAG	GCTTATAAAT	AAAGCAGTGA	CACTGCTTAC	TGGGAAATGC	120
TGTACCAAAA AATGTTATCT	TGCT				144

- (2) INFORMATION FOR SEQ ID NO:829:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

GAATTCGGCC AAAGAGGCCT AGCGGACTAG GAGTCAATAA AGTGAȚTGGC TTAGTGGGCG 60 AAATGTTATG CTTTGTTGTT TGGATATATC TGGAG 95

- (2) INFORMATION FOR SEQ ID NO:830:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 610 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

GAATTCGGCC	AAAGAGGCCT	AGTGGCTACC	TAAATTGAGT	ATCTGGCAAG	AGTAAGATTA	60
AGCAGTAATT	TGTTCCAAAG	AAGAATCTTC	TACCAAGGAG	CAACTTTAAA	GAATGAAATT	120
AACTTTCTTC	TTGGGCCTGT	TGGCTCTTAT	TTCATGTTTC	ACACCCAGTG	AGAGTCAAAG	180
ATTCTCCAGA	AGACCATATC	TACCTGGCCA	GCTGCCACCA	CCTCCACTCT	ACAGGCCAAG	240
ATGGGTTCCA	CCAAGTCCCC	CACCTCCCTA	TGACTCAAGA	CTTAATTCAC	CACTTTCTCT	300
TCCCTTTGTC	CCAGGGCGAG	TTCCACCATC	TTCTTTCTCT	CGATTTAGCC	AAGCAGTCAT	360
TCTATCTCAA	CTCTTTCCAT	TGGAATCTAT	TAGACAACCT	CGACTCTTTC	CGGGTTATCC	420
AAACCTACAT	TTCCCACTAA	GACCTTACTA	TGTAGGACCT	ATTAGGATAT	TAAAACCCCC	480
ATTTCCTCCT	ATTCCTTTTT	TTCTTGCTAT	TTACCTTCCT	ATCTCTAACC	CTGAGCCCCA	540
AATAAACATC	ACCACCGCAG	ATACAACAAT	CACCACAAAT	CCCCCCACCA	CTGCAACAGC	600
AACCACCAGC						610

- (2) INFORMATION FOR SEQ ID NO:831:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 564 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

GAATTCGGCC	AAAGAGGCCT	AGGAAGAAAC	AAGAACAAGA	AAAAAGATTA	TATTGATTTT	60
AAAATCATGC	AAAAACTGCA	ACTCTGTGTT	TATATTTACC	TGTTTATGCT	GATTGTTGCT	120
GGTCCAGTGG	ATCTAAATGA	GAACAGTGAG	CAAAAAGAAA	ATGTGGAAAA	AGAGGGGCTG	180
TGTAATGCAT	GTACTTGGAG	ACAAAACACT	AAATCTTCAA	GAATAGAAGC	CATTAAGATA	240
CAAATCCTCA	GTAAACTTCG	TCTGGAAACA	GCTCCTAACA	TCAGCAAAGA	TGTTATAAGA	300
CAACTTTTAC	CCAAAGCTCC	TCCACTCCGG	GAACTGATTG	ATCAGTATGA	TGTCCAGAGG	360
GATGACAGCA	GCGATGGCTC	TTTGGAAGAT	GACGATTATC	ACGCTACAAC	GGAAACAATC	420
ATTACCATGC	CTACAGAGTC	TGATTTTCTA	ATGCAAGTGG	ATGGAAAACC	CAAATGTTGC	480
TTCTTTAAAT	TTAGCTCTAA	AATACAATAC	AATAAAGTAG	TAAAGGCCCA	ACTATGGATA	540
TATTTGAGAC	CCGCCGAGCT	CGAG				564

- (2) INFORMATION FOR SEQ ID NO:832:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 424 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

- (2) INFORMATION FOR SEQ ID NO:833:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

GAATTCGCCA	AAGAGGNCTA	GTCTACATCA	GCTAACTTTC	CTACAAGATT	ATCAAATTTT	60
ACACAGTATT	TTTCTGTATT	TAATGACTGC	CATGGTCTGC	AAAATTATGT	GATTAGACAA	120
TGAATGACGC	TTAAAGAATG	ATGACCTATT	TTCTAAAGTA	CACTCAAAAT	ATTAAACTTT	180
AGAGACAAAG	CAAAATCTAT	CATAAAGTTG	GCTTCTGTTG	ATAGAAACAG	AGAGGTAGGT	240
TAATAATCAC	TGTCCTAAGA	TAAGCNAGAA	TGCTTAGAAA	TAAAAGTTGA	GACCCTGCTT	300
CAAAAAAGAG	AAGTTGAACC	TTCCAGCCCT	GAGTTTCTAA	TATTACATGA	AAATTATGAA	360
AATGAGCATT	AAGCCAGTCG	CAG				383

- (2) INFORMATION FOR SEQ ID NO:834:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

GAATTCGGCC	AAAGAGGCCT	ACTACGTAGT	TGGAGCTNTT	TCTTCCCCCA	GCAAAGCCAG	60
AGAGCTTTGT	CCCCGGCCTC	CTGGACACAT	AGGCCATTAT	CCTGTATTCC	TTTGGCTTGG	120
CATCTTTTAG	CTCAGGAAGG	TAGAAGAGAT	CTGTGCCCAT	GGGTCTCCTT	GCTTCAATCC	180
CTTCTTGTTT	CAGTGACATA	TGTATTGTTT	ATCTGGGTTA	GGGATGGGGG	ACAGATAATA	240
GAACGAGCAA	AGTAACCTAT	ACAGGCCAGC	ATGGAACAGC	ATCTCCCCTG	GGCTTGCTCC	300
TGGCTTGTGA	CGCTATAAGA	CAGAGCAGGC	CACATGTGGC	CATCTGCTCC	CCATTCTTGA	360
AAGCTGCTGG	GGCCTCCTTG	CAGGCTTCTG	GATCTCTGGT	CAGAGTGAAC	TCTTGCTTCC	420
TGTATTCAGG	CAGCTCAGAG	CAGAAAGTAA	GGGGCTTACT	CGAG		464

- (2) INFORMATION FOR SEQ ID NO:835:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

GAATTCGGCC	AAAGAGGCCT	ACTGGGAGTT	CGGAGTGATT	GTTTCCTGTT	ACAGGCCAAA	60
AAATTTGTTT	GGTTACTTAG	TGGTAGCATT	TTGAGAGGAA	AGTTTACAGA	AAACTAGGGT	120
TATTTTGTGA	TTATGCTTGA	ATTGTCTTTA	TTGTTTCCAA	GGCATCTTTT	TTTTTTCCTT	180
CTAGTTATCA	AGATGTTAGG	TTCTGTGCCC	TTGTGGGCCT	TCCCTCTGCC	CAAAAAAAGC	240
ATGGATGAGC	AGAGTAATAT	CATTAAAATG	GCAGTCTTTG	TTAGTTTTTC	TAGAAAAGAT	300
GGTCTCGAG						309

- (2) INFORMATION FOR SEQ ID NO:836:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

GAATTCGGCC	AAAGAGGCCT	AAGGCAGGTT	TTTTTTTCTA	TGCTTATTGA	TTTAGCCTAT	60
CTATTTATAA	CAGTATAATT	CAGAATATAA	ATATGGAACA	AGTTTCATAA	GGAAGTTTAT	120
CTTTAACTCA	GACATTATAT	CATTAATACT	TCAAATCTCA	TTATACCATT	ATGACCTGAA	180
TGCTACATTT	TTCTTCCTGT	ATGGAGAGCT	TAGGGAAAAA	TTGTGGCCTG	ATGTCTTCAT	240
CCATTCACTT	ATCATAGAGT	ACATAATGAT	CTCAAATATC	CAAAAATGGT	TATATTCAGC	300
TGCATATTTC	TAAGAAAACA	GGCAGGACTC	GAG			333

- (2) INFORMATION FOR SEQ ID NO:837:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 706 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

GAATTCGGCC	AAAGAGGCCT	AATTGATTTC	CCATGAGTCT	TGTAATCTTT	GCTCTGCTGA	60
TTGCGTTTGC	CGTCTCTAGA	CCATCTCGCT	TCGAACAAAT	CGCAAAAGAG	GTGAATTCCA	120
GAAGAACGAC	CTGGATTGCA	GAAGAATCGG	CTCCGTTCCG	TGACTATGCT	CGTTTGATCG	180
GTACCCTTCC	AAATACGGTC	CCTCTTCCGA	GTAAGACTGT	CGATGTCGTG	AAGAACCTTC	240
CTGAGAGTTT	TAACGCATTG	GAAAAGTGGC	CGGAATGCAA	GTCCATCACG	GAAATCCGTG	300
ATCAAGGAGA	ATGTGCTTCA	TGTTGGGCAC	TGGGGAGTGG	CGGAGGTGGC	CACGGATCGT	360
CTTTGCATTT	CTTCCAACGG	AAAGGATCAA	TCCCGTCTCT	CTGCCGAGGA	TCTGTTGGGA	420
TGCTGTGACT	CTTGTGGAAT	GAAATGCAAG	GGAGGGTACA	CGGGGAATGG	CCTGGGAGTA	480
TGTACGTCAG	GTGGGAATTG	TGACGGGTGG	AGCGAATGGA	AACAAGGAAT	GGTGTAATGA	540
GTACGCGTTC	CCGAAGTGCA	GTCACGGTAT	TCAGGGCTCC	TATCCTGAAT	GCTCTTCCAT	600
CCCCCTGAA	GATCCGGAGT	GTTCAACGAC	TTGCATAAAG	GGGTATCCCA	TCCCATATGA	660
TCAGGACCGT	CACAAAATGA	AGTCAGCCTT	CCAGCTGGCA	CTCGAG		706

- (2) INFORMATION FOR SEQ ID NO:838:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

GAATTCGGCC						60
ATCGTTGGCC	TATCATTCCA	AACTCCCTAC	AGTGTGGCTT	CAGCTTATCT	CTCTCTGTTT	120
TTTACAGGAA	TCCTAAACTC	TAACCCAGGG	ACCCTCAACA	TCTGTGCTGG	GTGGACTGTG	180
GCCACATTTT	CAGCTGGCCA	GTGTAAGGGT	TTTAGAGGCC	CTTACATGAG	AAGAAATACA	240
ATTTTTAAGT	CTCTGAGATG	ATGTGCTTCT	TACATTTTTG	GAATTAAAAT	GCCTCTTTAC	300
TTATAAAATG	CTGGTAGTAA	TAGATGGTCA	TTATCTCACT	GTCATTTGTG	AAAGAAAAA	360
CGATTGTAAT	AGAATTCTTG	CTATTTTTTT	TCTCTAAGGG	AGGTAAGTTT	TCTCCCTAAG	420
CAAACTTTAT	GGAATGCACA	ATGCTTGGCT	TTCACCTTCT	TTTATTCTCA	CTACCACCGG	480

- (2) INFORMATION FOR SEQ ID NO:839:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 589 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

GAATTCGGCC	AAAGAGGCCT	AGAATTAAGG	TGTATTATGA	GCAGTTGAAG	ATATATAGGA	60
AATTTTTTCC	CAAACCACTA	TCTCTGCTCG	TTCTATTCAT	TCAGTCTGTT	TATGTTATTC	120
CTTCATTCAT	TCATTTTATA	GAACAGTGGA	GTGCCTACTG	TATGCATCTA	TTGTTCTGGG	180
TCCTGGGGAA	AGAAAACAAA	GTTCCTGCTT	TCATGGAACT	TACATTATAT	TGGCGGAGAC	240
AGTAACAGAC						300
CTGGGAGAGA	GTAGTAGGGA	GTGCTATTTT	CGAGGTGGTT	GTCAGGAAAG	GCCTCACTGA	360
GGAGGTGGCA	TTTTGAGTAG	ACCTGAGCGC	AGCGGGGGCG	TAAGCCCAGG	CAGCATGTGG	420
AGGAAGAGTG	TTCTTGGTGA	AAGGAACAAG	GATAGAGGCC	CGAAGCTAGA	GAGCTCAGCA	480
TGATCAAGGA	ACAGCAAGCC	CCGTGTGGCT	GGAATGGAGT	GAGCAAAGGA	ATGAGCAGTA	540
GAAGGTGAGT	GAGTTGGGAG	GTCACCAGAG	ACCATGGCAA	AGACTCGAG		589

- (2) INFORMATION FOR SEQ ID NO:840:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

GAATTCGGCC	AAAGAGGCCT	AGGGACTAAC	TGCAACGGAG	AGACTCAAGA	TGATTCCCTT	60
TTTACCCATG	TTTTCTCTAC	TATTGCTGCT	TATTGTTAAC	CCTATAAACG	CCAACAATCA	120
TTATGACAAG	ATCTTGGCTC	ATAGTCGTAT	CAGGGGTCGG	GACCAAGGCC	CAAATGTCTG	180
TGCCCTTCAA						240
TAAAAAGTCC						300
GAGAATGGAA	GGAATGAAAG	GCTGCCCAGC	AGTTTTGCCC	ATTGACCATG	TTTATGGCAC	360
TCTGGGCATC	GTGGGAGCCA	CCACAACGCA	GCGCTATTCT	GACGCCTCAA	AACTGAGGGA	420

GGAGATCGAG

(2) INFORMATION FOR SEQ ID NO:841:

430

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 101 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:	
GAATTTTTAC TTGTCTATAG TCTAGTATTG TTATACCATG TGGTCTTGTT ATAATCATGG TTTCCATTCT GTGAGTCTTC AGATTATAGG CCTCTTTGGC G	60 101
(2) INFORMATION FOR SEQ ID NO:842:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 479 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:	
GAATTCGGCC AAAGAGGCCT AAATGGCGTC GTGGCATTGA GGGGCATCCC TCCTAGAACC TCCAGGAAAA GCTCGCGGAA GACGAGGTTC TGCGGAAGAG GAGGCTCCAA GCAGTCTGGG AAGTGTAGTC CAGTTGGCTT AGCAGTAGTT TCGTTGGGG GGAGCCGAGG TTCCGGGAAG GGGCTAGGCC GGCTTGAAAA GAGATTATGA CTGTACCTTT TAACTTTGTA GCTGGAACAC AAGAAGTGTT TGTTTAATGA ATGACGTACA CATTTAAGAT CTGTTTGGAC GCGGAGGATA ATCCTGTGAA TTGCTAATAG TTCACTGGGT TTGGCCCTTA GTGTTGACTT CAGTATGCTG AGACGGAAAC CAACACGCCT AGAGCTAAAG CTTGATGACA TTGAAGAGTT TGAGAACATT CGAAAGGACC TGGAGACCCG TAAGAAACAG AAGGAAGATG TGGAAGTTGT AGGAGGCAG	60 120 180 240 300 360 420 479
(2) INFORMATION FOR SEQ ID NO:843:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 270 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:	
TGGAAGAGCT AACTCGTCTG GCCTTTGAGC TCTTTGCTGA AGAGCAAGCA GAGGGTCCCA ACCGCCTGCT GTACAAAGAC GGCTTCAGCA CCATCCTGCA CCTGCTGCTG GGTTCACCCC ACCCTGCTGC CACAGCTTTG CATGCTGAGC TGTGCCAGGC AGGATCCAGC CAAGGCCTCT CCCTCTGTCA GTTCCAGAAC TTCTCCCTCC ATGACCCACT CTATGGGAAA CTCTTCAGCA CCTACCTGCG CCCCCCACAC GCATCTCGAG	60 120 180 240 270
(2) INFORMATION FOR SEQ ID NO:844:	
(i) SEQUENCE CHARACTERISTICS:	

361

(A) LENGTH: 413 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:	
GAATTCGGCC TTCATGGCCT ACACAGCCAG TATCAGAACC TCAAGAAAAC GAGGACACTG GGGACAGGGA CCAAAATTCA GACCACTTTT TTCTCTTGCC TTTCAATAGG ATATTCTGTT AATTGAATTC ATCTGAAAAT CAAGGTCATT GCAGAGAAGT CAGCATTCTA GAGCACAGAA	60 120 180
CAGGGCAAAA CAGGACGAAA GATGGATTTG GAGACCAAAT GGAGAAGGAA GAACAGAGAT ACGTGTGCTC CAAATATGAC ACCCAACTTC TTTACTCAGA GCAGTTACAT GTCAGATTAT ATTTTAGTTT TTCATTTCTC CTATAGGCAT ACATACTACA AGTCTATAAT AGAAAACTAG TGGCTGGGCG CGGTGGCTCA CGCCTTTAAT CCCAGCACTT TATGGCGCTC GAG	240 300 360 413
(2) INFORMATION FOR SEQ ID NO:845:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 126 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:	
GAATTCGGCC TTCATGGCCT AGGCTCTGTC TACCAAAAAA AAAAAAAAAA	60 120 126
(2) INFORMATION FOR SEQ ID NO:846:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 269 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:	
GCTTCATGGC CTAGTTGAAT AGTCAGTTAG AAATGGAAAG AATGAAAGTT GAACAAGAAA GACAAAGCCT TAGAACAAAA GACACAGCCC TAGAACAGAA GGACAAGGCC CTGGAACCAA AAGACAAAA CTTAGAAGAA AAAGACAAGG CCCTGGAACA GAAGGATAAG ATTCCAGAAG AGAAAGACAA AGCTTTAGAA CAAAAGGGCA GAGACTTAGA GCAAAAAGAC ACAGCCCTAG AACAGAAGGA CAAGGCCCTA GAACTCGAG	60 120 180 240 269
(2) INFORMATION FOR SEQ ID NO:847:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 264 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

GCGATTGAAT	TCTAGACCCA	CCTTCAGACC	ATCTCGGAAG	ATCTAAAAAG	CCTGACCATG	60
GACCCTCACA	AACTGCCCTC	CTCAAGTGAA	CAGGTGATTC	TGGACTTGAA	AGGTTCTGAT	120
TACAGCTGGT	CGTATCAGAC	GCCACCCTCT	TCCCCCAGCA	CCACCATGTC	CAGAAAGTCC	180
AGTGTCTGCA	GCAGCCTGAA	CAGTGTCAAC	AGCAGTGACT	CCCGGTCCAG	CGGCTCCCAC	240
TCGCATTCCC	CCAGCATTCT	CGAG				264

- (2) INFORMATION FOR SEQ ID NO:848:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

GAATTCGGCC	TTCATGGCCT	AGAACATTCC	AAATTTTCTT	GGTTTCAATA	CCCTTTTTTT	60
TCTTTTGAGG	GGAAAAGAGG	GGAGAAAAAC	AGGAGTGATG	TCATTTCTTT	TTCATGTATT	120
CCAATTAAAG	AAACAAGGGC	AGGTCGTATA	ATGGCATATT	AATACATTAG	ACTTAATCTA	180
GAACCCCTGT	AGCTTTTTGA	TGTGTTTTAT	TTCTTATCTC	TTTGAATTCC	TGTTTGGTTA	240
CTTGGCTTCC	AATGGAGGTG	AACTTAACAA	CCATACTTGA	ATATTCCGTC	TTGACTTTGT	300
AAACTGTGGC	TACTTGAAAT	GAAGTTTATC	TGGGGTCTCG	AG		342

- (2) INFORMATION FOR SEQ ID NO:849:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

GAATTCGCCT	TCATGGCCTA	GGTTATTCTA	TTATTTGTAG	CTGAAATAAT	TCCTGGCACA	60
AATGACTTTG	AAATTTATCT	CTGAACATCC	CAAATTCATT	ATTAGCAAAT	ATCAGAAACT	1.20
TCACATCACT	CCAGTCTGTT	ATTTCACATG	GTTTTCTTAG	GGCCTGGAAA	GTTTTTACAG	180
CTGGCTTTTA	TTGACTGTGG	TGGCTGATAT	GCTGAAGAAT	GGAGCTCATT	GGTTTGAGGC	240
TTCTGCCAG						249

- (2) INFORMATION FOR SEQ ID NO:850:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

GAATTCGGCC	TTCATGGCCT	AGACATGAAT	TCTTTGACTT	GTGCTCATTC	TTTCTGAACT	60
TATTGAGGCT	TATATATATC	AAATAAGGTT	AATTTACACA	ATAATTATTT	TTAATAATTA	120
ATAAACTCAT	TCATGTAGTA	TATTTTAAAA	CATTATTTCC	TCTCATTTTT	CCTTCTCTTT	180
TTTCTTCCTA	TATATTTTTA	AGGTTTCAAG	AGAAAACGGG	CTTCAGTTTT	TAAAAAAATG	240
TAGACTTGCA	TTTTTACTGT	GCTTATTTAA	AATAATGGAT	ATAATTTATA	TTAAGGTCCA	300
AATTATTTA	TTCACAGGAT	AATCATGGTC	TCTGATAAAA	GATGCCCACA	TTTCTGTGTA	360
CTCACAGTTG	TTGTATATTT	TTCAATTTCA	ATTTTGAAAG	TAAACTCAAC	ACTCGAG	417

- (2) INFORMATION FOR SEQ ID NO:851:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

GAATTCGGCC	TTCATGGCCT	AGCTAGCTAT	TGTAAATACA	AATAATAAAG	TCTGCATTTC	60
CTGTCTTCTT	TAAGCCTTCA	TTGCCTATTA	AATCATTACA	TTTTAGATTA	GATATTATAT	120
TTTGATCATT	TGAGGAACCA	AATTAAAAAT	ATGGAATAAG	TATGGCATTG	AATTATACAT	180
GCCTATTGCT	AATATATTCA	TATTTTATAG	GATTTAATGA	AACAGTCTCC	CAGCTCGAG	239

- (2) INFORMATION FOR SEQ ID NO:852:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

GAATTCGGCC	TTCCCTAGGA	AAGTTCTTCA	CATCAGGAAA	CATTAGATCA	TATACAGAAA	60
CAAACTAAAT	TTGATAAAGT	AGTTATGGAG	TTTTTGCATG	AGTGTATGGT	GAATAAATTC	120
AAGAAAACAT	CTATTCGTAA	GCAACAGACA	AATAATCAAA	CAGAAGTAGT	TAAAATAATT	180
GAAAAAGATG	TTATGGAAGG	TGTTACTGTA	GATGATCACA	TGATGAAGGT	AGAGACAGTT	240
CATTGCAGCG	CTTGCAGTGT	GTATATCCCT	GCTTTACATA	GTTCAGTTCA	GCAGCACTTA	300
AAATCTCCTG	ATCATATCAA	AGGGAAGCAG	GCTTATAAGG	AACAAATAAA	AAGAGAGAGT	360
GTCTTGACTG	CTACAAGCAT	TTAAATAAT	CCAATAGTGA	AGGCGCGATA	TGAACGTTTT	420
GTTAAGGGTG	AGAATCCTTT	TGAAATTCAA	GACCATTCTC	AGGATCAGCA	AATAAAAGGC	480
AGACTCGAG						489

- (2) INFORMATION FOR SEQ ID NO:853:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

GAATTCGGCC TTCATGGCCT ACTTCACTAA CCTTTTTTGT TTTAAAATGA ACCTGCTACT TAAAAAAAAT ACACATCACA CCCATTTAAA AGTGATCTTG AGAACCTTTT CAAACCAGAT GGAGCATTGC TTGCAAATTT TTTTTCTCTA TGTTTGCATG CGCTCGTGTG TGTGTGTCCA GGCAAGAACA CATTTTATAA AAATAAGAAC ACTTGGGCTG GGCATGGTGG CTCATGCCTG TGATCGCAGC TCTCTCGAG	60 120 180 240 259
(2) INFORMATION FOR SEQ ID NO:854:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 217 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:	
GAATTCGGCC TTCATGGCCT ACACAGCTGC AGTCAACATC CACAACTACC GGGACCACAG CCCCTACTGC TGGCTGGTGT GGCGTCCAAG CCTTGGCGCC TTCTACATCC CTGTGGCTTT GATTCTGCTC ATCACCTGGA TCTATTTCCT GTCGCCGGGC TACGCTTACG GGGTCCTCTG GCACAGAACC CCAAGGCGGG CAACAGCAGG GCTCGAG	60 120 180 217
(2) INFORMATION FOR SEQ ID NO:855:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 246 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:	
GAATTCGGCC TTCATGGCCT AGACCTGCCT CGAAAATAAA TAAATAACCC ACAGAGCTGA GCACAGGCTT CTTCATGCTT TTCCTTTGGA AGGTGTCCTA GATATATGAT GATTTCTTT TTCTTTCACC TCCTCTTGAT TGTCACAAGT AGCTTGCTTG GCTCAGGAAC AACAGAAGAG AATAAAGAAA ATGACCTCAG ACCTTCCTTA CCTCAGTCTT ATGCAGCGAC CGCAGCCAGA CTCGAG	60 120 180 240 246
(2) INFORMATION FOR SEQ ID NO:856:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 334 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:	
GAATTCGGCC TTCATGGCCT ACTGTCTCAA AAAACAAACA AACAAAAGA AAGAAAGAAA AAGGAAAGGT AGACTTATAT AAAATAGACA GTAAAGCATA GGGCAGCAGA AAGGAAAACC TACTCCGCAA AAGTCACTTG TTTTAACCTC ATCCAGGAGC TTCCTCTAAG TTCACCTTTA	60 120 180

240

300

334

TTTTTCACAC GTCCTGGGTC CAAATCCCAC CATGCTCTGC CGTATTCTTG CCCTTTGCTC

TGTTGTTGAA AGAGTCATGA GCGAGGCCTC TCTATGGATG GTTCCAATGA GCCACATGAA

CAAAGCCATC GTCAGTAAGC AGCCACTTCT CGAG

(2) INFORMA	TION FOR SEQ ID NO:857:	
(i) s	SEQUENCE CHARACTERISTICS: (A) LENGTH: 129 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:857:	
	TGATCAACTT AATTCCTTTT CTTTATCTTC CCTÇCCTCAC TTCCCTTTTC TTTTCCAAGC TGTTTCGCTT TGCAATATAT TACTGGTAAT GAGTTGCAGG	60 120 129
(2) INFORMA	TION FOR SEQ ID NO:858:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 260 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:858:	
TTCAGAAAAA TAGAAAATAA TGTTTTGAGT	ACCATAATTT GGCCACTCAG CTGTCATCAG GAACTAAGCC AACATTCCTT GACTTTGGAG AGGGCAAAC ACTTCTGACA GTCATACTGT GTACTTATTT GCTGCTCTCA GGCTTCAGTA TCCAGTCAAA TATAATATAG AACTCTAGTC CCTACTACAA TAATATTTTC ACAATAGACT ACCAGTTATG AAGTTCTCAC CATGCTCGAG	60 120 180 240 260
(2) INFORM	ATION FOR SEQ ID NO:859:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 217 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

GAATTCCTGT	CCCACCTGCT	GAATGAGTGC	GTGCCAGCTG	AACATCAGCG	TGGCTTCGTT	60
CTTCAACACA	TTTACAAAAG	AAGTAAAAAT	AAACAGTTTT	TTCTTCTCAA	TTCTCCTCCC	120
TGCTTTTTTC	CTTTGGAACC	ACAATCATGC	CCCAGTAAGT	GCTTTCCTAG	GTGAGAGGTG	180
TGTGTCCCAG	GTTGAAGGCA	AGGCCAGTGG	TCTCGAG			217

- (2) INFORMATION FOR SEQ ID NO:860:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

(ii) MOLECULE TYPE: cDNA

	TTCATGGCCT AGAATATTTT TATCATCCCA AAGCTAAAAC ATTAAAAAAT TTCTTAGAGA TTGATGCAAC TTGCATATCT AATCGAG	60 107
(2) INFORMA	ATION FOR SEQ ID NO:861:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 279 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:861:	
ACAAAATTTT ATTTTTTTTT CATGATCTCA	CCTGCCTCGA GGGCATCCTT TACTTTTTT TTTAATTCAG CACAAACCAA AAAATTTGAT GAGATTTGAA GTTGGACAAA AGTGTTATGC AGTTTTAAAA TTTTTTTTTGA GACCAGATCT CACTCTGTTG CCCAGGCTAG AGTGCAGTGG GCCCAAACCT CTACCTCTTA GGCTCAAGCG ATCCTCCCAT TTCAGCCTCC GGAGGCTGAA ATGGGAGGAT CAACTCGAG	60 120 180 240 279
(2) INFORMA	ATION FOR SEQ ID NO:862:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 266 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:862:	
TTTTGCAAAT CCTTTGCATC GTTTGATAAT	CGTGACCTGT TTTCCAGAAT TTATGATATT TCTATGGTTG GTATTCTCAA GTGTCTTGGT GTGGAACTTT TTCATTTGTT TTGCTGGGGA ATTGATGGAT AAGATGCTTA TATTTATTCT TCAGTTCTGG GAAACTTCCC TGTATTATTT TGCTTTCTCT CTGCTTTCTC TTTTCCGTTT TTTGGAATTG CTTGTTTGTG CTGCAGAGAA CTCGAG	60 120 180 240 266
(2) INFORM	ATION FOR SEQ ID NO:863:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 355 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)) MOLECULE TYPE: cDNA	
(xi)) SEQUENCE DESCRIPTION: SEQ ID NO:863:	
CTCATATAAT	TTCATGGCCT AGTGCTGTGG TAGTTTGTGC CTTTAGAGGG ATTTGTGTAT TTAATTTTTT GACATTCACT TTTTCACAAT ATTCTGTTAG AATTCTTTTA GGTGATATCT ATACTTTCAT TTATGTCTAG TAACTTGAAT CTTCTCTCTT	60 120 180
	367	

TTGTTCTTTC TCGGTCAAAC TAATAATACG TCAATTTTAC TGATATATCA GAAGAACCA CTTTCAAGTT TATTAATTTT CTCTATTGTT TTTATTTTCA CTACTTATCT CCATGCTAAC CTTTATTATT TCTTCCTTCT GTTTACTTTG GGTTAAGTCT GCTCTTTCAC TCGAG	
(2) INFORMATION FOR SEQ ID NO:864:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 205 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:	
GAATTCGGCC TTCATGGCCT AGCTTACTTT ACAATTCTGC TGTTTGTCAA GTGTTCCTAAGTTTTTTTT AAAGGTATGT TAACTATTTT TCCCTTTTGG TTTATATTTG TAGGAATCTTGCCTTTAAG TGTGCCCGTG CAGAAGAATT ATTTAACATG TTGCAAAGAGA TTATGCAAAATAATAGTATA AATGTGGAGC TCGAG	Г 120
(2) INFORMATION FOR SEQ ID NO:865:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 368 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:	
GAATTCGGCC TTCATGGCCT AGTCACTTGT TCTGTAGAAT ATGTTCAAAT CTGATTTTG CTTTTTGTTT TCTTGTGTTA TTACCTTGTT CCTCTATCCC CTGTTTTTTC TGAAAATGA AGTTAGCTTA GAAGTTTCAT TCCATTCTGG TTCAAAATGC TTAAGTGCTT TATGTCGTG CATATTAGGA AACACAGTAT CTAGTGGTCC CAATTTTAGT GATTCAAAAA TCAGTCTCT GGTTCAGAGA TTAATCAGTA GATTCAGAGA TCTCTCCATT GTAAATTTCT TAATTAACC TTGAATTGCT AATGTTCTGT TCACTGATCG TTGTGGCCCA AATTATTTAT TTCACTAGG GACTCGAG	A 120 T 180 A 240 T 300
(2) INFORMATION FOR SEQ ID NO:866:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:	
GAATTCGGCC TTCATGGCCT AAGGAGCAGC AGGAACATGG TACATAAAAT CATCCTGCT CTTATAATGG CAGGAATCAG TGGGATATGG TATTTGTGCA GCATGCTGGG GCATCCACT GAAAGGCCTG AAGGAAGACT CGAG	
(2) INFORMATION FOR SEQ ID NO:867:	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

GAATTCGGCC TTCATGC	GAT TGAATTCTAC	ACCTGCCTTG	AGCCCCTCCA	CCCCCAAATC	60
CTTCCTCTCC TCCCAGT	CCC ACCCCTTGC	CCACGGAGTC	CTGGGGACGC	AGTGCCCCAG	120
CTGGGAAGAG GGCGGGA	TCG GGCACTGGTT	CCTCCTTGTC	CCCGCTTTCT	TGGGGGCTTG	180
CTACTTTTTG TCTTCTA	TTG TGTGGCTTTC	TGAGTATTTG	AACCCCAGTC	CTGTGTCACC	240
TTCCTTTTTC CTTCGCT	GTC CCCTCGAG				268

- (2) INFORMATION FOR SEQ ID NO:868:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

GAATTCGGCC	TTCATGGCCT	ACAGAACTAT	AATTTATCTT	AGTTTAAGCC	ACTGGTAAGT	60
GTAATTGTAA	TTGTAATTTG	TTACATCTGC	TATAGTGAAA	CTAATACTGA	AATTTAGAAA	120
AGATGGGTAA	CTTATTATGT	GGTGAAGTTT	AAAAAAGATA	AGTAACTCGT	TGAAGATCAC	180
ATAATTAGAA	AAGAAAGCAG	TAGAGCTTGG	CCTTGAACTC	AACCAGTGTG	ACTCCAGAGC	240
TTGTAGAACA	GAATAACCAC	CTCCAAGGCC	AGCTGAATCT	GACCACAGTC	TGGTGGAATT	300
CTAGTACATC	TCGTTGAGAA	GTGGGATTGC	CGGAGGGGAG	TTGGTTATTC	ATGAAGGTGA	360
TGATGTTTGT	CCAATGTCCT	CGAG				384

- (2) INFORMATION FOR SEQ ID NO:869:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

GAATTCGGCC TCATGGCCTA CTTGG	SAGAGT TTTGTAAGGA	GAGTGGCAAA CA	TAGCACGG 60
ACTAATGCCA CGAACAACAT GAATC	TAAGC CGAAGCAGCA	GTGATAACAA CA	CTAATACT 120
TTGGGGAGGA ATGTGATGAG CACAG	CAACT TCTCCTCTTA	TGGGTGCTCA GA	GTTTCCCT 180
AATTTGACCA CACCTGGTAC TACAT	CAACA GTGACTATGT	CAACATCCAG TG	TTACTAGC 240
AGCAGCAATG TAGCTACAGC AACAA	ACACTC GAG		273

- (2) INFORMATION FOR SEQ ID NO:870:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

GAATTCGGCC	TTCATGGCCT	AGGTCAGGAG	CCTTCTTGGA	GTCCCAATTC	TGCATCCCCA	60
AATGATAAAG	ATGGGGTGAA	GGAACTGAGA	GCCATGAGTT	GGAGAGTCCT	CTTGCTTGAG	120
GTCCCTGAGA	ATGTGGTCCC	GGAGTATCCG	GATCACTGGA	AGCCAGGACT	TCAACGCATT	180
GGGTAGTGAG	GGATGGAGGG	AGGGGCTGGA	CGCAGAAGCA	GGATGAAGTC	TGCTGGGTGT	240
GAGCCTCCAA	GGAGGTAGAA	CAAAGAGGGC	AACTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:871:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

GAATTCGGCC	TTCATGGCCT	ACCAGACTCC	CATAATAATA	AACCCTGGTA	ATAAACAAAG	60
GAACTCCTTC	CAGTTTCAGT	GTATCAACCA	CCACGTACCA	GATAAAATCT	TATTTCACCT	120
TTCACAATTT	ACCAGTGTTG	GGCTGTGAAT	TAATATTTTT	ATTTTTCTGT	GCATTCATAA	180
ATTAAGATTA	TTTTATTGTA	TTGTAACTGT	AATTTTGAGA	CTAAAGTCTA	AAAACAAGAC	240
ATCATGAAAT	GGAGCTGGAG	GATACTCGAG				270

- (2) INFORMATION FOR SEQ ID NO:872:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

GGTTTAGAAA	GGGCACAAAC	AGTGCAAACC	TGTTCATGAA	CCTTTACATG	TCATGAACAG	60
GGCAGAATGC	TTCAGGAAAG	AATTGTCGAA	AGTAAAAAAG	CAAATAATGG	ATGCAGCTTA	120
TTCTAGTTAT	TGAAGAATCC	AACGGGATGG	AAGCTAAATG	TAGCACATGG	CATGGGCGAT	180
GTCTCAACAG	TGAGTGGGAT	AACAAGTCGT	TTTAATGGTT	CAGGGCCAAT	AACCGGGGAG	240
GGTGAGGAAC	GGCATCTCTG	TTTTGAGTAA	ACAAGAGTGA	TTTCCTTCCC	TGACACTGAA	300
AAATGAAACC	TTTGGGGAGA	TAGAGGAAGC	GATCTCGAG			339

- (2) INFORMATION FOR SEQ ID NO:873:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

GAATTCGGCC	TTCATGGCCT	AACCTTTAAA	CCCTAAAATC	CAGGAAAAGA	AAATAAATAC	60
ATTATCATGG	ACCTGAGGGA	TTTTTACCTG	TTGGCTGCTC	TGATTGCCTG	TTTAAGGCTG	120
GATTCCGCAA	TAGCTCAAGA	ACTTATTTAC	ACTATTAGAG	AGGAATTGCC	TGAAAATGTG	180
CCCATAGGAA	ACATACCAAA	GGATCTGAAC	ATTTCTCACA	TCAATGCTGC	CACAGGGCCA	240
CCTCG						245

- (2) INFORMATION FOR SEQ ID NO:874:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

GAATTCGGCC	TTCATGGCCT	AGTTTTCTTC	ACTGGCATTC	ACAAATTTAA	GCCATTGCTG	60
CCTCATTAGC	CTTGTATTTT	GTGTGCATAT	CATATATCCA	GACCTGTATG	TTCACTTTAA	120
GCATTCTTAT	ATCACACTGT	CTCCTCATCT	ACCATATGGT	AAATGTTAAA	ACTCCACATT	180
TGTCTGCATC	AGGGAAAATG	CATGGGCACA	CATCCTCCCC	CCCTTCCCTC	GAG	233

- (2) INFORMATION FOR SEQ ID NO:875:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

GGACAGGAAG	TCAACTTCAA	GCAGATTGAC	TTGAAACGGG	ATCTCATTTA	GGAAGCATAA	60
GTGTCCAATC	AAAAACTGTG	TATTTTTTA	AATTTGGAAA	ATACTCAAGT	TCCAGTTGCT	120
TATCATTCTC	CTTCACTTTC	TGAAAACCTG	GCAATCCCAT	GTGGACTTCT	GGTAGAATGA	180
GCAATGCAAA	GAACTGGCTT	GGACTTGGCA	TGTCCTTGTA	CTTCTGGGGG	CTGATGGACC	240
TTACGACCAC	CGTTCTCTCG	GACACCCCAC	ACCTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:876:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

GAATTCGGCC	TTCATGGCCT	AGTCCTCAAA	TTAGTTATTG	CATTATTTTC	AAGTATTGTA	60
TTATCATTTA	TTGATATTGG	TAGTGTTTCC	TAAAACAGGA	AATACATAAT	TTGGCATCCT	120
TATTCTTAGT	TTTATACCTA	AAGAACCTAG	TAACTCACAG	GAGAACGTAG	TAACATTATC	180

ACTIGITAAT CAAGCITTCA GIGAAACAGI TIATCAAACC ATTITITITA TITIGATICA GCAAATTIGI CAACTAAATI TAATTIAAAA GIAGAGGICC AAAGCICGAG	240 290
(2) INFORMATION FOR SEQ ID NO:877:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 260 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:	
GAATTCGGCC TTCATGGCCT ACTCAAATTG GAAAGAAAGA TTCCTTGAGA CTTACTTTTA AAATCTAAAG TGTGAGGNNA ACANCAGAGT AAAGNCCAGA CTCATTNNAC CTTCGATGTC TGCATAGATC CAGNAGTTGT ACATTTTACC TAACAACATC ACTTTTGTTG AACATTCCAA CTCCAGAATG ATCCCCAATC ACCCTAATCT CAGAATGCTG GAATGATGTC TGTTGGCAAA CCCAGGACTC CACACTCGAG	60 120 180 240 260
(2) INFORMATION FOR SEQ ID NO:878:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 180 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:	
GAAGCGACCA TTCGTCCAAC AGGTATGGCT GGTTTTTGTG CAATGAGAGA ATGTCCACTC GCAATGATGA GCCTGAGAAG GCAAGTCGTC CGTTTGATGT GGATCGCGAT GGTTTTGTTA TGGGTGAAGG TGCCGGGATT CTTATTCTGG AATCACTCGA ACATGCTGAG AAACGTGGAG	60 120 180
(2) INFORMATION FOR SEQ ID NO:879:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 497 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:	
GAATTCGGCC AAAGAGGACT ACACAGAGCC CCTGTTTGGG AATTTGAGAT TCTGTGTCAT GCTGGTTTTC CTTTCAGAAT TGCTTGAAAT CGAGTTCTCT TAGCCACTGG ACACCTAGTT TTCAGGAGAA TGTCCCAAGA TTGTTTATAT ATACAAAATG GCAAAAGTAC TGTTTTTCGA ATTGATAATT CAAGCAAAGG CTTCTCTTTA CTGTCACTGA TTTTTTTTTT	60 120 180 240 300 360 420 480 497

- (2) INFORMATION FOR SEQ ID NO:880:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

GAATTCGGCC	AAAGAGGCCT	AGCAAAATCA	AATTCAACCC	ATGAGTCACA	GTGCTTTCTT	60
CAACAAGAAA	ACATTGAACA	CAGAAAGCAA	TTGTGAATAT	AAGGACCCTG	GGAAAATGAT	120
TCGCACGAGG	CCCCACCTTG	CTTCTTCACA	GAAACAACCT	CAGAAATGTT	GCTTATTTAC	180
AGAAAGTTTG	AAGCTGAACC	TAGAAGTGAA	CGGTCAGAAT	GAAAGCAATG	ACACAGAACA	240
GCTTGATGAC	GTTGTTGGGT	CTGGTCAGCT	ATTCAGCCAT	AGCTCTTCTG	ATGCCTGCAG	300
CAAGAATATT	CATACAGGAG	AG				322

- (2) INFORMATION FOR SEQ ID NO:881:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

GGCCCACCTG	TGTCCTGGTT	GAGGGTCTCC	AGGGTTCTTT	GGGGCCCGAG	GCCAATGGTG	60
GCAGAGTCTA	CATAGAACTA	TGCTTCGTGG	TGTTCTGGGG	AAAACCTTTC	GACTTGTTGG	120
CTATACTATT	CAATATGGCT	GTATAGCTCA	TTGTGCTTTT	GAATACGTTG	GTGGTGTTGT	180
CATGTGTTCT	GGACCATCAA	TGGAGCCTAC	AATTCAAAAT	TCAGATATTG	TCTTTGCAGA	240
AAATCTTAGT	CGACATTTTT	ATGGTATCCA	AAGAGGTGAC	ATTGTGATTG	CAAAAAGCCC	300
AAGTGATCCA	AAATCAAATA	TTTGTAAAAG	AGTAATTGGT	TTGGAAGGAG	ACAAAATCCT	360
CACCACTAGT	CCATCAGATT	TCTTTAAAAG	CCATAGTTAT	GTGCCAATGG	GTCATGTTTG	420
GTTAGAAGGT	GACAATCTAC	AGAATTCTAC	AGATTCCAGG	TGCTAGGCCT	CTTTGGCCGA	480
A						481

- (2) INFORMATION FOR SEQ ID NO:882:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

GAATTCGGCC	AAAGAGGCCT	AGGGAAGAGT	GGAACAAAAG	TCAGTCGTAC	ATTCAGCTAC	60
ATCAAGAATA	AAATGTCTAG	CAGCAAGAAG	AGCAAAGAAA	AGGAAAAAGA	AAAAGATAAG	120
ATTAAGGAGA	AGGAGAAAGA	TTCTAAAGAC	AAGGAGAAAG	ATAAGAAGAC	TGTCAACGGG	180
CACACTTTCA	GTTCCATTCC	TGTTGTGGGT	CCCATCAGCT	GTAGCCAGTG	TATGAAGCCC	240
TTCACCAACA	AAGATGCCTA	TACTTGTGCA	AATTGCAGTG	CTTTTGTCCA	CAAAGGCTGC	300
CGAGAAAGTC	TAGCCTCCTG	TGCAAAGGTC	AAAATGAAGC	AGCCCAAAGG	GAGCCTTCAG	360

387

GCACATGACA CATCATCACT GCCCACG

(2) INFORMATION FOR SEQ ID NO:883:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 443 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:	
GAATTCGGCC AAAGAGGCCT AACGCAGCCA TGGCTCGTGG TCCCAAGAAG CATCTGAAGC GGGTGGCAGC TCCAAAGCAT TGGATGCTGG ATAAATTGAC CGGTGTTTT GCTCCTCGTC CATCCACCGG TCCCCACAAG TTGAGAGAGT GTCTCCCCCT CATCATTTTC CTGAGGAACA GACTTAAGTA TGCCCTGACA GGAGATGAAG TAAAGAAGAT TTGCATGCAG CGGTTCATTA AAATCGATGG CAAGGTCCGA ACTGATATAA CCTACCCTGC TGGATTCATG GATGTCATCA GCATTGACAA GACGGGAGAG AATTTCCGTC TGATCTATGA CACCAAGGGT CGCTTTGCTG TACATCGTAT TACACCTGAG GCGGCATAA CACAGCAAGA CGAGAAGACC CTATGGAGCT TTAATTTATT AATGCAAACA GTA	60 120 180 240 300 360 420 443
(2) INFORMATION FOR SEQ ID NO:884:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 353 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:	
GAATTCGGCC AAAGAGGCCT AAACATCATT TGTACTCTAA TCCAATCAAA GAAGAAATGA CTGAGTCTAA GTTCTCTAAG TACTCTGAAA TGAGTGAGGA AAAACGAGCC AAACTTCGTG AAATTGAGCT CAAAGTTATG AAGTTTCAGG ATGAATTGGA ATCTGGGAAA AGACCTAAAA AACCAGGCCA GAGTTTCAG GAGCAAGTAG AACACTACAG AGATAAACTT CTTCAACGAG AGAAAGAGAAA AGAGTTAGAA AGAGAAAAGA AAAGAGACAA GAAAGATAAA GAAAAATTGG AATCTCGCTC CAAAGACAAG AAGGAAAAAA ATGAGTGTAC TCCGACAAGG AAG	60 120 180 240 300 353
(2) INFORMATION FOR SEQ ID NO:885:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 475 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:	
GAATTCGGCC AAAGAGGCCT ACAATTTTT GCCTTTTTAC CCTTCTGTCC TTTAATGCCA TCTCTTTCTC AATTATTTC TCTCATTTT TTTCTGAGCA GACTTATACA AAAAGGAACA TAAATTAAAT TTGCCAAATA TCAAAAGAGA GGAACTTTTT ATTTTTATT TTTTTGGAAC GGAGTCTCAA TCTGTCTCCC AGGCTGAGT GCAGTGACGC AATCTCAGCT CACTGCAACC TCCGCCTCCC AGTTCAAGAG ATTCTCTGCC TCAGCCTCCC GAGTAGCTGG GATTACAGGT	60 120 180 240 300
374	

ACCCTCTACC ATACTCAGCT	AATTTTTGTA	TTTTTAGTAG	AGACTGGTTC	ACCATGTGGG	360
CCAGGCTGGT CTCGAACTCC	TGACTTCAGG	TGTTCTGCCT	GCTTTGGCCT	TCCAAAGTGC	420
TGGGATTATA GGCGTGAGCC					475
(2) INFORMATION FOR S	EQ ID NO:88	5 :			

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

GAATTCGGCC AAAGAGGCCT AGGGGTGTTA ATTAGCTCAG CTGTAGCAAT CAT	TTTCATAA 60
TGTATATCAA AACATCCCAC TGTATACTTT ATACTTTTTT ATAAAAATAA ATA	ATTCTTAC 120
AAAAGGACAG GCGCTGTGTC TGTCTGGCTC ACCATTGTAC CCAATACCCA ACA	AGGGTGCC 180
AAGTACCCAA TACCCAACAG GGTGCCAAGG AACACAAAAG GCACTCAAAA TAT	TGTTTGTT 240
GATTGGAGTT TACAAGGAAG AAAGGTATTT TCTTATCCCT CTCTTCCCTT CCC	CACCCAAA 300
CATAGCTTCT TCTAAGAAAA GAAACTGAGG CTGGGCAAGG TTAAAAAGCTA GCT	TCCTGGTA 360
CTTTTGCATC CACACTCAGT TTACCTGTGC CTTAAACCAG ACTTCATCAA ACT	TTCAGTCT 420
TCACAAGTCA CTTCACCATT TTTGCTCTAC CTACTTACTG CCTGTGTAGG CCT	TCTTTGGC 480
CGAG	484

- (2) INFORMATION FOR SEQ ID NO:887:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 184 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

GAATTCGGCC AAAGAGGCCT AGTGGGACAT	AAGGCTGGAA	GGTAGCACAC	ACAGCACCAT	60
ATTCTTTTTT ACTTGCATGC GAGTTACTTT				120
TTCTATTACT ACATTCCTTT TCTTTGTTTG				180
CCNC				184

- (2) INFORMATION FOR SEQ ID NO:888:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

GAATTCGCCC AAAGAGGCCT AGTTTGCGAC TTACTTTTAA TTTCAAATCA GCTGCAGATG
TTTGGGAGCC TTCTCGAG
78

(2) INFORMATION FOR SEQ ID NO:889:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

GAATTCGGCC AAAGAGGCCT					60
TTATTATTGG TTGGCAACCA	GGGTGTAGGA	AAAAACAAGA	TTGTTGACAC	ATTCCTTCAC	120
CTGCTCAACA GACCCCGAGA	ATATATTCAG	CTACACAGGG	ATACCACAGT	ACAAACTCTT	180
ACGCTTCAGC CTTCGGTTAA	AGACGGACTT	ATTGTATATG	AAGACTCACC	TTTGGTTAAA	240
GCAGTAAAGT TGGGTCATAT					300
ACGTGTATTT TAAAAACTCT					360
ATTGTTGCAA ATTCTGCTAA					420
TTTAGGATGA TTGTTCTGGC	AAATAGACCT	GGATTTCCTT	TCCTAGGCAA	TGATTTCTTC	480
GGTACCTTAG GTGATATTTT	TAGCTGCCAT	GCAGTTGATA	ACCCCAAACC	CCACTCGGAG	540
CTCGAG					546

- (2) INFORMATION FOR SEQ ID NO:890:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

GAATT	'CGGCC	AAAGGGCCTA	GAGATTTCAT	GTATTTCTCT	TCACTTCCAA	GAGAGTGGAT	60
AGAAT	'GGAGA	AATCTAGATT	GATCTTTACA	GCTCCAGATA	AAGGGACTAA	AAATATTGGT	120
				GTTGGTTTCT			180
AACTA	GGTTT	TTATTACTAA	GTTTTGGAAA	TGGGGTAACC	ATTTTTTTCT	CATATCAAGG	240
ATATG	TACAT	ATTTCCCATT	TCCCCATAAT	TAAAAACAAA	CAACTCCCAT	CCACTTCTTA	300
TAAAT	AGTTC	TTAACTTGGG	CTTAGTAACA	ATGTATATTG	TGCCAGTAAT	ACAGAAAAGG	360
TGGGA	GTATA	AAGACCATCC	TGTCCTGTTA	GAATCCTATA	GAACCAAGGT	GCTGGATTAT	420
GGTGG							427

- (2) INFORMATION FOR SEQ ID NO:891:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

GAATTCGGCC	AAAGAGGCCT	AATTTTATTG	AAACTGCTTA	TGTATGTCAA	AGGAGCCCAC	60
					CTTTTATTTC	120
					TCCAGACCTA	
TAAGGAAATG	ԴՐԻՐԻՐԻՐԻ	ATGAAAAATG	ACAACTCCAT	CCTTLLIAC	CTCATGTCTT	180
TOCOCOMO	CCCCTAATAC	CACTORAGA	ACAAGICGAI	GGTTAAACTT	CTCATGTCTT	240
IGGIGCIIIG	GCCCIAAIAG	CACTGGACAA	CACCACGACC	ACATGGAAAC	ATATTTTTGG	300

AAGCAAAACT TTAATTTTAT ATAACGTATG CTATGGAGAA CTCGAG	346
(2) INFORMATION FOR SEQ ID NO:892:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 95 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:	
GAATTCGGCC AAAGAGGCCT AGTGGAGAGT GAAGCTTAAG ACTGCAATTG CAGAAAAAGT CCATGAGGAG AGAAGAAGGA GAAAAGGGGG AAGAG	60 95
(2) INFORMATION FOR SEQ ID NO:893:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 424 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:	
TTTTTTTTT TTTTTTTAA ATACTTCGCA TACTCTCAA TGCCCAAAAA TAGCAAGGTG GTAAAAAGAG AATTAGATGA TGATGTTACT GAGTCTGTCA AAGACCTTCT TTCCCAATGA AGACGCAGCT GATGATGCTT TTAAGACAAG TGAACTAATT GTTGATGGCC AGGAAGAGAA AGACCAGCTT GGAACAGTAA ACTACAATAC ATCCTGGCCC AAGTTGGATT TTCTGTAGGT TTAGGAAATG TGTGGCGATT TCCATACCTA TGTCAGAAGA ATGGGGGCGG TGCATATCTT TTACCATATT TAATACTACT TATGGTAATA GGTATTCCCC TTTTTTCTT GGAACTCTCT GTGGGTCAAA GAACCACTCT CGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:894:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 390 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:	
GCCAAAATCA AGCAAAGTAT GAAGAAAGAT AAAGAAGGGG AAGAAAAAGG GAAGCGAAGA GGATTCCCCA GCATCCTGGG ACCCCCACGG AGACCAAGCC GTCATGACAA CAGTGCAATT GGCAGAGCCA TGGAACTACA GAAGGCGCCC CACCCTAAGC ACTTATCCAC ACCCTCATCT GTGAGTCCTG AACCTCAGGA CTCTGCCAAG TTGCGCCAGA GTGGGTTAGC AAATGAAGGA ACAGACGCTG GATACCTGCC TGCCAATTCC ATGTCTTCTG TAGCTTCAGG GGCCTCTTTT TCCCAGGAAG GAGGGAAAGA GAATGATACA GGATCAAAGC AAGTTGGAGA AACATCAGCA CCTGGAGACA CCTTAGATGT CACCCTCGAG	30
(2) INFORMATION FOR SEQ ID NO:895:	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 595 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GAATTCGGCC	TTCATGGCCT	AGTAGCTGGT	ATTTATTCCC	CAAAGTAATA	ATGTTGAAGT	60
ATGGGTCTCA	TCATTCCCAT	ACACAGAAAC	ACAAAACACT	TTGATCATAA	ACTTTTTTCT	120
TCAGAAGCCA	AACTAACTTG	CAGAATAATA	GAGCCACTGG	TTTAATGTTT	CCTCAAGATA	180
GGTTTTAGTG	TAAGCTAGTA	TTCTGTGTGT	TCGTAGAAAT	GATTCAATAC	CTGCAGCTGG	240
TGAATTAGGA	ATTGTATTTG	TTGCCTTTTT	TATATTAGAT	GAGGTGCAAA	AATTTTAATG	300
CTAGTCAGTA	TGCACCACCA	CAGGAAAGTT	AGATCCCATT	AGCACTTGAA	ACTACAGCTT	360
TGGAAACTTA	GGCTAAGTTA	ATTTGGATTT	GTTACTTGAT	TCACCTACTG	ACCTTTTCTT	420
TTGTTTGAAG	TGCTTATCAG	CATAATGAGC	TAAGTGTCAT	GCATATTTGT	GAAGAAACAC	480
CCTTTTTGGT	CCCTTTTGGG	ACAGAGAGGT	ACTCCTTGAT	CTTTATGAAT	GACAGGTTAC	540
TGTTTTGCCT	TATTGCTTAA	CTTAATGTAG	TGAAATAAAG	CAGACGAGGC	TCGAG	595

- (2) INFORMATION FOR SEQ ID NO:896:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

GGCTGATCCG	CGTGAACATG	GAGGACTTGC	GAGAGCAGAC	TCACACCCGC	CACTATGAAT	60
TGTACCGACG	CTGTAAGCTT	GAAGAGATGG	GGTTCAAGGA	CACTGACCCT	GACAGCAAAC	120
CCTTCAGTCT	TCAGGAGACA	TATGAAGCAA	AAAGGAATGA	ATTCCTGGGA	GAACTGCAGA	180
AGAAAGAAGA	AGAAATGAGA	CAAATGTTTG	TTATGAGAGT	GAAGGAGAAA	GAAGCTGAAC	240
TTAAGGAGGC	AGAGAAAGAG	CTTCACGAGA	AGTTTGACCT	TCTAAAGCGG	ACACACCAAG	300
AAGAAAAGAA	GAAAGTGGAA	GACAAGGAGA	AGGAGCTCGA	G		341

- (2) INFORMATION FOR SEQ ID NO:897:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

GAATTCGGCC	TTCATGGCCT	ATGCCTTAAT	TTTGCTGTTT	GCCCTCGGAT	CTCTGGGTTT	60
GATTTTTGCG	TTGACTTTAA	ACAGACATAA	GTATCCCCTT	AACCTGTACC	TACTTTTTGG	120
ATTTACGCTG	TTGGAAGCTC	TGACTGTGGC	AGTTGTTGTT	ACTTTCTATG	ATGTATATAT	180
TATTCTGCAA	GCTTTCATAC	TGACTACTAC	AGTATTTTTT	GGTTTGACTG	TGTATACTCT	240
ACAATCTAAG	AAGGATTTCA	GCAAATTTGG	AGCAGGGCTG	TTTGCTCTTT	TGTGGATATT	300
GTGCCTGTCA	GGATTCTTGA	AGTTTTTTT	TTATAGTGAG	ATAATGGAGT	TGGTCTTAGC	360
CGCTGCAGGA	GCGCCACTCG	AG				382

(2) INFORMATION FOR SEQ ID NO:898:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

GAATTCGGCC	TTCATGGCCT	ACGAGCCTCA	CATCACTTGT	ACAAGCCACC	TGGGAGAAGT	60
	AAGATCCTAA					120
	ATAAGAGTCA					180
	CCACGATCCT					240
CAATACGTAC	CTGCCTTTGA	GTGAACCTTC	AATGCCAACT	AGGAAGGGCG	CTTCCAAAAC	300
GACGTTATTT	GTAACTCCTA	GGAAGACAAA	CACGGGTCAG	AACCCATACT	CTGCGGGCCT	360
TGAAATGGAA	AATCTCTCCT	CTAGACAGAC	TCATCCTGGC	CGTAAATATC	AGGAGACTCG	420
AG						422

- (2) INFORMATION FOR SEQ ID NO:899:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 806 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	60
NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	120
NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	180
NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	240
NNNNNNNNN	NNNNNNNNN	$\mathbf{NNNNNNNNNN}$	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	300
NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	360
NNNNNNNNN	NNCNTTGCAN	GNTTTGGTTC	CNTTTNTTCC	TTGTTTNTTT	TTTTGCACAA	420
TATTTCAAGN	TTTACNAGGC	ATACATCAAT	CCAAGTTCGG	AATTTTAATT	AAGAATTCGG	480
CGTTCATGGC	NTAAAAGAAN	TTGATGCTAC	CCCCGGAAAT	GCCAGAAGAG	GANATACATT	540
GAAATAGACN	GTGATGAAGA	GCCCAGGGGT	GAATTACTTT	TTNTTCGGGA	CANTGAACGC	600
NTTCATAAAA	AGCCAAAGTC	TGACAAAGAG	ACAAGAGTNG	CAANTNCAAT	GGNTGGANAG	660
ACAGACCGAA	AAGAATTTNT	GAGGAAGAAA	ACCAAAACAA	ATCCATNNTC	CAGNTCGACA	720
AATNAAGAGA	AGNAAANACA	GAAGAACTTT	ATGATGATGC	GGTATAGCCA	GAATGTCCGG	780
TCAAAAAATA	AGCATTCCTT	CTCGAG				806

- (2) INFORMATION FOR SEQ ID NO:900:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

GAATTCGGCC	TTCATGGCCT	AGGAGGCCT	GTTTCAGAAT	TGCTTTAATA	GTTCCCTTCC	60
AGTTGAATTT	ACCTTTTGCA	GGAGCCTCAT	CGTCTTCTGG	TTCTCCGCCC	TCAGGATGCT	120
CTGGGAGCTT	CATCTTTTTC	TTCTTAGAAT	CTGTTTCAAC	TTCCGAGTGC	CTCCGCTTCC	180
TCTTCCCTGC	CCCACGCGTG	CCTCTTCCTC	ACTGGCGCTG	TCCTTGCGCT	GCTTCTTCTT	240
CTTGCTCCTC	TTCCCTGCAG	AGCCATTGGC	CTCAGGGACT	TCCTCCCCAC	CAGCCTCAAG	300
GTCAGCCTCC	TGCCTCGAG					319

- (2) INFORMATION FOR SEQ ID NO:901:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

GAATTCGGCC	TTCATGGCCT	AAGAAAAGAC	AAGGTCCCCA	TAAGAGTGGC	GAGAGGAACA	60
GAGCCAGGAC	ATCGGAAAGC	AAGCCCCTGT	GTTCCCAAAC	CGCAGAAGAG	GGAGCTCTGA	120
TGTTAGACAA	GCCACCCTCC	TACAAGCGAA	GGGAAAGTAA	CTTTGAGCAA	AAATGAGCAA	180
CAGAAAATGA	GATCAAGGTC	AGATCTCATA	CAAAGTTGCA	AGATGAAAGA	ATGAGCAGCA	240
GAATAACCTC	CCTGTGATGT	GGAAAGTGTG	CCAGGAAAAC	AGACCCAAAC	GCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:902:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

GAATTCGGCC	TTCATGGCCT	AGGGGTTCTT	TCTCCTGCAC	GATGCCAGGT	GGTACTGGAA	60
TCTGCTGAGT	GGGATTCGGT	GGTGAGGATC	ATAAGGGCAA	ATTTCAAAGG	CTTCTGGCTC	120
CATGAGAAAT	TCTTGAAGCA	GGGTATCTCA	CTGCTAGAGT	CTAACGGAAA	TGCTTCTTGT	180
GGAGAAGCCC	TTTTGTAAGA	AGGATGGAGT	TGTCCTCTGC	CCAGTTTTGG	CCCTTGGGAT	240
TCTGTAGGTG	ACGGTCTTAA	CTTGTGGTCT	GTTCTCTAGG	ACTGTGAGTG	GTGGATTAGA	300
AGAGAGATGA	GGAGCTGCCA	AAAGCAGCTA	CACAGAGAAC	AGAGTTAGCA	AATGGCACCC	360
GAGACAGAAC	TATAGCAGAT	GCAAGAGCCA	AAAACCCACA	GCCGCATTGA	ATTCTAGACC	420
TGCCTCGAG						429

- (2) INFORMATION FOR SEQ ID NO:903:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

GAATTCGGCC TTCATGCCTT GTAACCATCA GGTAGATACA GCACCAACGG TAGTGGCTCT 60

TTATGACTAC	ACAGCGAATC	GATCAGATGA	ACTAACCATC	CATCGCGGAG	ACATTATCCG	120
AGTGTTTTTC	AAAGATAATG	AAGACTGGTG	GTATGGCAGC	ATAGGAAAGG	GACAGGAAGG	180
TTATTTTCCA	GCTAATCATG	TGGCTAGTGA	AACACTGTAT	CAAGAACTGC	CTCCTGAGAT	240
AAAGGAGCGA	TCCCCTCCTT	TAAGCCCTGA	GGAAAAAACT	AAAATAGAAA	AATCTCCAGT	300
CCTCGAG						307

- (2) INFORMATION FOR SEQ ID NO: 904:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

GAATTCGGCC	TTCATGGCCT	AGGACCTCGT	AGGTCCCTAC	AGCACCACAG	TGCTCTTCAT	60
CTCTCAGAGG	ACTGAACCAC	CAGCCAGCAC	CAACAGAGAC	ACTGTGGAAA	GCACAAGGAC	120
CCGACGGGCA	CTGAGTGACG	AGCAGTGTGC	TGCCGTCATC	CTTGTGCTGT	TTGCTTTCTT	180
TTCCATTTTG	ATTGCCTTTA	TCATTCAGTA	CTTTGTAATC	AAGTGAAAAT	ATAACTTTAT	240
TTTTTAACTC	TATTACATTT	TATTTTGTCA	TGTACTAAAA	TTATTTCTGT	ATTGCTTTNA	300
TAAAAAACAG	TGGCACCTCG	AG				322

- (2) INFORMATION FOR SEQ ID NO:905:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

CTAATTATTA GCATCATCCC TCTACTATTT TTTAACCAAA TCAACAACAA CCTATTTAGC TGTTCCCCAA CCTTTTCCTC CGACCCCCTA ACAACCCCCC TCCTAATACT AACTACCTGA CTCCTACCCC TCACAATCAT GGCAAGCCAA CGCCACTTAT CCAGTGAACC ACTATCACGA AAAAAACTCT ACCTCTCTAT ACTAATCTCC CTACAAATCT CCTTAATTAT AACATTCACA	60
CTCCTACCCC TCACAATCAT GGCAAGCCAA CGCCACTTAT CCAGTGAACC ACTATCACGA	120
	180
AAAAAACTCT ACCTCTCTAT ACTAATCTCC CTACAAATCT CCTTAATTAT AACATTCACA	240
	300
GCCACAGAAC AACTCGAG	318

- (2) INFORMATION FOR SEQ ID NO:906:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 553 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

GAATTCGGCC	TTCATGGCCT	ACAGGAAACA	TACAAAGCTG	CTCATAGTGG	GAGTCTTTTT	60
GCTCATGTTC	GTGTGCGGCC	TCTTCTTCAC	TCGACCTTCA	GGCAGCTACT	TCATCAGACT	120
GCTGAGTGAC	TACTGGATAG	TCTTCCCCAT	CATCGTCGTT	GTCGTATTTG	AAACCATGGC	180

TGTATCCTGG	GCCTATGGGG	CCAGGAGGTT	CCTTGCAGAC	CTGACGATCC	TGTTGGGCCA	240
CCCCATCTCT	CCCATCTTTG	GTTGGCTGTG	GCCCCATCTG	TGTCCAGTTG	TGCTGCTAAT	300
			TATGAAGCCG			360
			ATACCCACCG			420
			CCCTGCATAC			480
		AGAGCGGAGA	CGGGCCTATG	ACAGCCTCCA	CATCCCTACC	540
CCTAAGTCTC	GAG					553

- (2) INFORMATION FOR SEQ ID NO: 907:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 557 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

GAATTCGGCG	TTCATGGCCT	AGTAGAGAAG	ANNNTATTGC	NGTGACAATG	AGGTTTCTAC	60
GTTCAGTGGC	AAGAGTTTTT	GTTATTCTGA	GTGTGGAAAT	GGCTTCATCC	AAAAAGAAAA	120
ACAACTTTAT	TCCACAGCCA	ATTGGAAAAT	GCAAGCGTGT	ATTCCAAGCA	TTGCTACCTT	180
ACGCTGTGGA	AGAATTGTGC	AACGTAGCAG	AGTCACTGAT	TGTTCCTGTC	AGAATGGGGA	240
TTGCTCGTCC	AACTGCACCA	TTTACCCTGG	CTAGTACTAG	CATAGATGCC	ATGCAGGGCA	300
GTGAAGAATT	ATTTTCAGTG	GAACCACTAC	CACCACGACC	ATCATCTGAT	CAGTCTAGCA	360
GCTCCAGTCA	GTCTCAGTCA	TCCTACATCA	TCAGGAATCC	ACAGCAGAGG	CGCATCAGCC	420
AGTCACAGCC	CGTTCGGGGC	AGAGATGAAG	AACAGGATGA	TATTGTTTCA	GCAGATGTGG	480
AAGAGGTTGA	GGTGGTGGAG	GGTGTGGCTG	GAGAAGAGGA	TCATCATGAT	GAACAGGAAG	540
AACACAGGAA	GCTCGAG					557

- (2) INFORMATION FOR SEQ ID NO:908:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

GAATTCGGCC	TTCATGGCCT	AAAAAAGTCA	GCCAGGTGTG	GTGATGTGCG	CCTGTGGTCC	60
CAGGTATTCA	CGAGCTGAGG	TGGGAGGATC	ACCTCAGCCC	GGGAGGTGGA	GGTTGCAGTG	120
AGCCCATATC	CCGCCACTGC	ACTCCAACCT	GGGAGACAGA	GCGAGACCCT	GTCTCCAAAA	180
АААААААА	AAAATCCGGG	ATCTATTTAT	GTAACTACTA	GAATCTTAAG	TTCAGAATTT	240
ACTCCATAAG	AGTATATAAA	AAACTTACTG	TGATTTTATC	CATGTTTTTC	CTAATATATA	300
ATAGGTCTAA	GTCTTGTACT	TTTCTGTCCT	GTCCACAGAG	CCTTGAAAAT	AATTTAGAGC	360
TCAGTCATTC	AGTTTGGATT	TATGTATAAA	TTGAAATATA	TTAATTACTT	ATTTATAGTG	420
CAGCTCGAG						429

- (2) INFORMATION FOR SEQ ID NO:909:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

GAATTCGGCC	TTCATGGCCT	AGTCCCTGAA	AAAAAAAAA	GAAAAAAAAA	ATTTAAATAG	60
AGGAAATACT	AGCTAAGTTT	AATGTAGGCC	AGTTCTAAAA	TAATGATTTA	TTGCTGCTGT	120
TGTTACATAA	TTTTCTTAAA	TATTTTAAAG	ATTGCACACT	GTCTGCTCGT	AGGCCATGAA	180

- (2) INFORMATION FOR SEQ ID NO:910:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

TACCTGCAGT	TGTACCGGGT	CACATGTGAC	CAAACCTACC	TGCTCCGATC	CCTGGATTAC	60
GTAAAAAGAA	CACTTCGGAA	TCTGAATGGC	CGCAGGGTCA	CCTTCCTCTG	TGGGGATGCT	120
GGCCCCCTGG	CTGTTGGAGC	TGTGATTTAT	CACAAACTCA	GAAGTGACTG	TGAGTCCCAG	180
GAATGTGTCA	CAAAGTGAGT	TTTAGAACTG	GAAACATTTT	CTCCCAATTC	CCAGTGGAAG	240
CTCTTGCTGT	AGAAAGATAT	TCAGAAAGGA	AACTATTTTT	CCATTCATCC	ATTGTTGTAA	300
ACAGATCACT	CCAAAATGTT	AATCTTGAGC	ATAGTGGTGG	GATCATATGC	CCTCTTTTTA	360
TCCAAGCATG	TGTGTGCCGG	TCTCGAG				387

- (2) INFORMATION FOR SEQ ID NO:911:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

GAATTCGGCC	TTCATGGCCT	AGTGTCTTGA	CAATGGTTGA	GCTGGTTTGG	ATCACAGGAA	60
CATTTATTTG	ATAACGATGG	AAGGAAAAA	CAGTGCTGTA	ATAAGTCGCT	TCTTAAAATG	120
TGGGGTGTTA	TTAAAAGAAT	AATGGGAAAG	TGCTACTGGG	AAGGCAAACA	CAGCAATTGT	180
ACTCTACAGA	CAGGGATTCT	CCTATTGGCC	ATTTTAGAAA	CATTCCCCAG	GCAACATGAG	240
ATTATCCAAG	TGGAGAGAAC	CAGAGTCAGA	GCCATTTCCT	AGGCCGACAG	AGCAGCGCTC	300
CAGATGAGAT	ACTGAAGGTT	TGAACTCAAG	TGATGGCAGT	AAGATCAGAA	AGCAAAAGGC	360
ATATCACAAA	GAAACCATAA	GATTCTCCAT	CTGGATATAT	AGAAGATAAA	TGGAAAGAGA	420
AACTCGAG						428

- (2) INFORMATION FOR SEQ ID NO:912:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

GAATTCGGCC	TTCATGGCCT	AGAAAACCAA	ATACTGCATG	TTCTCACTCA	TAGGTGGGAA	60
CTAAACAATG	AGAACACTTG	GACACAGGGC	TGGGAACACC	ACAACTTCTT	TTTCAGTTCA	120
TAACTCATAG	TCCACGATCC	ATGTGCTCTT	TGACTTGACT	TTTCTTAAAC	TCCTATTTTA	180
TGTGCTTCTG	ACTTGCTTTC	CCTTCTTATT	TGTAATCCAC	ACTAGCCTCA	AAAGATGCAT	240
GAACTGTGAA	TTTTCACTTC	CAGGGCCATG	GATAGTTGAA	CATCTAGTAG	TGAATTTCCT	300
CTTTCAGAAG	TAAATAAAT	TCATTCATTC	CCCTGGATCT	AGAAGGACAC	ACTCGAG	357

- (2) INFORMATION FOR SEQ ID NO:913:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

CAGCCTGGGT	GGCAGAGCAA	GACTCCATTT	CAAAAAAAAA	AAAAAAAAGC	CCAAGTCACT	60
TGCTGTTTCT	GGATCCAGTA	ACGCTGCCTC	AAATTTGATT	CAGTCACCTC	ACATACTTAA	120
CATTCTGGCT	TTCCTTTCCT	CTGTTTCTGG	CATCTGGAGA	TTTCCTTTTT	TTGTGTGTGA	180
GCTCATTTAT	GGTTATCTGT	TGTTATGTTT	AATACAACCA	TTCCTGGCTG	AGGCTGCCAC	240
ATCTAGAGCT	GGTAAACTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:914:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

GAATTCGGCC	TTATGGCCTA	GTGATATGTC	ATAATCCCTT	CTGTGGGCTG	GGCCCACATA	60
AGGAGAGTCA	AATCACTTGG	GTGCTGGGAA	GAGGCACATG	TCACACGTGC	AAGAAGGTCC	120
AAGGATGAGA	TTAAAAATTC	CACAAAGGTC	CAAATTCTAG	GGCCCAGACA	GAAGAGAAGA	180
GTCACATCAT	CTAGATGATG	AATGAAAAGA	TATGTCATTA	TTCTCCTTTG	GGCAGTGCTT	240
CTGCAGAAAA	GTTGCACCTT	CTAGGTGTTG	GACTCAGCAA	TATATCACAA	TGTCTGCAGT	300
ATTTTGGAAG	GAGAGGAGAG	TCACCATTAC	TTAGGTGCTA	GGCCCAGCAA	TACATCTCAA	360
GCACTTCTTG	GGCAAAGCCC	AAGCAGTAAA	AAAGAGTCAC	ATTACCTAGG	TTCTGGGTAT	420
AGCAATATGT	CACAAATGCC	CCTAAGAAGA	GGGCCCAGGA	AAAGACTCGA	G	471

- (2) INFORMATION FOR SEQ ID NO:915:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

GAATTCGGCC	TTCATGGCCT	AGAGTGCCTG	ACCTTCCCTG	TTCAAGAATT	TATAAAGATT	60
CCTAACAGCA	ATTCTAGAAA	AAGGATAAAG	ACCTCCACTT	GGCTTTCAGA	AGCCTCCAGC	120
ATCTGGCCCA	AGCTAATACA	GCCTTAAAAC	TAATCTGGTT	ATAGCCCAGC	CCCTCATTTC	180
ACAAAGAAAA	CTGAGACCCC	TGGCTATCTA	TTAACTCGCT	CCAACCAAAC	ACATCATCTA	240
TCCCCTCTCT	TCCTCCAGAT	AACACTCACT	TACCAGGCTA	CAGTGAGGTC	CACGTCTCTG	300
ATATGAGGCT	CCTGTCCACA	AGTTTGGTAA	CCTTCATCTG	CCTCATCACC	AGTGAGCACC	360
CAGCACTTAG	CACTGTGCCC	GACACAGAAA	TGAACACTCT	GCTCCTCCGG	GCCGGCGTGG	420
GTGCGCCGCT	GCGGCCACCG	GCAGCGCTCG	AG			452

- (2) INFORMATION FOR SEQ ID NO:916:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

GAATTCGGCC	TTCATGGCCT	ACAAATGGTT	GGTTTATGTT	ATGATAGCAA	TTTTCTGCAT	60
AGCATCAGCA	ATGAGTCTGT	ACAACTGTCT	TGCTGCACTA	ATTCATAAGA	TACCATATGG	120
ACAATGCACG	ATTGCATGTC	GTGGCAAAAA	CATGGAAGTG	AGACTTATTT	TTCTCTCTGG	180
ACTGTGCATA	GCAGTAGCTG	TTGTTTGGGC	TGTGTTTCGA	AATGAAGACA	GGTGGGCTTG	240
GATTTTACAG	GATATCTTGG	GGATTGCTTT	CTGTCTGAAT	TTAATTAAAA	CACTGAAGTT	300
GCCCAACTTC	AAGTCATGTG	TGATACTTCT	AGGCCTTCTC	CTCCTCTATG	ATGTATTTTT	360
TGTTTTCATA	ACACCATTCA	TCACAAAGAA	TGGTGAGAGT	ATCATGGTTG	AACTCGCAGC	420
TGGACCTTTT	GGAAATAATG	AAAAGAATGA	TGGAAATCTC	GAG		463

- (2) INFORMATION FOR SEQ ID NO:917:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

GAATTCGGCC	TTCATGGCCT	AACGTACTTG	AAAAGGCTTT	CCTTTACACT	TCCAGGACCA	60
AACAGCAACT	TCCTGCCACA	CACTTCCACC	CTATCACTGG	GAGAAATCCT	TTTCTGGACA	120
TGAGCCTTTG	ACCTGGGTGG	GGCAGAAAGA	ACCACAAACT	CCATCTCCCA	ATAGAACTTT	180
GAAATTCACT	CAGCTTTTCC	TTTCATGCTG	TTTGTTGCCT	GCTTGTTGCA	CTCCTCCTGC	240
CCCAGAACTG	CAAGATTTTT	AGCTTCACCC	CTTTCTGAGA	GTAATGTTAT	CTTTTATCAG	300
AATCAGTATC	AGTTCCCCTG	TATTCTGTGC	TTCATCGAAT	TTGCAAGACT	GACCTCTTTT	360
AAGCATTTAA	TTCACTCCCA	GAATCTCGAG				390

- (2) INFORMATION FOR SEQ ID NO:918:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

GAATTCGCCT	TCATGGCCTA	CAGTGACAAT	GAACAAAACC	AGCACACCAC	ACAAATGAGT	60
GATGAGGAAG	AGGATGATGA	TGGCTGTGAC	CTTTTTGCTG	ACTCTGAGAA	GGAGGAGGAA	120
GATATTGAGG	ACATTGAAGA	AAATACTAGA	CCTAAAAGAA	GCAGACCTAC	ATCGTTTGCA	180
GATGAGCTGG	CTGCCCGCAT	CAAGGGGGAT	GCCATGGGTC	GAGTGGACGA	GGAGCCGACA	240
ACCTTACCCT	CAGGAGAAGC	AAAACCTCGG	AAGACACTCA	AAGAGAAGAA	GGAAAGGAGA	300
ACTCCTTCAG	ACGAGTCTTC	ATCATCCAAA	CCTGGAAAGA	AAATCCCAGC	AGCTCTCGAG	360

- (2) INFORMATION FOR SEQ ID NO:919:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

GAATTCGGCC	AAAGAGGCCT	AGTGCTATTG	AAACATTGGT	AACAGCAATT	TCTTTAATTA	60
AACAATCCAA	AGTCTCTGCA	GATGATCGTT	GCAAAGTTCT	TATTAGCTCT	CTGCAGGATT	120
GCCTTCATGG	AATCGAGTCC	AAGTCCTATG	GGTCTGGATC	CAGACGTGAA	CGATCAAGAG	180
AACGGGACCA	TAGTAGATCA	CGGGAAAAGA	GTCGTCGCCA	TAAATCTCGG	AGTAGAGATC	240
GCCACGATGA	CTATTACAGA	GAGAGAAGCA	GAGGTCGAG			279

- (2) INFORMATION FOR SEQ ID NO:920:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

GAATTCGGCC	TTCATGGCCT	ACAGAACTTG	AAGCCATCAA	TAAAAGAGTA	AAAGACACTA	60
TGGCACGATC	AGAAGATTTG	GACAATTCCA	TTGATAAAAC	AGAAGCTGGA	ATTAAGGAGC	120
TTCAGAAGAG	TATGGAGCGC	TGGAAAAATA	TGGAAAAAGA	ACATATGGAT	GCTATAAATC	180
ATGATACTAA	AGAACTGGAA	AAGATGACAA	ATCGGCAAGG	CATGCTATTG	AAGAAGAAAG	240
AAGAGTGTAT	GAAGAAAATT	CGAGAACTTG	GATCACTTCC	CCAGGAAGCA	TTTGAAAAGT	300
ACCAGACACT	GAGCCTCAAA	CAGTTGTTTC	GAAAACTTGA	GCAGTGCAAC	ACAGAATTAA	360
AGAAGTACAG	CCATGTTAAC	AAAAAGGCTT	TGGATCAGTT	TGTAAATTTC	TCCGAGCAGA	420
AAGAAAAGTT	AATAAAGCGT	CAAGAAGAGT	TAGATAGGGG	CCCACTCGAG		470

- (2) INFORMATION FOR SEQ ID NO:921:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

GAATTCGGCC	TTCATGGCCT	AGCAGTGGCG	TTGGAAGGAG	ACGCGGAGGG	GCAGTGGCGT	60
TGGAAGGAGA	AACGGAGGGG	CAGTGGCGTT	GGAACGGGGG	CAGTGGCGTC	GGAAGGGGAC	120
GCGGAGGGC	AGTGGCGTTG	GAAGGAGAGA	CCAGGGCCGC	GGGGCTGCTT	CTTGTAAAGG	180
GCCAAGCTGT	GAGGACTTCG	GGCTTTGCGG	CCGCTTTTGT	CTATGTCCCA	TCTCCTTCTT	240
TGTTTTGTTT	TTCTCAAACC	CTTTAAAAAC	GTGAAAACCA	TTTCTAGCTT	GGGGCCCTA	300
TAAAAATAGG	CCTCGCTGGC	CCTAGTTTGA	TGACCCCTGA	AACAGACAAT	TCAAGGAGAA	360
GCTTAGTGAA	AGAGTCACTT	ATAGCTTCAT	AAAAATAAGA	GAAGATATAG	TATCCATAAA	420
ATAATAATAA	GATTGTATCC	ATGAGGTTCC	TCGAG	·		455

- (2) INFORMATION FOR SEQ ID NO:922:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

GACATGACCC	TGGACAAAGA	ACAAATAGCG	AAGGATTTGC	TTTCAGGGGA	AGAAGAGGAA	60
GAGACGCAAT	CATCTGCTGA	CGACCTCACC	CCGTCCGTGA	CCTCCCACGA	GGCCTCCGAC	120
CTCTTCCCTA	ACCGGAGTGG	ATCTCGTTTC	CTGGCTGATG	AAGACAGAGA	GCCTGGCTCT	180
TCTGCCTCCT	CCGACACCGA	GGAGGACTCT	CTTCCTGCCA	ACAAATGTAA	GAAGGAGATC	240
ATGGTGGGAC	CTCAGTTCCA	AGCTGACCTC	AGCAACCTGC	ACTTGAACCG	GCACTGTGAG	300
AAGATCTACG	AGAACGAAGA	CAAGCTACTC	GAG			333

- (2) INFORMATION FOR SEQ ID NO:923:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

GAATTCGGCC	TTCATGGCCT	AAGCAGCCTT	TCACCAGGGC	TCCATCTGTG	AAGAGTCTCA	60
GCCATGACTT	TGAGCTGAGC	TTGGGAGAAG	TAAAGCAACT	GTTAAGGCCA	GCCCTTGCCC	120
CTCAGACCTG	CCATGAAAGG	AATGAGCCCT	AGACTGACTC	CTGCAGCACC	CCCGGGACAG	180
GCTGGGACCA	GCTGTTTGTC	TCCAGGTGTC	AGAGTCCCTC	CTCCTCCTCC	AACCTCTCCA	240
TTGAATTCTA	GACCTGCCTC	GAG				263

- (2) INFORMATION FOR SEQ ID NO:924:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

ATTTTGGGGA	CCAAGAACCT	GTACAAGGAT	TTGTGATGAA	CTTTTCCAAT	GGGGAAATTA	60
TCGACATCTT	CAAGCCAGTG	CGCAAGCACT	TTGATATGCC	TCATGATATT	GTTGCATCTG	120
AAGATGGGAC	TGTGTACATT	GGAGATGCTC	ATACCAACAC	CGTGTGGAAG	TTCACCTTGA	180
CTGAGAAATT	GGAACATCGA	TCAGTTAAAA	AGGCTGGCAT	TGAGGTCCAG	GAAATCAAAG	240
AAGCCGAGGC	AGTTGTTGAA	ACCAAAATGG	AGAACAAACC	CACCTCCTCA	GAATTGCAGA	300
AGATGCAAGA	GAAACAGAAA	CTGATCAAAG	AGCCAGGCTC	GGGAGTGCCT	GTTGTTCTCA	360
TTACAACCCT	TCTGGTTATT	CCGGTGGTTG	TCCTGCTGGC	CATTGCCATA	TTTATTCGGT	420
GGAAAAAATC	AAGGGCCTTT	GGAGCAGATT	CTGAACACAA	ACTCGAG		467

- (2) INFORMATION FOR SEQ ID NO: 925:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

GCCATCCTCT	GACAAAAGAA	AGAATATGTA	CTCAGGTGGA	GAGAATGTTC	AGATGAATGG	60
GGATACGCCC	CATGATGGAG	GTCACGGAGG	AGGAGGACAT	GGGGATTGTG	AAGAATTGCA	120
GCGAACTGGA	CGGTTCTGTG	GTGGACTAAT	TAAAGACATA	AAGAGGAAAG	CGCCATTTTT	180
TGCCAGTGAT	TTTTATGATG	CTTTAAATAT	TCAAGCTCTT	TCGGCAATTC	TCTTCATTTA	240
TCTGGCAACT	GTAACTAATG	CTATCACTTT	TGGAGGACTG	CTTGGGGATG	CCACTGACAA	300
CATGCTCGAG						310

- (2) INFORMATION FOR SEQ ID NO:926:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

GAATTCGGCC	TTCATGGCCT	AGTGGAGACC	TGGCCAAGGT	ACAGAGAGCT	GTGTGCATGC	60
TGAGCAACAC	CACAGCCATT	GCTGAGGCCT	GGGCTCGCCT	GGACCACAAG	TTTGACCTGA	120
TGTATGCCAA	ACGTGCCTTT	GTTCACTGGT	ACGTTGGGGA	GGGGATGGAG	GAAGGTGAGT	180
TTTCAGAGGC	CCGTGAGGAC	ATGGCTGCCC	TTGAGAAGGA	TTATGAGGAG	GTTGGTGTGG	240
ATTCTGTTGA	ACCACACCCT	GAGGAAGAAG	GAGAGGAAAA	CCTCGAG		287

- (2) INFORMATION FOR SEQ ID NO:927:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

CCGCGCACCA ACAACAGCAA CAACTCCACT GCGCCGGGCT GAGGAGCAGG AATTAGGAGC

60

TCGCGAATAA	TATGAAAGGG	ATCCGCAAAG	GGGAAAGCCG	AGCAAAGGAA	TCCAAACCCT	120
		TGCGCTAAAT				180
		TTTACGTTTT				240
		TTGGGGGTCC		GGATGGAGGT	GGGCTGACTT	300
GTAGATGGAG	AGAGGCTGGC	AGCTTACTCG	AG			332
(2) INFORMA	ATION FOR SE	EQ ID NO:928	3:			

-
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

AGCCTGCCAT CCCAGGCTTC	AGATTGGAGC	CGATACTCAA	GCAGCTTACT	GGAATCCGTC	60
TCTGTTCCTG GAACACTAAA	TGAGGCTGTT	GTAATGACTC	CATTTTCATC	GGAACTTCAA	120
GGAATTTCAG AACAGACCCT	CCTGGAGCTG	TCCAAAGGAA	AGCCCTCCCC	GCATCCCAGA	180
GCCTGGTTTG TGTCTCTTGA	TGGAAAGCCA	GTTGCACAAG	TGAGGCACTC	CTTTATAGAC	240
CTGAAAAAGG GCAAGAGAAC	CCAGAGCAAT	GACACCAGTC	TGGACTCTGG	GGTGGACATG	300
AATGAGCTTC ACTCAAGTAG	AAAGCTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:929:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

GAATTCGGCC	TTCATGGCCT	AGTGAGTGGG	TGATATCTGT	AAAGTGCATT	GTCTTCAGTT	60
		GGAATGGCGG				120
GTGCCCTTCT	CATCCCAGAC	CTGAGCCCCC	CCCAAAACCT	GTCTGGACTT	TGATCAGGAT	180
AAGAACGTTG	CAGGGCGAGG	CAAGTTCCTG	AAGCCGAAGA	GGTCTGGGCT	GGGGCCTACT	240
GGAGAAAGGG	CATAGACTGG	CTCGAG				266

- (2) INFORMATION FOR SEQ ID NO:930:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

GCGAAAATAA	CCTTTTCTAA	TGAGGATGTC	TGATACTGTT	ACTGTAAAAG	ATGAAACTGC	60
AACAATGAAG	GATTTGGAGG	CAGAAGTGAA	AGATACAACC	AGAGTTGAAA	ATCTTATCAA	120
ATCAGAAAAC	TATGGGAAGA	TTTTGGTAGA	GAAGAATGAA	CATTGTATTG	AGAACAATAT	180
AGATTTGCAG	GAGAAAATTC	AGATCCAGTT	AACACAATCA	TTTGAGAAAG	AAGAGAAGCC	240

AAGAGATCCC AGTCTCGAG	300 319
(2) INFORMATION FOR SEQ ID NO:931:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 255 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:	
GAATTCGGCC TTCATGGCCT AAAGAAGAGC AGGAAGTCCA ATGTGGCCGA AGCAGAGTGA GCAAGGGCAG GAGTACCAGA GGAGGAGATA GGACGCCAAA GAGTTAAGAA AAGGAGGAAT GCAGAACCTT TCCATCAAAA ATAAAATAAT ACATAACCAT GGTTATGTGG GGTGGGGTTG TCTCTTTCTT TTGGAAAGAA GAAGGGCTTT CTGGGAATAG ATGGCCAGGC CAGGCAGCAA GCTGCTAAAC TCGAG	60 120 180 240 255
(2) INFORMATION FOR SEQ ID NO:932:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 588 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:	
GAATTCGGCC TTCATGGCCT AGCATTTCA AAAATTCAGT GCAAGCGCCA GGCGATTTGT GTCTAAGGAT ACGATTTTGA ACCATATGGG CAGTGTACAA AATATGAAAC AACTGTTTCC ACACTTGCAC CTGATCAAGG AGCAGTGCTT CTCCATTTGT TTTGCAGAGA AATGTTTTC ATTTCCCGTG TGTTTCCATT TCCTTCTGAA ATTCTGATTT TATCCATTTT TTTAAGGCTC CTCTTTATCT CCTTTCTTAA GGCACTGTTG CTATGGCACT TTTCTATAAC CTTTTCATTC CTGTGTACAG TAGCTTAAAA TTGCAGTGAT TGAGCATAAC CTACTTGTTT GTATAAATTA TTGAAATCCA TTTGCACCCT GTAAGAATGG ACTTAAAAGT ACTGCTGGAC AGGCATGTGT GCTCAAAGTA CATTGATTGC TCAAATATAA GGAAATGGCC CAATGAACGT GGTTGTGGGA GGGGAAAGAG GAAACAGAGC TAGTCAGATG TGAATTGTAT CTGTTGTAAT AAACATGTTA AAACAAACAA AAATTGTTAT TTTTCTTTTC CTTCGGTCAG AGCTCGAG	60 120 180 240 300 360 420 480 540
GTCTAAGGAT ACGATTTGA ACCATATGGG CAGTGTACAA AATATGAAAC AACTGTTTCC ACACTTGCAC CTGATCAAGG AGCAGTGCTT CTCCATTTGT TTTGCAGAGA AATGTTTTC ATTTCCCGTG TGTTTCCATT TCCTTCTGAA ATTCTGATTT TATCCATTTT TTTAAGGCTC CTCTTTATCT CCTTTCTTAA GGCACTGTTG CTATGGCACT TTTCTATAAC CTTTTCATTC CTGTGTACAG TAGCTTAAAA TTGCAGTGAT TGAGCATAAC CTACTTGTTT GTATAAATTA TTGAAATCCA TTTGCACCCT GTAAGAATGG ACTTAAAAGT ACTGCTGGAC AGGCATGTGT GCTCAAAGTA CATTGATTGC TCAAATATAA GGAAATGGCC CAATGAACGT GGTTGTGGGA GGGGAAAGAG GAAACAGAGC TAGTCAGATG TGAATTGTAT CTGTTGTAAT AAACATGTTA	120 180 240 300 360 420 480 540
GTCTAAGGAT ACGATTTGA ACCATATGGG CAGTGTACAA AATATGAAAC AACTGTTTCC ACACTTGCAC CTGATCAAGG AGCAGTGCTT CTCCATTTGT TTTGCAGAGA AATGTTTTC ATTTCCCGTG TGTTTCCATT TCCTTCTGAA ATTCTGATTT TATCCATTTT TTTAAGGCTC CTCTTTATCT CCTTTCTTAA GGCACTGTTG CTATGGCACT TTTCTATAAC CTTTTCATTC CTGTGTACAG TAGCTTAAAA TTGCAGTGAT TGAGCATAAC CTACTTGTTT GTATAAATTA TTGAAATCCA TTTGCACCCT GTAAGAATGG ACTTAAAAGT ACTGCTGGAC AGGCATGTGT GCTCAAAGTA CATTGATTGC TCAAATATAA GGAAATGGCC CAATGAACGT GGTTGTGGGA GGGGAAAGAG GAAACAGAGC TAGTCAGATG TGAATTGTAT CTGTTGTAAT AAACATGTTA AAACAAACAA AAATTGTTAT TTTTCTTTTC CTTCGGTCAG AGCTCGAG	120 180 240 300 360 420 480 540
GTCTAAGGAT ACGATTTGA ACCATATGGG CAGTGTACAA AATATGAAAC AACTGTTTCC ACACTTGCAC CTGATCAAGG AGCAGTGCTT CTCCATTTGT TTTGCAGAGA AATGTTTTC ATTTCCCGTG TGTTTCCATT TCCTTCTGAA ATTCTGATTT TATCCATTTT TTTAAGGCTC CTCTTTATCT CCTTTCTTAA GGCACTGTTG CTATGGCACT TTTCTATAAC CTTTTCATTC CTGTGTACAG TAGCTTAAAA TTGCAGTGAT TGAGCATAAC CTACTTGTTT GTATAAATTA TTGAAATCCA TTTGCACCCT GTAAGAATGG ACTTAAAAGT ACTGCTGGAC AGGCATGTGT GCTCAAAGTA CATTGATTGC TCAAATATAA GGAAATGGCC CAATGAACGT GGTTGTGGGA GGGGAAAGAG GAAACAGAGC TAGTCAGATG TGAATTGTAT CTGTTGTAAT AAACATGTTA AAACAAACAA AAATTGTTAT TTTTCTTTTC CTTCGGTCAG AGCTCGAG (2) INFORMATION FOR SEQ ID NO:933: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 520 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	120 180 240 300 360 420 480 540
GTCTAAGGAT ACGATTTGA ACCATATGGG CAGTGTACAA AATATGAAAC AACTGTTTCC ACACTTGCAC CTGATCAAGG AGCAGTGCTT CTCCATTTGT TTTGCAGAGA AATGTTTTC ATTTCCCGTG TGTTTCCATT TCCTTCTGAA ATTCTGATTT TATCCATTTT TTTAAGGCTC CTCTTTATCT CCTTTCTTAA GGCACTGTTG CTATGGCACT TTTCTATAAC CTTTTCATTC CTGTGTACAG TAGCTTAAAA TTGCAGTGAT TGAGCATAAC CTACTTGTTT GTATAAATTA TTGAAATCCA TTTGCACCCT GTAAGAATGG ACTTAAAAGT ACTGCTGGAC AGGCATGTGT GCTCAAAGTA CATTGATTGC TCAAATATAA GGAAATGGCC CAATGAACGT GGTTGTGGGA GGGGAAAGAG GAAACAGAGC TAGTCAGATG TGAATTGTAT CTGTTGTAAT AAACATGTTA AAACAAACAA AAATTGTTAT TTTTCTTTTC CTTCGGTCAG AGCTCGAG (2) INFORMATION FOR SEQ ID NO:933: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 520 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	120 180 240 300 360 420 480 540

ATTTGTGGGC	CTCCAGATGG	AGGCCCTACC	TTCTCAGCAA	GGGAAGAAAC	CCCTCTCTCT	240
TTGACCTCTC	TCCCCTGCAC	AATTAGAAGG	TTCTGAAGAG	TGACTTCATT	ATTGGTGGGT	300
GAGTATATGT	TTATTGGGCA	TCTGTGGTGT	GCCAGATGTT	GTGTTGAGTG	CTGGGTGCAG	360
AGGTAAATGG	GATATCTGGT	TACCGCCCAC	ATGGGGCTTA	TAGTGGGGGA	AGTGGGGGAG	420
TAAGTCAGGA	CACACGTAAG	CAAACGCTAG	AATGGATAGA	TATTGTGATT	AGAGCATTGG	480
AGAGAAAGAA	CAGGATGTTT	CAAGAAAGGA	CAGTCTCGAG			520

- (2) INFORMATION FOR SEQ ID NO:934:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

GAATTCGGCC	TTCATGGCCT	ACTTTTTTC	TCAAGGTGCA	ATGAAAGCCT	TCCACACTTT	60
CTGTGTTGTC	CTTCTGGTGT	TTGGGAGTGT	CTCTGAAGCC	AAGTTTGATG	ATTTTGAGGA	120
TGAGGAGGAC	ATAGTAGAGT	ATGATGATAA	TGACTTCGCT	GAATTTGAGG	ATGTCATGGA	180
AGACTCTGTT	ACTGAATCTC	CTCAACGGGT	CATAATCACT	GAAGATGATG	AAGATGAGAC	240
CACTGGGGAG	TTTCTCGAG					259

- (2) INFORMATION FOR SEQ ID NO:935:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

AACAAAATGA	AACAAACAAA	AGACAGAGGC	CAAGAAAGGC	TAAGTAACTT	GCCTAAGACT	60
ATATAATAAG	TCACAGGGCA	GGGAATAAAA	CTCAGTTTTC	CTGACTTCCA	TTAAGGTTGT	120
CTTTTCCTCA	CTCCACATTG	CCTGTCATTT	TTTTTCTGAT	TATTCTTAAG	AAGGAGTGAG	180
GAGAGAGAAT	AGAGAAACAG	ATTTTTTCT	CGGACTATCT	TTTCTGTAGG	GAAAAACCAC	240
TGAAGCCCTA	TTAGCCTGGA	AGCTGCTTAT	AGGGTTACAA	TACTGTGTGT	CCTGCAGAAC	300
CTGTGAAGCT	CTTCTGTATT	TTCTGGACTT	TCCTGGAAAG	TCATTTAGAT	ATAATGTAAT	360
ATATATA	AAGTAGTTTA	GATATAATGA	GGTTTTCAAT	AGGCTTCCTC	GAG	413

- (2) INFORMATION FOR SEQ ID NO:936:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

GAATTCGGCC TTCATGGCCT	ACCCTGAGAG	TAAGCCAAAA	AAGGAAGAAA	AAAATATGGA	60
AGTAAATATG AAAGAGTGGA	TTTTACGATA	TGCTGAACAA	CAAAATGAAG	AAGAAAAGAA	120

TGAGAATTCT AAAAGTTTAG AAGAGGAGGA AAAATTTGAC CCTAATGAAA GGTACTTACA TCTTGCAGCA AAACTGCTGG ATGCAAAAGA ACAAGCAGCT ACCTTTAAAC TAGAAAAAAA CAAGCAGGGC CGTCTCGAG	180 240 259
(2) INFORMATION FOR SEQ ID NO:937:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 263 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:	
GCGAAACCGT GGTCAGCTGC AAGAAGGCAC AGGAGAACAT GAAGCAAAGG CACGAGAACG AAACGCACAC CTTAGAAAAA CAAATAAGTG ACCTTAAAAA TGAAATTGCT GAACTTCAGG GGCAAGCAGC AGTGCTCAAG GAGGCACATC ATGAGGCCAC TTGCAGGCAT GAGGAGGAGA AAAAACAACT GCAAGTGAAG CTTGAGGAGG AAAAGACTCA CCTGCAGGAG AAGCTGAGGC TGCAACATAA GAGGGAGCTC GAG	60 120 180 240 263
(2) INFORMATION FOR SEQ ID NO:938:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 384 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:	
GAATTCGGCT TCATGGCCTA TTCCACTACT AGGCTGACAT GCAAAATCCT AAGAGAAGTC AGTCTTCAG GATTGATCCT GGCATTTGTG CTTGCTGTTC CCCGTGCCTG GAGCACCTGT CCCAGCTCCC CTGTGGCTGG CTCCTTCTCA CCATCCAGGG TTCAGTCCAA ATATCTCCTT CAAAGAGAGA TCTTCCAGGG TCACCTAATC CAGAGAGTGC CCTCTATGGT TGCCACATCC CCCCGACCCA CCACCCACCA CCCCCCACTT CAACTCCTTT ATGGCACCTG CCCCTCCCTG AAATTCTCAC TGTTGCTTAT TTGTTATCTA GCCCTCTCAT CAGAATGTAG ATCCACTGGT GACAGGGGAC TTGTGTGCCT CGAG	60 120 180 240 300 360 384
(2) INFORMATION FOR SEQ ID NO:939:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 262 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:	
GAATTCGGCC TCCATGGCCT AGTTGTGTTT TTTGGGCTTG CTATTAATGC AAACTCTGAT TGCAAATGGA TGTCATGTTT CATACCTTTT TTATCAGGAA AAAAGCAGCA AGCCTTCAGG TGTTCCAGTG ATGCCTGACA CAATTGAGCT GGACTTTATG CTGCTCTTTA CAGTAAGAGG TGTTGCATTG TATGTGGGGA CTATGTGCAC TGGCGTCTAA GACAGTGACC TCAACAATAT TAGCTTTGCA CAAACCCTCG AG	60 120 180 240 262

- (2) INFORMATION FOR SEQ ID NO:940:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

GAATTCGGCC	TTCATGGCCT	AGTGGAGGAC	TGCTTTTGTG	AACATGAGAA	AGCAGCGCCT	60
GGTCCCTATG	TATTTGGGTC	TTATTTACAT	CCTTCTTTAA	GCCCAGTGGC	TCCTCAGCAT	120
ACTCTTAAAC	TAATCACTTA	TGTTAAAAAG	AACCAAAAGA	CTTTTCTCCA	TGGTGGGGTG	180
ACAGGTCCTA	GAAGGACAAT	GTGCATATTA	CGACAAACAC	AAAGAAACTA	TACCATAACC	240
CAAGGCTGAA	AATAATGTAG	AAAACTTTAT	TTTTGTTTCC	AGTACAGAGC	AGAACTCGAG	300

- (2) INFORMATION FOR SEQ ID NO:941:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 194 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

GAATTCGGCC	TTCATGGCCT	AGTATATCTG	AAAAGTACAC	TGTGTTTTGA	AATTATAAAT	60
TTTCATTCTG	AATGAGGTTT	CTTTTTTTGA	TTTTCTTTAA	AAAAAAAAA	CAACCTGCTT	120
TGATTTGCTT	TACATTCCTT	GCCCTCCATT	TTTCTTATTA	TATTGTAAAC	ATTAGAAAAA	180
TGAACACCCT	CGAG					194

- (2) INFORMATION FOR SEQ ID NO:942:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 581 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

GAATTCGGCC	TTCATGGCCT	AGTGAGGATA	AAGATAAGGA	ACAGGCCAGG	CACAGTAGCT	60
CACGCCTGTA	ATCCCAGCAC	TCTGAGAGGC	CGAGGCAGGT	GGATCACATG	GGGCCAGGAG	120
TTTGAGACCA	GCCTGGACAA	CATGGTGAAA	CCCCGTCTCT	ACTAAAAATA	GCCAGGTGTG	180
GTGGCACACA	CCTGTAATCC	TAGCTACTTG	GGAGGCAAGG	TGGGAAGTTT	GTTTGAACCA	240
GGAGGCAGCG	GTTGCAGTGA	GTCAAGATCA	TGCCACTGCA	CTCCAGCCTG	GGTGACAGAG	300
TACGACTCTG	TCCCAAAAAA	AAAAAAAAAG	ATAAGGAACA	GACCCAACCC	GAATCCACAC	360
AACCTGACAC	ACAGGAAAGT	CTTGCCCATC	CATCCACCTA	CCTCCCCAAC	CAGAGTAGTG	420
AAGCTATAAC	CCCAGAGAGA	TACCTTTGAT	GTGAGCACTG	TCCAGCATGG	GCACCAAGGC	480
ATTCACCTGC	TCCAGGAGTG	CAACCTGGGA	AAGGATAAAC	TGCTCCTCTA	AAGCAAAAAT	540
GGACAAGATA	GTTGCAGTGA	AGCAAACCTG	GGCATTGCTA	G		581

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:	
GAATTCGGCC TTCATGGCCT AAAACAGGCA ACAATGACCT TTTATTTTCT GTTTGTCCCC	60
ACCTCCCCAG CCTTCCACCT CCTGTTCTTC CTACCTTCTT CCTTTTTGAC TAAATAATCC	120
CCACCTCCCT TGATCATACA GTGAGGCTAC AGTGACTGAG GGGAGAATCC CCTCCTGTTC	180
ACTCTCCCAA CCCTGCTCCA GCCCCTCAGC TTCCCAGACC CTCATGCAGT TGGTTGTAAA TTCTCCCAGT GAGCTCGAG	240
TICICCAGI GAGCICGAG	259
(2) INFORMATION FOR SEQ ID NO:944:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 360 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:	
The state of the s	
GAATTCGGCC TTCATGGCCT AAAACCTCAC GTGGCCTCTG ATTTCATTGT GGGTGCATCC	60
ACAGGTGGCC CGAGCTGTTC TTTCAGCTGC TCCAAGGATT GAGACCCAAG TCATCATGAA	120
AAAGGCCCAA GTACAGTCTT AATGCGATAA ATCCACTAGC TAAGACGTCG AGTGCCAAGA	180
CCAGCCTTCC AGCCGAGGTT TGGACAAAGT CTCAGGTTCC CGTGACTCAG GGTAAGGTGC TGGGGCTGCC AGAGGACCTG CCCCAGCAAG ATTTTTGTCA AGAGCGAGAC TCCATCAGCC	240
CAGGCAGACG GGAGCAGGTT CTTGGCCAGC GTAGACAGCA GCAAACAGCA GCTCCTCGAG	300 360
	300
(2) INFORMATION FOR SEQ ID NO:945:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 206 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) TOPOLOGI: Timear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:	
GAATTCGGCC TTCATGGCCT AGTGCAGGAG ACGCCCTCAC CGGAGATGGG GACCGAGTCC	60
ACACGGCTCT CACTGCAAAT GCTTTGGGAA AAACAAGACA GTGTACTTTG TGATCATATA	120
AAACAGCAAA ATAAAATAGT CGTGGGCACA GGGCCAGTGA TTCTGCAGTT AGAGCCGTGT	180
GGACTCGGTC CCCTCTCCGG CTCGAG	206
(2) INFORMATION FOR SEQ ID NO:946:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 272 base pairs	
(B) TYPE: nucleic acid	

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

GAATTCGGCC	TTCATGGCCT	AGGTTCCCCG	GCGTGGCATG	GATGATGACA	GAGGCCCTAG	60
ACGTGGTCCT	GAGGAAGATA	GGTTCTCTCG	TCGTGGGGCA	GACGATGACC	GGCCTTCCTG	120
GCGTAACACA	GATGATGACA	GGCCTCCCAG	ACGAATTGCC	GATGAAGACA	GGGGAAACTG	180
GCGTCATGCG	GATGATGACA	GACCACCTAG	ACGAGGACTG	GATGAGGACA	GAGGAAGCTG	240
GCGAACAGCT	GATGAGGACA	AAGGACCTCG	AG			272

- (2) INFORMATION FOR SEQ ID NO:947:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

GTTTTGCTTA	GATTTTGCTT	TGGTTAGGTT	GCGTTTTGGG	GTTTGCCTTT	TTTTGTTGTC	60
GCTTAAATGC	AATTTGGTTG	TAAAGATTTG	ATTCCTTTGT	GTTCATCTGT	TCCGCTTCTC	120
AGCGGTCCAT	CTCAGCGTCT	CCCTTCAGGA	ACCGCTGAGT	GTCCTCTCTT	AACATCCAAG	180
CCTTTTAATG	AAATCGTACT	GAAATCTGTA	TCAGCTAAGA	GTCCTCCAAT	CCTGGTCCCA	240
TTAACTCCAA	GTGCCTTTTT	GACAGTGACA	ACAGACAGTC	CCTCGGCACT	CGAG	294

- (2) INFORMATION FOR SEQ ID NO:948:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

GAATTAGAAT	CTCTAAAGAA	ACAGGAGGGA	CTTCTTAAAA	ATATTCAGGT	CTCACATCAG	60
GAATTTTCAA	AAATGAAACA	ATCTAATAAT	GAAGCTAACT	TAAGAGAAGA	AGTTTTGAAG	120
AATTTAGCTA	CTGCATATGA	CAACTTTGTT	GAACTTGTAG	CTAATTTGAA	GGAAGGCACA	180
AAGTTTTACA	ATGAGTTGAC	TGAAATCCTG	GTCAGGTTCC	AGAACAAATG	CAGTGATATA	240
GTTTTTGCAC	GGAAGACAGA	AAGAGATGAA	CTCTTAAAGG	ACTTGCAACA	AAGCATTGCC	300
AGAGAACCTA	GTGCTCCTTC	AATTCCTACA	CCTGCGTATC	AGTCCTCACC	AGCAGGAGGA	360
CATGCACCAA	CTCCTCCAAC	TCCAGCGCCA	AGAACCATGC	CGCCTACTAA	GCCCCAGCCC	420
CCAGCCAGGC	CTCCACCACC	TGTGCTTCCA	GCGTATCTCG	AG		462

- (2) INFORMATION FOR SEQ ID NO:949:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 624 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

GAATTCGGCC	TTCATGGCCT	ACTCAAAGAG	ACAACAAATA	GCATGGTAGA	ATCAATTAAA	60
CACTGCATTG	TGTTGCTGCA	GATTGCCAAA	AGTACTATTA	ATCCCGTAGA	TGCAATATAT	120
CAACCTAGTC	CTTTGGAACC	TGTGATCAGC	ACAATGCCTT	CCCAGACTGT	GTTACCTCCA	180
GAACCTGTTC	AGTTGTGTAA	GTCAGAGCAG	CGTCCATCTT	CCCTACCAGT	TGGACCTGTG	240
TTGGCTACCT	TGGGACATCA	TCAGACTCCT	ACACCAAATA	GTACAGGCAG	TGGCCATTCA	300
CCACCGAGTA	GCAGTCTCAC	TTCTCCAAGC	CACGTGAACT	TGTCTCCAAA	TACAGTCCCA	360
GAGTTCTCTT	ACTCCAGCAG	TGAAGATGAA	TTTTATGATG	CTGATGAATT	CCATCAAAGT	420
GGCTCATCCC	CAAAGCGCTT	AATAGATTCT	TCTGGATCTG	CCTCAGTCCT	GACACACAGC	480
AGCTCGGGAA	ATAGTCTAAA	ACGCCCAGAT	ACCACAGAAT	CACTTAATTC	TTCCTTGTCC	540
AATGGAACAA	GTGATGCTGA	CCTGTTTGAT	TCACATGATG	ACAGAGATGA	TGATGCGGAG	600
GCAGGGTCTG	TGGTGAAGCT	CGAG				624

- (2) INFORMATION FOR SEQ ID NO:950:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

GATTCTAGAC	CTGCCTCGAG	CACGCTTGGA	GAAGCCCCGT	CTCTACTAAA	AATACAAAAT	60
TGGCCGGGCA	TGGTGGCGCA	TGCCTGTGGT	CCCGGCTACT	CTGGAGGCTG	AGGCGGGAGA	120
ATCACTTGAG	CCCAGGAGGT	GGAGTTGAGG	TGAGCCGAGA	TCGTGCCATT	GCACTCCGGC	180
CTGGGTGACA	GAGTGCAACT	CCGTCTCAAA	ААААААААА	AAGCATTCAC	GTCAATCTCA	240
AGAGAACCTG	CTACTAATGC	TTTCTTTGAT	AGGCAGTATG	ATAGGTTGGA	AAGAATATAA	300
ACTGGGATCA	AGCTTGGGTT	CCACTTACCA	GCTGTAGTAT	GTTGAGCAAA	TTATTTAATC	360
TAACACTCGA	G					371

- (2) INFORMATION FOR SEQ ID NO:951:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 283 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

GCGATTGAAT	TCTAGGGTTT	TTTTTTTTT	GGGATCCTGG	GTAAAATTTT	ATCCAAAAAA	60
CGGGATTTTT	TTTTTTTTAA	AAAAGGAAAT	TTGAATTCAA	AATTTTGGGC	AGCCCCGGCT	120
TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTGGTGGGTT	CTGAGTCTTC	180
ACTTTATTAC	TATGTCACCA	GAAGTCACCA	CCTTCACTTG	GTTCACCACA	GATGGATGGA	240
TGTCATAAAG	GAGGGTGCCA	CGGGGCCACT	GGATTCACTC	GAG		283

- (2) INFORMATION FOR SEQ ID NO:952:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

GCTTGGCAGA	TGCTAACTTC	ATGGAAGATG	GTAATAGGAA	CAGATACTGC	TCTCTGCCCC	60
TGCTTCTTGG	ATTCTTCAGC	TCCTACCGCT	GATTCGGATT	ATCCCCTTTT	GACCCTCTTG	120
GGGATCCAGA	CTGCTGCCAG	GAGGCTGAGT	AGATACCTCA	GTTATCTGTA	TGTTATTTCT	180
GAGAGGCTTT	GGCGGATCCT	CTTCACTTGG	CATCCTGTGG	CATCCCTAGG	GTCTGGTGGT	240
AGCAGTAATA	GCAACAATGA	TATCTTACAT	CTGGAACAAC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:953:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 614 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

GAATTCGGCC	TTCATGGCCT	AATTCTAGAC	CTGCCTGTCT	TGAGAGGAAC	CTTCCCTGTG	60
CTGGCTCCTG	TTGTTATCTG	TACCTAAGTT	ACTCAGTTCT	GAGTGCATGT	CTGGTAAATG	120
CTGGCCATTT	CTTTGAAGTT	CTGACTCAGA	ATCGGCCTCC	ATTAGAGAAC	TCAGTTCTCC	180
AAACCCAGTC	ATGATCTGCC	TTAAAATTGA	CCGAAGAGCC	ACTGATGATG	GCTCAACAAG	240
CTCATTCTCA	GAAATCCTAC	GAAGAGGAAC	TGTTATGGTA	CTAACATAGG	TTCGAATACC	300
TGACCGCTCT	AAACGAGAAA	TGGTTCGGCG	AAAGCCCCCA	CTATTGCTTT	CAATAGTGAC	360
TGTATTTTCT	GCTAGCCCTA	CTCTGGATCG	AGTTCTATTT	GCAATACTAT	CCCGATCTCT	420
ATTTTCTCCA	GGACGGATCC	TTCTCACTTG	AAGGTCCAGT	GTGATTGTTG	GATGTCGTCG	480
TACAGCAGTT	GAGGATCTGC	TGGATTCTTC	TCCTTCTTCT	ACTGTTATTC	TTGACACAAG	540
CCTTGAATTA	GAGAATGGGG	TATATGCAGT	ACCTCTGCGT	TCTCGTTCTC	TATCTTGCTC	600
TAAAAAGACT	CGAG					614

- (2) INFORMATION FOR SEQ ID NO:954:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

GAATTCGGCC	TTCATGGCCT	ACAAGGATTT	CAGGATGTTC	TTCCTCTGGA	CTGCTCTGTT	60
CTGGGGTGGA	GTCATGTTTT	ACTTGCTGCT	CAAGAGATCC	GGGAGAGAAA	TCACTTGGAA	120
GGACTTTGTC	AATAACTATC	TTTCAAAAGG	AGTAGTAGAC	AGATTGGAAG	TCGTCAACAA	180
GCGTTTTGTT	CGAGTGACCT	TTACACCAGG	AAAAACTCCT	GTTGATGGGC	AATACGTTTG	240
GTTTAATATT	GGCAGTGTGG	ACACCTTTGA	ACGGAATCTG	GAAACTTTAC	AGCAGGCGCT	300
CGAG						304

- (2) INFORMATION FOR SEQ ID NO:955:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

GAATTCGGCC	TTCATGGCCT	AGTAGCTATT	AATCTGTGGC	TATGAAATGA	TCAGAAATGC	60
TAAGTGAGAT	CAATATTTGT	TTGGAAAAAA	AATCTTGGGA	AACAACCCAA	GGGTTTTCGC	120
TGTTGTTGTT	TTTCTTTTTC	TATTTTTGTN	NACTTAGTCC	TTTAGCTAGT	GGATTTAATT	180
TTGTTGTGCC	TGCTTCATTT	TGCAATAACA	ATGCAGTAGA	ATTTAAAACT	TGGACGCTCG	240
AG						242

- (2) INFORMATION FOR SEQ ID NO:956:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

GCTGCGCTGT	ACTTCAGATA	CTTTTTTCGA	GGAACATTTG	TGATTTGTGG	CATAAAGTAA	60
CTGTCTAAAG	GAAATCTTCT	GAGAGGATCT	GGTCATTTTA	TGAAAGGGGC	AATTAAGGGG	120
AAATGGAAGC	AGATCTTTTA	AAGAAGGAGC	ATTTGAAATT	AGCCCAGGAA	TCATGTCCGG	180
CGAGTCCTGC	TCTTTTGTAC	CTGGGCATAA	TAGTCAGCCA	CACAGAGCTA	GAGTTAGTTC	240
AAGAATTGTC	TTTCCTGATC	GTGCTATATT	TTTGGAAACA	CGCCGTACTC	GAG	293

- (2) INFORMATION FOR SEQ ID NO:957:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

GCAAAGAATG	GTAACGTGCT	TATCATGGGA	GTGTTTTGAG	AAACTTAGCC	AAAGCTTCAG	60
CAGAAAAATC	CCCGAGAAAG	ACCAGAGAGT	TCTTCACCAC	AACAATGTTC	CTGCTCATCC	120
CTCTCATCAA	ACAAGGCCAT	TTTGCAAGAG	TTTTGATGGG	AAATCACTAG	GCATCCACCC	180
TACAGTCCTG	GTTTGGCACC	TTCTGACTTT	TTGTTTCCTA	ATCTTAAAAA	AATTTTTCAG	240
GGCAACTCTC						253

- (2) INFORMATION FOR SEQ ID NO:958:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 466 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

GAATTCGGCC TTCATGGCCT ACAACATCAG CTCCTGTCTG GTTCTCAGC TGCACGACCT CAAACTACAA CCTCAGCTCT TCCCCGAGTC TTCTGCTGCA TGACCCTCAA TCTAGAACAT AAGCTCCTCT CTGGGTGTCC ACCTGTAGGG ACCTCAAATT AGAACGTCAG CTCCTCCCAG AGTCTTCAGC TGCATGACCC TCAATCTTTA ACATCAGCTC CTCTCCAGGT CTGCAGCTCC ATGACCCTAA AAATACATGA GCAGCTCCTC CCTGAATCTT CAGCTGTACG ACCCTCAAAC TACAACATCA GCTCCTGTCT GCACCTCCAG CTGCAGGGCC CTCAAACTAG AATATCAGCT CCTCCCCGAG TCTTCAGCTG CACGACCCTC AAACTAGAAC ATCAGCTCCT GTACAGATTT CCAACTGTAG GGCCCTCAAA CTAGAACATC AGCTCCTCCC CTCGAG	60 120 180 240 300 360 420 466
(2) INFORMATION FOR SEQ ID NO:959:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 137 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:	
GGAGCATGTC CTGTTATTTA TTTAACTTTT CCATTTTCAT TTTTTATTTG GGTAAGATAA TTGCTTATGA TAAGCCTTGG GTGTGGAGAG CCGGTGCATA CAGAGTGGCG AGGCAAGCTT CAATCTGCAG TCTCGAG	60 120 137
(2) INFORMATION FOR SEQ ID NO:960:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 317 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:	
GAATTCGGCC TTCATGGCCT AGAGCCGCGG CTCATGCGCG GTGCACAGAG GCTTGTTTCA CATCTGTAAC AACAGGAGGA GGCCCAGCCT CGTGATGAGG AATAGCAAGG AGAGAATTCA GCTCCAGTTC AAAAGCCTAC AAAATCTGAG ACTGTCATTG CTTTTATAAG GATTCCAGCT TTCCCTCCTG GCCAGAAATG TTCAGCCTGG ACTCATTCAG AAAAGATCGG GCCCAGCACA GGCAGCGTCA GTGCAAACTT CCCCCACCCC GCCTTCCACC CATGTGTGTC AACCCTACCC CAGAAGGAAC CCTCGAG	60 120 180 240 300 317
(2) INFORMATION FOR SEQ ID NO:961:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 470 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:	
GAATTCGGGC TTCATGGCCT ACTCTGCTCA ACCTGCACAT CACCCACCAC AGTCACCAGC ACAAATTCAG ATGCAACTAC AGCACGAATT ACAACAGCAA GCCGCATTCT TTCAGCCTCA	60 120

GTTTCTAAAC	CCAGCCTTTT	TGCCTCATTT	TCCTATGGCC	CCAGAAGCAC	TGCTGCAGTT	180
TCAGCAGCCT	CAGTTTCTCT	TTCCATTTTA	TATACCTGGG	ACGGAGTTCA	GCTTGGGGCC	240
AGATTTGGGC	TTGCCAGGCT	CTGCCACATT	TGGGATGCCT	GGCATGACAG	GAATGGCTGG	300
CTCCTTGCTT	GAAGACCTAA	AGCAGCAGAT	TCAAACCCAA	CATCACGTTG	GTCAAACTCA	360
ACTCCAGATA	CTACAGCAAC	AAGCACAACA	ATACCAAGCC	ACACAGCCCC	AGCTGCAGCC	420
TCAAAAACAA	CAGCAGCAGC	CACCACCTCC	ACAGCAACAA	CAAGCTCGAG		470

- (2) INFORMATION FOR SEQ ID NO:962:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 603 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

GAATTCGGCC TTCATGGCCT	AGGAGAANGA	CGTGCTGGTG	AACGTGAACC	TGGTGGATAA	60
GGAGCGGGCA GANAAAATG	TGGAGCTGCG	GAAGAAGAAG	CCTGACTACC	TGCCCTATGC	120
CGAGGACGAG AGCGTGGACG	ACCTGGCGCA	GCAAAAACCT	CGCTCTATCC	TGTCCAAGTA	180
TGACGAAAAA CTTGAAGGGG	AGCGGCCACA	TTCCTTCCGC	TTGGAGCAGG	GCGGCACGGC	240
TGATGGCCTG CGGGAGCGGG	AGCTGGAGGA	GATCCGGGCC	AAGCTGCGGC	TGCAGGCTCA	300
GTCCCTGAGC ACAGTGGGGC	CCCGGCTGGC	CTCCGAATAC	CTCACGCCTG	AGGAGATGGT	360
GACCTTTAAA AAGACCAAGC	GGAGGGTGAA	GAAAATCCGC	AAGAAGGAGA	AGGAGGTAGT	420
AGTGCGGGCA GATGACTTGC	TGCCTCTCGG	GGACCAGACT	CAGGATGGGG	ACTTTGGTTC	480
CAGACTGCGG GGACGGGGTC	GCCGCCGAGT	GTCCGAAGTG	GAGGAGGAGA	AGGAGCCTGT	540
GCCTCAGCCC CTGCCGTCGG	ACGACACCCG	AGTGGAGAAC	ATGGACATCA	GCACACTCTC	600
GAG					603

- (2) INFORMATION FOR SEQ ID NO:963:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 415 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

GAATTCGGCC	TTCATGGCCT	ACAACAGCGT	TAGGTTTTTT	TTTTNGTTNG	TTNGTTNGTT	60
TNGTTTTTT	CCAACCCTCT	TTCGGATGGA	CGGGGAAAGA	GAGAAAGAAA	AANCGAGGGA	120
AAATCNACAA	AATGTGCGAT	GCAAAGAGTC	GATTTTCGCG	${\tt GGGTTTGTCA}$	ACTTCGCCAC	180
TGCCGCACGC	GAATCGACGT	CGTCACGTGA	CGGTCTGCCT	CCGCCCTTAT	TAACTCTCAG	240
CCCAGCGGCG	GTTTCCAGGA	CCTCAGACTT	TTTGCCGAGG	CGGCAGTCCC	TAGACGAAGC	300
GAAGGAGGCG	GCGCCTGCCC	CGCCCACAAG	AGCTGCCGCG	CGCGGGTGTT	ATAGCTCCAC	360
CCCATCTGCA	AAGGAAGGGG	GAGCGGAAAG	AGCGGGATCT	AGCGGGGAAC	TCGAG	415

- (2) INFORMATION FOR SEQ ID NO:964:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 964:

GAATTCGGCC	TTCATGGCCT	AGCGGGTCTT	CAGACAAGTG	GAAAAGGTGA	GAGAGGAGAT	60
CAGGGCGCAG	AGCCCCGTGG	AGGCTGAGTT	TCCATATGGG	CAACTGAGCA	CATCCTGCCA	120
CTCCCACCTC	GTGCCTCAGA	ATNGACACCA	GGCTACTCAT	CTGGAGGTGA	CCAAGCAGCC	180
AACCAATCGG	GTCCCCTGGA	GGTCCTCAAA	TGCCTCCCCA	TACCTTGTTC	CAGACCTCGA	240
G						241

- (2) INFORMATION FOR SEQ ID NO:965:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

GAATTAATAG (CCTGCAGGTT	AATTACTCCC	TGAAGGGTAT	TGTGGAAAAG	TATAACAAGA	60
TCAAGATCTC '	TCCCAAAATG	CCAGTATGCA	AAGGACACTT	GGGGCAGCCT	CTCAACATTT	120
TCTGCCTGAC '	TGATATGCAG	CTGATTTGTG	GGATCTGTGC	TACTCGTGGG	GAGCACACCA	180
AACATGTCTT (CTGTTCTATT	GAAGATGCCT	ATGCTCAGGA	AAGGGATGCC	TTTGAGTCCC	240
TCTTCCAGAG	CTTTGAGACC	TGGCGTCGGG	GAGATGCTCT	TTCTCGCTTG	GATACCTTGG	300
AAACTAGTAA	GAGGAAATCC	CTACAGTTAC	TGACTAAAGA	TTCAGATAAA	GTGAAGGAAT	360
TTTTTGAGAA (GTTACAACAC	ACACTGGATC	AAAAGAAGAA	TGAAATTCTG	TCTGACTTTG	420
AGACCATGAA	ACTTGCTGTT	ATGCAAGCAT	ATGACCCAGA	GATCAACAAA	CTCAACACGC	480
TCGAG						485

- (2) INFORMATION FOR SEQ ID NO:966:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

GAATTCGGCC	TTCATGGCCT	AACGGCTCCC	TCACTTGTGA	ATTAAAGTCA	GACACTGCCG	60
TAAGGTTCTT	CTGGTTCCTG	CTTTGTGGAG	AAAGCTTTCA	GCAGCAATAT	CTGGGATCAC	120
TGGTGTATTA	AATGTCAGGC	CTCGCATCAT	TATTCTGCCC	TGAGCTGATG	GTAAACCGGG	180
CACCCAGCCT	TTTAGCTTTC	ATCCAGCACG	AGGGAACTTG	CCTTCAGATG	TGACACGTAC	240
AAGTCAAAAA	AGCTCAGAGT	CAGCTCCAAC	GTCTATTGGA	TCCCACTCTA	TCGCCTTTAA	300
AAAGGAAAAG	AAAATCGAAA	CGAACTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:967:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

GAATTCGGCC	TTCATGGCCT	AGGGTCGCAG	ACTCAAATGC	CCACAGGGGC	CAGGTTAGGT	60
TAGCGGCTGA	AGCAGTCTGG	GGAGAGGCAA	AAAGCAATGG	CAGGGAGGTG	GGACAGAGGA	120
ATGTGGGCCC	CAAACTATGG	GGGCAGCTGC	TACTCAGTGC	CAGCTGTTCG	TCGCCATGGG	180
GGGAAGCGGG	ACCAGAGCCG	CCGGGTCTTC	GGCTTTTTCA	AGAGGACGCA	TAACTCCGGA	240
					GAAGGAGGCC	300
CACTCATCCT	C)) mmmc) C)	C110010		COOTOACAGI	GANGGAGGCC	300
GACICAICGI	CAATTTCACA	CAAGTACTCG	CCGGAGTCCT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:968:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 531 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

GAATTCGGCC TTCATGO	SCCT AGGATGCAGC	CGAAAAGGAT	CGCAAGCTTC	AGGAGAAAGA	60
GAAGCAAATC GAAGAG	CTGA AGAGGAAACT	GGAACAAGAG	CAGAAGCTCG	TGGAAGTGCT	120
GAAAATGCAA CTTGAG	STTG AAAAACGAGG	GCAGCAGCAG	CGGCCCCTGG	AAGCCCAGCC	180
CAGTGCCCCA GGTCAT	ICTG TCAAGTCAGA	TCAGAAGCAC	GGCAGCCTTG	GCTCCTCCAT	240
CAAAGATGAG GCCTCAG	CTCC CTGACTGCTC	CAGCTCCAGG	CAGCCCATCC	CAGTAGCCAG	300
CCACGCTGTA GGCCAG	CCCG TCTCTACAGG	TGGCCAGACC	CTTGTTGCCA	AAAAGGCTGT	360
AGTTATCAAG CAAGAG	STCC CTGTGGGCCA	GGCAGAGCAG	CAGAGTGTCG	TCTCGCAGTT	420
TTATGTGAGT TCCCAGO	GGAC AGCCACCGCC	TGCTGTTGTT	GCTCAGCCCC	AGGCTTTACT	480
GACCACGCAG ACTGCT	CAGC TGCTGCTCCC	AGTGTCCATC	CAGGGCTCGA	G	531

- (2) INFORMATION FOR SEQ ID NO:969:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

GTGCCTCGAG	AAACTGCCTA	TTCAGAAACA	CAGAAACACC	GAGACCTCAA	AATCCCCTGA	60
GAAGGACGTT	CCCATGGTAG	AAAAGAAGAG	CAAGAAACCC	AAGAAGAAAG	AGAAAAAACA	120
				GAGAAGAAGG		180
				CCCGCCCCCG		240
ATCCACGGGG	GAGCTCAGTG	TGAACACTGT	CACTACCCCG	AAGGACGAGT	GTGAGGACGC	300
					ACAAGAAATC	360
	AAGAACAAGA			~2.01.ca.100	ACMOMMIC	388
						200

- (2) INFORMATION FOR SEQ ID NO:970:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 365 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

GAATTCGGCC	TTCATGGCCT	AGCTTACACT	GGGCCAAGTG	CTTGCCAAGG	ATTCTCATGT	60
GACATTTCTT	TCAGTCCTGC	CGAGGACTTT	ATGAGGGAAG	CACCCTGTTT	TACAGAGGGA	120
AGGGGGCCTA	TGGGGTCTAC	AGCAGTGAGA	GCCTAGAGTT	CAGTCTGCGT	CTCTCTGATT	180
CCAAAGCCTG	TGATTGTGAC	TTCCATACTC	TCCCTAAGAC	ACATTCATAC	ATTCAACTGA	240
ATATTTATTG	AGCACCTACT	GTGTGCTAGG	GATAGAGCAG	TAAATGAATC	AGGCAAAAAT	300
TATTTACATT	CCACTGGGGC	TGACAAACCC	AAACAAGGAA	GAGGTGTAGT	GCTTCGGGTC	360
TCGAG						365

- (2) INFORMATION FOR SEQ ID NO:971:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

GCAAAAGTAA	TATGATTTGT	TTAAAATACT	CAGTCAACAG	GTATTTCCTG	TTTTATAAAA	60
CCATAGAAAG	TAGAATATGG	TTCTCCCGAA	TAAAAACTGA	TCCATTTTAC	CTTTTTCTTT	120
				GCTTTTTTCC		180
				TGCTTGGACA		240
GCCAGTTGGT	TCCCTGTAAT	GTTTGTGGGC	GTACCTTCCT	GCCAGACAGA	CTGATTGTTC	300
ACCAACGATC	TTGTAAACCC	AAAGCTCTCG	AG			332

- (2) INFORMATION FOR SEQ ID NO:972:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

GCGCCCTCAC	CCCTCCAATC	CCCCCTCTGA	CCCCCTCTTC	CTCACATGGG	GTCGGGGGCC	60
TGGGAGTTCA	TTCTGGACCA	GCCCACCTAT	CTCCATTTCC	TTTTATACAG	ACTTTGAGAC	120
	CACAGCACAC					180
TGTCAGCAGG	ATTGGCGTGT	GGGAAAGCTC	TTGAGCTGGG	CACTGGCCCC	CCGGACGAGG	240
	TTCACACACA					273
TGGCTGTGTG	TTCACACACA	CACACACCTC	GAG			273

- (2) INFORMATION FOR SEQ ID NO:973:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi)	SECTIONCE	DESCRIPTION:	SEO	TD	NO - 973
141	SECUENCE	DESCRIPTION:	350	ıυ	NO:3/3

GAATTCGGCC	TTCATGGCCT	ACTCTGTCTC	AAAAAAAAT	AGTAAGTTGT	GTAAAGAAAA	60
ATATTAATTA	TATAATATGG	CAGTTCCTAT	GAGAGTGTGG	CAAAAATCAA	GAGGGCTTGG	120
AAGTTTTTTC	TTTGCTCTTG	CAACTGGCTG	GATGCAGTTC	ATATATTTT	CAACCAGTAG	180
GTGGCACCCC	AACCTAATTT	TTTGCAGTTG	TAACCTGGTG	GCAGAAGGGG	CAGGACTGAT	240
GGCTTGGGCA	AGACTGTTAT	GCCAAGTTCT	CGAG			274

- (2) INFORMATION FOR SEQ ID NO:974:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

GAATTCGGCC	TTCATGGCCT	AGTGAGATAG	TACCAGATTT	AGAATATAAT	TTTATCTTTC	60
TTTAGCAACA	AGCCCTAACA	ATATCCAAAC	TAAATAAAT	CATTACATGA	ATTTACTTTT	120
TACAATCATT	CTCCTAAGGC	TCGAG				145

- (2) INFORMATION FOR SEQ ID NO:975:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

GAATTCGGCC	TTCATGGCCT	AGGAAATAAC	AGTTATTTCA	TCATAAAACA	GTCCCTTCAA	60
ACACACAATT	GTTCTGCTGA	AGAGTTGTCA	TCAACAATCC	AATGCTCACC	TATTCAGTTG	120
CTCTGTGGTC	AGTGTGGCTG	CATAGCAGTG	GATTCCATGA	AAGGAGTCAT	TTTAGTGATG	180
AGCTGCCAGT	CCATTCCCAG	GCCAGGCTGT	CGCTGGCCAT	CCATTCAGTC	GATCATCTCG	240
AG						242

- (2) INFORMATION FOR SEQ ID NO:976:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

CATGTGCACA CTCGCACATG CACATATGGG CACGTGGGAA GACGGGAGAA GTACTGTCAA

AGTATAAGGA ACTGCAGAGG TTGGGATTTA CTGGAAGGGA AGGGAGCACA CTCGAG

116

(2) INFORMATION FOR SEQ ID NO:977:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

GAATTCGGCC	TTCATGGCCT	AGCATGGCAA	CAGATATGTG	GAGCATTGGA	GTGTTAACAT	60
ATGTCATGCT	TACAGGAATA	TCACCTTTCT	TAGGCAATGA	TAAACAAGAA	ACATTCTTAA	120
ACATCTCACA	GATGAATTTA	AGTTATTCTG	AGGAAGAATT	TGATGTTTTG	TCTGAGTCGG	180
CTGTTGATTT	CATCAGGACA	CTTTTAGTTA	AGAAACCTGA	AGATCGAGCC	ACTGCTGAAG	240
AATGTCTAAA	GCACCCCTGG	TTGACACAGA	GCAGTATTCA	AGAGCCTTCT	TTCAGGATGG	300
AAAAGGCACT	AGAAGAAGCA	AATGCCCTCC	AAGAAGGTCA	TTCTGTGCCT	GAAATTAATT	360
CGGATACCGA	CAAATCAGAA	ACCGAGGAAT	CCATTGTAAC	CGAAGAGTTA	ATTGTAGTTA	420
CTTCATATAC	TCTAGGACAA	TGCAGACAGT	CAGAACTCGA	G		461

- (2) INFORMATION FOR SEQ ID NO:978:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

GAATTCGGCC	AAAGAGGCCT	AATGATGATG	AATAAGTTGG	TTCTAGCGCA	GTTTTTTTT	60
TTTCTTGTCT	ATAAAGCATT	TAACCCCCCT	GTACACAACT	CACTCGAG		108

- (2) INFORMATION FOR SEQ ID NO:979:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 505 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

GATGGCGTCG	GGCAGCGGGA	CAAAAAACTT	GGACTTTCGC	CGAAAGTGGG	ACAAAGATGA	60
ATATGAGAAA	CTCCCGAGA	AGAGGCTCAC	GGAAGAGAGA	GAAAAGAAAG	ATGGAAAACC	120
AGTGCAGCCT	GTCAAGCGAG	AGCTTTTACG	GCATAGGGAC	TACAAGGTGG	ACTTGGAATC	180
CAAGCTTGGG	AAGACAATTG	TCATTACCAA	GACAACCCCT	CAATCTGAGA	TGGGAGGATA	240
TTACTGCAAT	GTCTGTGACT	GTGTGGTGAA	GGACTCCATC	AACTTTCTGG	ATCACATTAA	300
TGGAAAGAAA	CATCAGAGAA	ACCTGGGCAT	GTCTATGCGT	GTGGAACGTT	CCACCCTGGA	360
TCAGGTGAAG	AAACGTTTTG	AGGTCAACAA	GAAGAAGATG	GAAGAGAAGC	AGAAGGATTA	420
TGATTTTGAG	GAAAGGATGA	AGGAGCTCAG	AGAAGAGGAG	GAAAAGGCCA	AAGCGTACAA	480
GAAAGAGAAA	CAGAAGGAGC	TCGAG				505

- (2) INFORMATION FOR SEQ ID NO:980:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

CGAGGGACAT	GAGGCTGAGC	TGGTTCCAGG	TCCTGACAGT	ACTGTCCATC	TGCCTGAGCG	60
CCGTGGCCAC	GGCCACGGGG	GCCGAGGGCA	AAAGGAAGCT	GCAGATCGGG	GTCAAGAAGC	120
GGGTGGACCA	CTGTCCCATC	AAATCGCGCA	AAGGGGATNT	CCTGCACATG	CACTACACGG	180
GGAAGCTGGA	AGATGGGACA	GAGTTTGACA	GCAGCCTGCC	CCAGAACCAG	CCCTTTGTCT	240
TCTCCCTTGG	CACAGGCCAG	GTCATCAAGG	GCTGGGACCA	GGGGCTGCTG	GGGATGTGTG	300
AGGGGGACCT	CGAG					314

- (2) INFORMATION FCR SEQ ID NO:981:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

GAATTCGGGC	TTCATGGGNT	ACTCATTGCT	ACATTGCTAG	TTGACCCGCA	GTTATATTTC	60
CTTTTTTTCT	TTTTAATAAA	AGGCAAGAGA	AACAATCCGT	TTTTGCCTTT	TCCTACCACA	120
TCTTTGACTT	TTCTGATTCC	TGCAAGTTTA	AGTTAAAAAC	ATCCTACCTT	CAAGCTACAA	180
AATGCAGCAC	ATCCCAGGAC	ATCCCTCACC	TGCTTTGCTT	GTTTATTAGA	CACAAGTGGC	240
TTTGTTCAGA	AAGTTACTGG	GAACCGCTAA	GGATAGTCAA	GGTGGAGAAC	ACAGGGTGGG	300
GTCTCAGAGT	CTGAGGCCTT	GGTTCAGGTT	CCTGATAACA	TTAAATATAG	AAAATACACA	360
GCACAAGGCC	AAACTCGAG					379

- (2) INFORMATION FOR SEQ ID NO:982:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

GAATTCGGCC	TTCATGGCCT	AGAAGATGGT	AAGGTTCGAA	TCTTTCGGGT	GATGGGAGTT	60
AAGTGTGAAC	AGGAACTGGG	ATTTAAGGGC	CACACTTCAG	GGGTATCCCA	GGTCTGCTTT	120
CTCCCAGAAT	CCTATTTGCT	GCTTACTGGA	GGGAATGATG	GGAAGATCAC	GTTGTGGGAT	180
GCAAACAGTG	AAGTTGAGAA	AAAACAGAAG	AGTCCCACAA	AACGTACCCA	CAGGAAGAAA	240
CCTAAAAGAG	GAACTTGCAC	CAAGCAGGGT	GGAAATACTA	ACGCTTCAGT	AACAGATGAG	300
GAAGAACATG	GCAACATTTT	ACCAAAGCTA	AATATTGAAC	ATGGAGAAAA	AGTGAACTCG	360
AG						362

- (2) INFORMATION FOR SEQ ID NO:983:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

GAATTCGGCC	TTCATGGCCT	AGGCCACTGA	TATTTTTCTA	AGTTAGCAAG	GCTCACTTGC	60
TTGCTTTCTT	GCCTCCCTTG	CCTCCATCCC	TCTCCCTTCC	TACCTTCTCT	ATTTACCTAT	120
TTCTCTCCCT	CCCTCTCTTC	TCCTCTCTTT	TTTTTTCCCC	CGCATATGCA	GCTTTTTGAT	180
TGTACTTGAT	TTTATAGAGA	CTGCACAGTT	CCAGCAAGAT	TGGGAGTCAG	GCATGGAGCA	240
GGCATCTCAG	GCTACCAGAA	AGAATTGGTC	ACCTAGACTT	TCAGTCAGGC	ATCCTCGTTT	300
GCATTGTCCT	GTAAGTCAAT	TAGTTGATAA	ATAGTTCCCC	CTTCATCCCT	TAAGTTTTGT	360
TTTTGTTTTT	GTTTTTAATA	TAGGTAAGTG	GGACTCTACC	TAAAATTTTG	CATCATACTT	420
ATGGGTAATA	TCTTTTTCAT	ATATTATTTA	TCAAAGTATG	AAGTTGAGTA	TTTTGCTTGT	480
ACCATTTCAA	TTCTGCATTA	TAGTAGTTCA	TTGTATAACT	GAAAGAAATG	ATTTCTTCAT	540
AAGTGACATT	AAATATGAAC	ATTCATCTCT	CGAG			574

- (2) INFORMATION FOR SEQ ID NO:984:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

GAATTCGGCC TTCATGGCCT ACGATTGAA	AT TCTAGACCTG CCCCCTCCCT CCATGCCTC	A 60
TCCCCGCCC CCTCCAGTCA TGCCGCAGC	CA GGTTAATTAT CAGTACCCTC CGGGCTATT	C 120
TCACCACAAC TTCCCACCTC CCAGTTTTA	AA TAGTTTCCAG AACAACCCTA GTTCTTTCC	T 180
GCCCAGTGCT AATAACAGCA GTAGTCCTC	CA TTTCAGACAT CTCCCTCCAT ACCCACTCC	C 240
AAAGGCTCCC AGTGAGAGAA AGTCCCCAC	CT CGAG	274

- (2) INFORMATION FOR SEQ ID NO:985:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

GAATTCGGCC	TTCATGGCCT	AGATAAGGAG	ACTTCAGAAG	AGAAGCCGCC	AGCTGAGGGA	60
AGTGAGGACC	CTAAGAAGCC	ACCCCGCCCT	CAGGAGGGAA	CAAGATCTAG	CCAGCGAGAT	120
CAGATACTCT	ATCTCTTTGG	GAGAACTGGC	CGAGAAAAAG	AGGAATGGTT	TAGGAGATTT	180
ATTCTGGCAT	CTAAGCTAAA	GTCGGAAATC	AAGAAGTCAT	CGGGTGTCTC	TGGAGGTAAA	240
CCAGGGCTTT	TGCCTGCACA	CAGCAGACAC	AACAGTCCGT	CCGGGCACCT	GACCCACAGC	300
CGCAGCAGCA	GCAAAGGCAG	TGTGGAGGAG	ATCATGTCAC	AGCCAAAGCA	GAGGGAGCTA	360
CTCGAG						366

(2) INFORMATION FOR SEQ ID NO:986:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 451 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

GAATTCGGCC	TTCATGGCCT	ACTCTCTTCC	AACCAAAAGT	CTTAATATGG	GAATATCCCT	60
CACCACGATC	CTAATACTGT	CAGTAGCTGT	CCTGCTGTCC	ACAGCAGCCC	CTCCGAGCTG	120
CCGTGAGTGT	TATCAGTCTT	TGCACTACAG	AGGGGAGATG	CAACAATACT	TTACTTACCA	180
TACTCATATA	GAAAGATCCT	GTTATGGAAA	CTTAATCGAG	GAATGTGTTG	AATCAGGAAA	240
GAGTTATTAT	AAAGTAAAGA	ATCTAGGAGT	ATGTGGCAGT	CGTAATGGGG	CTATTTGCCC	300
CAGAGGGAAG	CAGTGGCTTT	GCTTCACCAA	AATTGGACAA	TGGGGAGTAA	ACACTCAGGT	360
GCTTGAGGAC	ATAAAGAGAG	AACAGATTAT	AGCCAAAGCC	AAAGCCTCAA	AACCAACAAC	420
TCCCCCTGAA	AATCGCCCGC	AGCATCTCGA	G			451

- (2) INFORMATION FOR SEQ ID NO:987:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

GAATTCGGCC	TTCATGGCCT	AGAGAAACTG	AGCAAAAATA	GCTGCCAAGA	GAAGAGGGAA	60
CGAGTGCTCG	GGGCGGGTTG	GAGGCAGATA	ACGAGAAGGC	AAGAAAATTC	TTTGTCTTTG	120
GCTCCTGCTG	TCAGCTCAGA	GGGGTCATCT	TGAGATGAAA	AAGAAAAGTC	CCCAGCCTTG	180
GGGAAGGAAA	GGAGAGGGTG	CCCCACGCAG	ATATGAAGCA	AAGCCATTGG	CAAGATATTC	240
TCTCTAAGGA	GAGCAGCGGT	CTTGCCAAAG	GCATCTTCTA	TTGTGTATTG	CCGTCATAAA	300
CCCTACCCTT	CCATGTAGAT	AGCCAGGACT	CGAG			334

- (2) INFORMATION FOR SEQ ID NO:988:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

GAATTCGGCC	TTCATGGCCT	AAGAGAAACA	AAAATGATTT	TGCTTTCCAA	GCTTGGTTTG	60
TGGCGTCTCC	CTCGCAGAGC	CCTTCTCGTT	TCTTTTTTAA	ACTAATCACC	ATATTGTAAA	120
TTTCAGGGTT	TTTTTTTTTG	TTTAAGCTGA	CTCTTTGCTC	TAATTTTGGA	AAAAAAGAAA	180
TGTGAAGGGT	CAACTCCAAC	GTATGTGGTT	ATCTGTGAAA	GTTGCACAGC	GTGGCTTTTC	240
CTAAACTGGT	GTTTTTCCCC	CGCATTTGGT	GGATTTTTAT	TATTATTCAA	AAACAAAATG	300
AAAAGGTTAT	TTACTTTTTT	TTTCCTGAAA	TGCTGACAAT	ATGTGATATC	TTAATATCTG	360
TAATTCTTAG	TGAAAGTTAT	GGTATAGTAT	AGGTGAAGCT	GTAGTGTTTA	TATCAATAGA	420
TGTGAATTCA	AATGAGCAAT	CTAATAATTA	TTTACTATTC	AATTATGTTA	ATTTTCTTCT	480
CTTTGTCTCC	CATTGTATCT	GCACTCGAG				509

- (2) INFORMATION FOR SEQ ID NO:989:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

GAATTCGGCC	TTCATGGCCT	AGGCTTGTGG	GCAGGGCCCG	TGCAGGTCAT	GGAGCCGGTA	60
GCATCTCAGA	GCTGGACAGA	GGAGGTAGGC	TGGGAGCAGG	CCCGGTTGGG	GACCAGTGGC	120
CCCTGCACAG	GAGCCAGAGG	GCCTGGGCAG	CTGTCTGTCC	AGAAAGCATG	CAAGACCCCG	180
TGCCACCCGG	GCACACAGGG	CTGTCGTGTC	TAGAAAGAGA	TCTCCTGGGG	TCACGGGCAG	240
GCAAAGCTGA	TTGATTTTGG	CCGTGAAGTT	TGACCTTGTG	ATGGAAACCG	AGCTCCCAGG	,300
GAGTGAGACA	AACTGCCTCC	CCGTGTCAGT	GGCCAATAAA	CCTGACTTGG	TTTTACAGCC	360
CCGAGAAATT	GCTCACTAAT	AGCCAGACAG	ATGCTCCCCC	TGCCTCGAG		409

- (2) INFORMATION FOR SEQ ID NO:990:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

GAATTCGGCC	TCATGGCCTA	CCCAAATCTG	AAGTCTTTGG	ATATGTTACT	GCTGAAGTTT	60
CTATCACTTC	TCACTCCTGG	TTCCTTGTTT	CCCTGTATGC	TTTTTTTTTT	TTTCCATGAG	120
TTCACTTTTT	TAAATTATAG	TTCTTCAAGG	CCTAGGATGC	AGGTGTGTTC	TTCCATAAAG	180
GGCTATTTTG	CCTCTGCCGA	GGTCCTCGAG				210

- (2) INFORMATION FOR SEQ ID NO:991:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

GAATTCGGCC	TTCATGGCCT	AGTAGATAGT	ACAAAATTCA	ACAGATATCA	AAGTGTGTTA	60
AGTTTACCTT	TCCACCCACT	TTCTCATTTT	TGTCTCCCCC	AGTTCCTTTT	GCATTATTCC	120
ACGTATATTC	TGTGCATATA	TACATTCATA	TACATTTATC	TGTATGTGTC	AGCTTCTTTT	180
TACACAAATG	ATACATAAAC	ACTGTTCTGG	ACCTTCCAAC	TTAGAATTAC	TGCAAACAGT	240
GTCGTGATGA	ATTACCTAAT	TCTGTGTATG	TGTGTATATT	GGTAGAAAA	ATTCCCGGAA	300
GTAGAATTGC	TAGAACAAAG	ATTTATGCAT	TTTAAATATT	CCTTTATTAT	AAAACTAATG	360
AAAGTAAACA	TGTTGGCTAT	GACCACGTAT	GCTCTATGCT	CAGTTTTTCT	AGAGTTGTGT	420
ATGCTTAATA	TAGGAGCCTG	CCTCGAG				447

(2) INFORMATION FOR SEQ ID NO:992:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

GAATTCGGCC	TTCATGGCCT	AGCCCATTGT	TGTTTATTTT	GAATTAATTT	CAAGCTTACA	60
GAAGAATTAT	AAGAATTATA	CAAAGAGCCC	TTGTATAGCC	TTCATCCAGA	TTCCTCATTA	120
ATAGTTATCT	CCCCCACACA	CGTAATGCAC	AGACACTGCA	TGCATTTTCC	TTTTCTTTTT	180
TCTCTTCTTT	CTTTTTCTTT	TTCTCTCTTT	CCCTTTCTCT	TCTCCCTCCC	CTCCCCACCC	240
CTCCCCTCCC	TTCCTCTCCC	TTCCCCTCCT	CCTACTTCAG	CCTCTAGAAT	AACTAGACTC	300
GAG						303

- (2) INFORMATION FOR SEQ ID NO:993:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

GAATTCGGCC	TTCATGGCCT	AGGATTTGGT	AGGGTAACTT	GAAAACTGAG	TTAAATGAGA	60
AAGGTAGAAA	AAATTCGTAC	TTTTTCTCCT	CCCCACAAAA	AATAAAAACA	GTAAAATCTT	120
TACCAACTGA	AAAAGCTGTT	GAAATTTTCT	GTATGTTAAA	AAAATGAGCT	TTGCAGTAAC	180
TCTTAAAATC	ACCTAGCAAA	ATAGGAACTA	TAATGTGCAT	CTTTCCTTCA	CTAAAACATT	240
TATTGCATCT	CTTCTTGATG	CTGATGATTG	AGGACACACA	TTCTGCTTTC	CTGGGGCTTA	300
TGGTTTTATA	TAAAAACCAA	AGCAAAGTAG	AAAGTATACC	TCCTACCAAG	GGGCTCGAG	359

- (2) INFORMATION FOR SEQ ID NO:994:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

GAATTCGGCC	TTCGGCCTTC	ATGGCCTAGA	GGAGGACCAA	GGCTTCAAAG	GCCCCTGCCC	60
GCGCGTCCTG	CAGGTTCCCA	TTGTCCGTGT	TAATAGCCTC	AGATGGGCAT	CAGTTGCCCT	120
GATGGGCTTG	GGCTCCACGC	CCGGGCTTGC	ATGTTTGGCA	AAATTACTCA	AGAGCATTTC	180
TTTTTTTTT	CTTTGAGACT	CCGTCTCAAA	ААААААААА	AAAGAGATCC	TCAGCTGTTG	240
TTTCTTGAAT	CAGATATTTG	GATCACTCTA	GCATCCAATC	ATGCAGCTCC	TAAATATGCT	300
CCTAAATCAT	GCAGGTCCAA	TCACGCACCT	GTTTTACGGT	TTATCAATTT	GTGCTCATCC	360
TGAACTAAAT	AAACAAATCC	ATGAGCCAAC	TGCAGCACCA	CTCGAG		406

- (2) INFORMATION FOR SEQ ID NO:995:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

GAATTCGGCC	TTCATGGCCT	ACCATCTTGG	AACCTCCTCC	CATGATTGCC	TTATTATTTT	60
AAATACATTA	ATGTAGATCA	ATGAAGAATA	AGAAAATAAG	CAATTTTATT	TTACCTTAAT	120
TTATTCTGTT	TCTGATGCTC	TTTGTCTCTC	TATGTAGGTC	TGACTTTTTG	ACCTACATTA	180
TTTTCTTTCC	CTCCTAGGAA	TTTTTAAAAG	CATTTCTTGT	AAGGCAGGGC	TACTGAAAAC	240
AAATTTCCTC	AATATTTGCT	TGTCTACAAA	AGTCTTTATT	TCTCCTTTAC	CTTTTAAGGG	300
AAATTTCACA	ACCTACAGAA	TTCTAGGTTG	GTGGGTTTTT	TCCCCCTCAA	TCCCTTAAGT	360
ATTTAATTCC	TCTCTTCTTG	CTTGCATGGT	TTGTAAGGAA	GAGTCAGATG	TAATTTTTAT	420
CTTTGCTTCT	GTATGGGTAG	GGTGCTTTTT	CTTCTAGATT	TTTTTTCCAG	AGTTTTTTTC	480
TTTATCTTTG	ATTTTCTGTA	CTTCAAATAT	ATTATGCCCA	GGTATAGATT	GTTTTTTGTT	540
CTTGTTTTGT	TTTCATTTGG	CATTTGTTCT	GCTTGGTGTT	CTCTGAGCTT	CCCGGATCTC	600
GAG						603

- (2) INFORMATION FOR SEQ ID NO:996:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

GAATTCGGCC	TTCATGGCCT	ACAGAGAATG	AAACATGGAG	CTCACATTCT	GATGGGGGAG	60
TAAAAATAAA	CATATCAGAT	GGTGATGAGC	TTTTCGGTTT	TCTATTTCTA	TTTATGAAGA	120
ATAAAATAAG	GTAATAGAGA	TAATGTGATG	AAAATTCTAA	CATTCTCTAC	CTTTCCTGAA	180
TTCTTAATCT	ATACCTTCTG	TTCTTACATT	TTCTACTTAA	TTTTATTTAA	TACAACTTGT	240
AGCTAAACTT	TTATTTTTCT	TTCACTCCTG	ATTCTTAACC	CCTATCCATG	CTAATTTTTG	300
CCTTCACTAT	TCCACAAAAC	TTACCCACTG	TCGTATTATT	ATCTTCTATT	AAAAGCCAGT	360
ATTCTCTTTT	CAGTTTTTAT	CCTTCTTGAT	CTACACTGAA	CATGATTGCC	TTTCTCTCTC	420
TTATATCACT	TGCTGCTATC	TGCAGTCCAA	CTAGCCTCGA	G		461

- (2) INFORMATION FOR SEQ ID NO:997:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

GAATTCGGCC	TTCATGGCCT	AGTGATTTGG	GTACAGACAC	AGCCAAACCA	TATCATTACA	60
GATATAAATC	TCTGAGTAAA	TCCGGTGTTT	GATTTCTTCT	AGCTTTTTAG	CTTATGAGTA	120
GAGGTCTTTC	TCCTCTACTC	CAAGAATTTT	CATAGACACA	CCACTTAGTA	CTTACGTTTA	180
CCACCATTGT	TATTATTTT	AAGAATGTAC	TACTTTATAT	TTTTAAACAT	GAAGGACTAG	240
CTCAAAATTT	TGTAGCTTCC	CCCCCCGCCC	CAATCTTTTT	TTTTTTTTTG	ACTCCTTTGT	300

GATGGGTAGT GGTTTAAAGA CAGCAAAACA TGACCTTAAC CAGAACACTA ACTAGCTTTA TACATAATTC AGCCTATGAA CATGTATCTG GCAAGAGAAA TTCCTGATCT GTGGTTCGGC AGATCCATGA GAGCTGCTTC TCCGGATTTT CTTTGCTGGC CCCTCTCGAG	360 420 470
(2) INFORMATION FOR SEQ ID NO:998:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 350 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:	
TTTAAAGAGA GTTGCGTTAT TTTCTCCAAA AGCATTTGTT GAGTTGGTCA TTTTGACAGT TAACTGTCGG TTTTTACCTG CATTCCTAGG TGCTAAAACT TACAAGTGTA TCTCTTGAAC ACAGGCATTG ATCCTCTACC AATGAATAAT TGAGAGAGGT AGGAATGACT GATTTTTCTA GTTGTAGTTT GAAAGATTAA TTTGATGAAT TGGAAAGTAT GGAAACTATT CTGTTACTAT TGCAAAGAAA GATTTATTTT TTTAAAAAAAT TTATTTTTAT TTATTTTTT	60 120 180 240 300 350
(2) INFORMATION FOR SEQ ID NO:999:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 266 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:	
GGAGTATTGT TACAATCACA TTTGAAGTAC CAGGAAATGC AAAGGAAGAA CATCTTAATA TGTTTATTCA GAATCTCCTG TGGGAAAAGA ATGTGAGAAA CAAGGACAAT CACTGCATGG AGGTCATAAG GCTGAAGGGA TTGGTGTCAA TCAAAGACAA ATCACAACAA GTGATTGTCC AGGGTGTCCA TGAGCTCTAT GATCTGGAGG AGACTCCAGT GAGCTGGAAG GATGACACTG AGAGAACAAA TCCATTGGTC CTCGAG (2) INFORMATION FOR SEQ ID NO:1000:	60 120 180 240 266
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 309 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:	
GTAATGGGAG ATGGACATCC ACTGTTTCAT AAGAAGAAGG GGAACAGAAA GAAGCTAGTA GAGCTGGAGG TGGAGTGCAT GGAAGAGCCT AATCACCTTG ATGTGGACCT GGAGACCCGG ATCCCTGTCA TCAATAAGGT GGATGGTACT TTGCTGGTGG GTGAGGATGC CCCTCGCCGG GCTGAACTGG AGATGTGGTT ACAGGGTCAT CCAGAGTTTG CTGTTGATCC CCGATTTCTA GCGTATATGG AGGATCGCAG AAAACAGAAG TGGCAAAGAT GTAAAAAAAA TAATAAGGCA	60 120 180 240 300

309

GGACTCGAG

- (2) INFORMATION FOR SEQ ID NO:1001:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

CACGTCAGGA	GAATAGAATG	GAAAATTTTT	ATTTCAACAG	AAAGAAGTTA	ATTTAGAAAA	60
TTAGTTTAAA	ATACATTTGA	AAACTTAAAG	AGCAAAAAGC	ATTTGTAAAC	AAACAAAAA	120
TAAACCAAAA	AAACCCTGAT	GAGGTTACTA	CTAATAGTAA	CTGTAGGAGG	CATCTACCTC	180
CCTAGATTGG	GGAAAGAAGT	AGTGGTTGAA	TTATCAGAAC	CTAGAAGCAC	AGAACAGGGG	240
CCCCTCAGAA	TGTGTTCTCA	GACTCCTGAG	GGAAGGATGC	TACCCAGCTA	CAGCTGGTTC	300
CTCGAG						306

- (2) INFORMATION FOR SEQ ID NO:1002:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

GAATTCGGCC	TTCATGGCCT	ACACCCTGCT	AATTTTTGTA	TTTTTTTTTG	TAAAGGCTGG	60
GTCTCACTAT	GTTGCCCAGG	CAGGGTCTCG	CTATGTTGCC	CAAGTGGGTC	TCGAACTCCT	120
GGGTTCAAGC	AATCCTGCCT	CGGCCTCCCA	AAGGGCTGGG	ATTACATGCA	TGAGCCATCA	180
CATCTGGCCC	CCACCCATCT	TAAAAGTCAG	AAATAAAAGC	CAGAGCCCCT	CCTTGACCTC	240
CTGGCCCCCT	CCGCTTTATC	ACCCCACCTC	TCTGCCTGTC	TTTATTGCAA	AACCCCCAGA	300
AGGTTATCAG	GCTCATGGTC	TTCCCTCCTG	TCCACACTGC	CCCAACTACA	CAATGAGATG	360
CCCCCATTCC	AACTCCCCAG	CCTCCTCTGC	TGGCGTCTCC	TCCTTCCTAA	TCTCTGAACA	420
TTGTCCCATC	CAAGGGCTCA	GTCCCAGGTC	CGTTCACCCC	TTGTCCACAC	TCACCCTGAG	480
AGCTTCCAGT	CTGTGGCCTC	CATGCCCTGG	AATGAGCCCC	TGTAAGATCC	ACAATCTCGA	540
G						541

- (2) INFORMATION FOR SEQ ID NO:1003:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 602 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

GAAACGCCTC	CTGATTTTGT	CTTACAATGG	AACTTAAAAA	GTCGCCTGAC	GGTGGATGGG	60
GCTGGGTGAT	TGTGTTTGTC	TCCTTCCTTA	CTCAGTTTTT	GTGTTACGGA	TCCCCACTAG	120
CTGTTGGAGT	CCTGTACATA	GAATGGCTGG	ATGCCTTTGG	TGAAGGAAAA	GGAAAAACAG	180
CCTGGGTTGG	ATCCCTGGCA	AGTGGAGTTG	GCTTGCTTGC	AAGTCCTGTC	TGCAGTCTCT	240
GTGTCTCATC	TTTTGGAGCA	AGACCTGTCA	CAATCTTCAG	TGGCTTCATG	GTGGCTGGAG	300

GCCTGATGTT	GAGCAGTTTT	GCTCCCAATA	TCTACTTTCT	GTTTTTTTCC	TATGGCATTG	360			
TTGTAGGTCT	TGGATGTGGT	TTATTATACA	CTGCAACAGT	GACCATTACG	TGCCAGTATT	420			
TTGACGATCG	CCGAGGCCTA	GCGCTTGGCC	TGATTTCAAC	AGGTTCAAGC	GTTGGCCTTT	480			
TCATATATGC	TGCTCTGCAG	AGGATGCTGG	TTGAGTTCTA	TGGACTGGAT	GGATGCTTGC	540			
TGATTGTGGG	TGCTTTAGCT	TTAAATATAT	TAGCCTGTGG	CAGTCTGATG	CGACCCCTCG	600			
AG						602			
(2) INFORMATION FOR SEQ ID NO:1004:									

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

GCGGCAATGA	TACCCACTGC	CAACCAACAA	AAATTGGCTG	CAACCATCCC	CTACCAGGAC	60
CGAGCCCCTA	CAGGTGAGCG	GCTCTGCCAG	GCCCTGGCTC	CTGCCCGCAT	GCACCCAAGC	120
CGGAGCCTGG	GGCAGCTCCT	ACGAGGCTCA	CCAGGGCCCC	AGCAGGATGC	CTGGGTCCCC	180
TGCTCCTGCT	TGGCCAAAGG	GAAGAGGAAG	CAGCAGGCAG	GGGCTGGGGA	GGCCTTCATG	240
AATTACATGA	ATTATCCTTC	TTTTTTTTT	TTTCCCCTTT	TTTTTTTTT	TTTTTTTTT	300
TTTTTTTTT	TTTTTTTTT	TGAGANNCCA	NTTNAAAAAA	AAAAGGGGGG	GGTGTCAGGG	360
TTTCATTCAG	AGCTCGAG					378

- (2) INFORMATION FOR SEQ ID NO:1005:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

GAATTCGGCC	TTCATGGCCT	ACTGTTTTAT	TTCCCGCTTT	TATTTTGCTT	TTGAAATCTT	60
TTTCCTTGGT	GGATTTGTAC	GTGTCTTCAC	TAGATGCCTC	AAATTAAGTC	TGACCACAAT	120
CCTACTCTAC	TTTCTACAGT	GGAGAGACCA	TCCTCCCTGC	CCCAGGGCTG	TCTCCACCCA	180
CCCCCCTTC	CCCACCCGCA	CCCTCGAG	•			208

- (2) INFORMATION FOR SEQ ID NO:1006:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

CTGATCTGTG	AACCTTACAC	GAGCAAGGAA	TTATTCCGGG	TTTTGGATAC	ACCCTACTTA	60
CTAAATGAAG	ACTGGGAATA	CTATCTCTCT	GGGAAGCTAT	TTAATAAATC	AAAAATGAAG	120
CTCACTTTTG	AACAAGTTTA	CAGTGACTGC	AAAAAAATA	GAGGCACTTA	CGGCACTCTT	180

CACCTGCAGA	ACAGCTTCAA	TATCAGTGAA	CATCTCAACA	TTAATGAGCA	TACTGGAAGC	240
ATAAGCAGTG	AATTGGAAAG	TCTGAAGGTA	AATCTTAATA	TCTTTCTGTT	GGGTGCAGCA	300
GGAAGAAAAA	ACCTTCAGGA	TTTTGCTGCT	TGTGGAATAG	ACAGAATGAA	TTATGACAGC	360
TACTTGGCTC	AGACTGGTAA	ATCCCCCGCT	CTCGAG			396

- (2) INFORMATION FOR SEQ ID NO:1007:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

GAATTCGGCC	TTCATGGCCT	AGATGGGGGC	TAGTTTTTGT	CATGTGAGAA	GAAGCAGGCC	60
GGATGTCAGA	GGGGTGCCTT	GGGTAACCTC	TGGGACTCAG	AAGTGAAAGG	GGGCTATTCC	120
TAGTTTTATT	GCTATAGCCA	TTATGATTAT	TAATGATGAG	TATTGATTGG	TAGTATTGGT	180
TATGGTTCAT	TGTCCGGAGA	GTATATTGTT	GAAGAGGATA	GCTATTAGAA	GGATTATGGA	240
TGCGGTTGCT	TGCGTGAGGA	AATACTTGAT	GGCAGCTTCT	GTAGCTCGAG		290

- (2) INFORMATION FOR SEQ ID NO:1008:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

GTGGTTCTGA AATCACCCTT	CCTTTTCACT	CCTCTGCCCT	GACTTCCTCT	CTCACCATGC	60
TCTCCTGCTC TCCACCTTC	CCCTCTTCAG	TGGGATTTCT	GCATTTCAGC	CAGAGGGACC	120
TGTCTGCAGC TACCAGATGO	TCCCCACCCT	GGGAGAGCTC	AGCGGCATGT	CTGCACATGG	180
GCCTTTTCAG CCTTCTTCAT	CCCGCAATTG	GAACTGACTT	TCCCACTCCC	ATCTCACACT	240
TGAGAATCTC TGTTTCTTGT	TTCTTGTTTT	TTATTTTATT	TTTATTTTT	CTCCCCCCTG	300
GCGGACTCGA G					311

- (2) INFORMATION FOR SEQ ID NO:1009:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

GGANCAGAGT	CCAANAGATN	AATTATATTC	AGAAAACTCT	GTTCAAGATA	GGGTATGATT	60
ACAAATTGGA	ACAGATCAAA	AAGGGATATG	ATGCACCTCT	TTGCAATCTG	TTACTGTTTA	120
AAAAGGTCAA	GGCCCTGCTG	GGAGGGAATG	TCCGCATGAT	GCTGTCTGGA	GGGCCCCGC	180
TATCTCCTCA	GACACACCGA	TTCATGAATG	TCTGCTTCTG	CTGCCCAATT	GGCCAGGGTT	240
ATGGACTGAC	AGAATCATGT	GGTGCTGGGA	CAGTTACTGA	AGTAACTGAC	TATACTACTG	300

GCAGAGTTGG AGCACCTCTT ATTTGCTGTG AAATTAAGCT AAAAGACTGG CAAGAAGGCG GTTNTACAAT TAATGACAAG CCAAACTCGA G	360 391
(2) INFORMATION FOR SEQ ID NO:1010:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 415 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:	
GGGGAAGAAA GGCGTAAGGA TGGTGAAGCT GAACAGTAAC CCCAGCGAGA AGGGAACCAA GCCGCCTTCA GTTGAGGATG GCTTCCAGAC CGTCCCTCTC ATCACTCCCT TGGAGGTTAA TCACTTACAG CTGCCTGCTC CAGAAAAGGT GATTGTGAAG ACAAGAACGG AATATCAGCC GGAACAGAAG AACAAAGGGA AGTTCCGGGT GCCGAAAATC GCTGAATTTA CGGTCACCAT CCTTGTCAGC CTGGCCCTAG CTTTCCTTGC GTGCATCGTG TTCCTGGTGG TTTACAAAGC CTTCACCTAT GATCACAGCT GCCCAGAGGG ATTCGTCTAT AAGCACAAAC GCTGTATCCC AGCCTCCCTG GATGCTTACT ACTCCTCCCA GGACCCCAAT CCCAGAAGCC TCGAG	60 120 180 240 300 360 415
(2) INFORMATION FOR SEQ ID NO:1011:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 407 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:	
GCCAGACTAC CACAAGCCCC ACCCACACTA TGCCAAGCCC TACCCATACC ACAGCAAGCC CCACTCATAC TTCCACAAGC CCCACCCATA CCCCCACAAG TCCCACCCAC AAAACCAGTA TGTCACCTCC CACCACTACA AGTCCTACCC CCAGTGGTAT GGGCCTAGTC CAGACTGCCA CAAGTCCCAC CCATCCTACC ACAAGCCCCA CCCATCCCAC CACAAGCCCC ATCCTTATAA ATGTAAGCCC TTCCACTTCT CTAGAACTTG CTACCCTCTC CAGCCCCTCC AAACACTCAG ACCCCACCCAC CCCAGGCACT CCCAGGCACT CCCCAGGCACT CCCCAGGCACT TCTCGAG	60 120 180 240 300 360 407
(2) INFCRMATION FOR SEQ ID NO:1012:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 291 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:	
GAATTCGGCC TTCATGGCCT ACGCCGCCGC CACAATGGGC CGCGGAGTTT GGGAATCTGA CGCGGATGCG GCATGTGATC AGCTACAGCT TGTCACCGTT CGAGCAGCGC GCCTATCCGC ACGTCTTCAC TAAAGGAATC CCCAATGTTC TGCGCCGCAT TCGGGAGTCT TTCTTTCGCG TGGTGCCGCA GTTTGTAGTG TTTTATCTTA TCTACACATG GGGGACTGAA GAGTTCGAGA	60 120 180 240

GATCCAAGAG GAAGAATCCC GCTGACCATT GAATTCTAGA CCTGCCTCGA G	291
(2) INFORMATION FOR SEQ ID NO:1013:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 351 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:	
GAATTCGGCT TCATGGCCTA TGGATTACCT GAGGAAGAAG AGATCAAGGA AAAAAAAACCC ACCAGTCAAG GAAAGTCAAG TAGCAAGAAG GAAATGTCTA AAAGAGATGG CAAGGAGAAA AAAGACAGAG GAGTGACGAG GTTTCAGGAA AATGCCAGTG AAGGGAAGGC CCCTGCAGAA GACGTCTTTA AGAAGCCCCT GCCTCCTACT GTGAAGAAGG AAGAGAGTCC CCCTCCACCT AAAGTGGTAA ACCCACTGAT CGGCCTCTCC GGTGAATATG GAGGAGACAG TGACTATGAG GAGGAAGAAG AGGAGAACA GACCCCTCCC CCACAGCCCC GGCAGCTCGA G	60 120 180 240 300 351
(2) INFORMATION FOR SEQ ID NO:1014:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 596 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:	
GCTCGAGTCG GATCCTCCT GAATGTGGAG CGATGGGGGG TTGCACACAG GCCGTTCTGC CCCAGCAGCT AACAAGAAAG ACCCTTGCAT TCCTCCCTGC ATCTCTCCT TTTGGGTCCT ACTAATGTCT GTTGAATTC TCTTTTTTCC AAAGCAAAAT CCTTCTCTGC ATTTTGTCTG CTTGTCTGTT TCCCAGAGCC GCAGGACTCT CTCCTTGTCT GGAGTTCCAG AGAGCCCCCA CTTTCTCTTT CTAAGCTGTG TTGTGTGTTT CCTGGTACAT TCTAGGTTCC CCAAAGATAA ACATGACTAA GGATTGGAAA GGAGGAAAGG CCGCGCAGAT TGTTAATCTG AAAGTCAATC CCCGGATTTA GCTCTCAAAA ATGCTTTATT TTTGGAGAAA AGCAATAGAG TAAGACAGAA GGACTTAACG CTTGCAGGGA AGTGGCTTC TGCCATGTAG AGCCAGGCTG GCAACCTGCC CTCTGCCATC AGGGAGTGAG CATGAACCTG GAAACCTCTA GGACGCAAGA GCGAGGCTGG CTGTCCCCTC GTGTGCAGTG CTTAGACCTT CTTGCCACAC ATCCCATCC CTCGAG	60 120 180 240 300 360 420 480 540
(2) INFORMATION FOR SEQ ID NO:1015:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 353 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:	
GAATTCGGCC TTCATGGCCT ACTTGGTTTT GCTGACCAAC AAATATGCAT AGTGTCTATT CACAGTTATA CAGTAATAGG TTAGAACAGA AATAAATGCC AGCTTCTTAT GATGCCTTTG CCAACAATCA GGCCATGTGT TTCAGGACCC TTCCTTCCTC TGACTTGTGT AGCATTACAC	60 120 180

TTGCTGGGAG TGATGGGAGC CACAGATACG TGCATGGAAG TTACTGCCTC GAG

(2) INFORMATION FOR SEQ ID NO:1016:

CTCAGCACAC GACTTCTTGA AAGAGTGAAC CTCCAGGGCT TGCTCTCTCA GATGCACCTG

GGCAGCAGCA GGAACTGTCT GACAGTCTCT CCTGTCTCCA TAAAGTAGCG GGCTGGCTCT

240

300

353

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 300 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:	
GAATTCGGCC TTCATGGCCT AATTATTAAG TAAAATAAGG GTTCCTTGAA TATAGGCACT GCAAATACCA TGACAGTGAT CTGATCACTG AGCTAACTAC TGAGTGACTC AGAGGCAGGT GATGTATACT GTGTGGAGTG GAATGGTGAG AGATTTCATC ACACTACTCA GAATTGCATG AAACTTAAAG CTTATAAATT GTTTAATTCT GGAATTTTTC ACTTAATATT TTCTGACTGA GATTGCCCAC GGGTAACTGA AACTGTGGAA AGCGAAACTG CAGATAATGG CGGACTCGAG (2) INFORMATION FOR SEQ ID NO:1017:	60 120 180 240 300
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 491 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:	
GCGATTGAAT TCTAGACCTG CTCGATCTCA TGGGGCAGAT GAAATTCTCT TCCTTAGAGG AAAGGGAAAG GTGAGGCCCC AGAGGACTTA TCTCAGCTGT ACATGCTCTG CCTGTGGAGA CATGGCTTTT CTTTGTGCTG TGGCAGACTG GGGCTTTGGA AGTGGTGTAT GTTTAACTTA CCTGAGAGTG AGAGATGTGT AGGAAGAATA GCTGGAAGAA AGTGAAAGAT GAGTGCCAGT ACTTTTGGCC TGTTATCCAG TAGAGAGAAA GTGACAGTGA AAGTAACGTG AGAGAGAAAG AGTGTGTGTG TATATGTGAG AGAGAGAAAG AAAGAGAAAG GAATGCTTGA TTGCTTGTTG TCACTGGGC CAGCTCTGAA ATCCAAAATC ATGCCTTGAT AACATTACAA AACCGTGATC CTGGGTTTGA GTGAATCCTA GAGACATTGT TCTTATGGCC GCCTGGTTTC CGCAGCATGA TCACCCCTCGA	60 120 180 240 300 360 420 480 491
(2) INFORMATION FOR SEQ ID NO:1018:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 323 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:	
GCTTTTCCAT GAAAGGTGGA TCGAGATCTA CTGCCAGTGG GTCAACAGGT TCTAAATTGA AATCAGATGA GTTACAGACC ATCAAGAAAG AATTAACCCA GATCAAAACT AAAATTGACT CCTTGCTAGG GCGCCTGGAG AAGATTGAGA AACAGCAGAA GGCGGAGGCA GAAGCTCAGA	60 120 180
418	

AGAAGCAATT GGAAGAGAGT CTAGTGCTGA TCCAAGAGGA ATGTGTGTCA GAGATTGCAG ATCACTCTAC AGAGGAGCCT GCTGAAGGAG GGCCAGATGC CGATGGAGAA GAGATGACAG ATGGGATAGA GGTTGGACTC GAG	240 300 323
(2) INFORMATION FOR SEQ ID NO:1019:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 319 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:	
GGTCACAATC TCCTTGCAGT CCAGGACTGG GCATACTCAT ATGCCTTCTG TGGTTGGCGT CCTTGTATTT ACCCCAGTTTT GGTTCTGGTT TCCTCTTTCA CACTTCCTGT CATTGGCTTA TACCCCCTACC TGTGTCATTG GCCTTAACAA GGACTTAAAG ATGCCGAAAG TTCAGTATAA ATCGAACTGT AAACCATCCA CATTTGCATA TCCTGCCCCT CTGGAAGTAC CAAAAGAAAA AGAAAAGGAAAA AAAGAAAAG AAAAGAAAAG GAACTCGAG CTGCTGTATT ATCTATAACT GCCAAGGCTA AAAAGAAGAAAA AAAAGAAAAG	60 120 180 240 300 319
(2) INFORMATION FOR SEQ ID NO:1020:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 450 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:	
GCGGGCATGG TGTGTAGCCT ATGGGTGCTG CTCCTGGTGT CTTCAGTTCT GGCTCTGGAA GAGGTATTGC TGGACACCAC CGGAGAGACA TCTGAGATTG GCTGGCTCAC CTACCCACCA GGGGGGTGGG ACGAGGTGAG TGTTCTGGAC GACCAGCGAC GCCTGACTCG GACCTTTGAG GCATGTCATG TGGCAGGGGC CCCTCCAGGC ACCAGTGAC ACCAGTTCTT GCAGACACAC TTTGTGGAGC GGCGCGGGC CCAGAGGGCG CACATTCGAC TCCACTTCTC TGTGCGGGCA TGCTCCAGCC TGGGTGTAG CGGCGGCACC TGCCGGGAGA CCTTCACCCT TTACTACCGT CAGGCTGAGG AGCCCGACAG CCCTGACAGC GTTTCCTCCT GGCACCTCAA ACGCTGGACC AAGGTGGACA CAATTGCAGC AAGACTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:1021:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 266 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:	
GAATTCGGCC TTCATGGCCT ACTAGACCTG CTTTTTGGAA GAGAATGCTT TTCACCTGTT	60

120 180

CTTTTTTTAA TCCACCTGGC ACTTTCCTCA GGACCCAAAC TTGTTCACTC TGCTGCTTCT TGATGTATCA ATTTTGGGAC ATCACCTGTT GTCTCCTTGC TGTGAATGAT GAGGATTTGG

CCCATATTAC CCCCGTTCCT TCCCCGGTCA TTCTCTCGGT TGCCTTTGTC ACTTTAAATC 240

ATTTACATAA ACCACAACTT CTCGAG	266
(2) INFORMATION FOR SEQ ID NO:1022:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 352 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:	
GAATTCGGCC TTCATGCCTA AGAAACTTAT TCGTCTTCAG CATGAGAATA AGATGTTAAA GCTTAACCAA GAAGGTTCGG ACAATGAAAA AATAGCCTTA TTGCAGAGCC TTCTAGATGA TGCAAATCTA CGCAAGAATG AACTGGAGAC AGAGAATAGG CTGGTGAATC AAAGACTTCT GGAAGTACAG TCACAAGTTG AAGAATTACA AAAATCTTTA CAGGATCAAG GCTCAAAAGC AGAAGATGCT ATTTCAGTCC TTCTAAAAAA GAAGCTTGAA GAACATCTAG AGAAGCTGCA TGAGGCCCAAT AATGAACTAC AGAAGAAGAG AGCCATTATT GAAGATCTCG AG	60 120 180 240 300 352
(2) INFORMATION FOR SEQ ID NO:1023:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 249 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:	
GAATTCGGCC TTCATGGCCT ACAAAAGCCA CCAGGTGAAT AAATGCCATT TTCTTTTTGC CTAGACATTG TTCATTTACT GAAAATGAAC AAGGTAATGC TCAGCATACA AAAAAAAATT AAAGTTCTCA AGATCCCATG CTTTCTGGAT TCCTCTGTAT TTATCACTCA AGTCATCCCC CTTTTTGTAA TCTCGCTTTT TGTCCTCGCT TTATTTAAAT CCTTTATATC ACTACCCCCA TCTCTCGAG	60 120 180 240 249
(2) INFORMATION FOR SEQ ID NO:1024:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:	
GAATTCGGCC TTCATGGCCT ACAGGAAATA GGCAAAAATA CCCAGGAAAA GGAAACAGTT TTATGCATTA GTGCTGTACC TTCTTCATAT TGTCAAAAAT AAAAGATAGT AGAGATTTAT TGAAAACATT TTAAATAAAG AAGTTGTGTT CATAATATAA AGCTGCCTTA AACTATATAT GAAAAAAACT GTAAATCATA GAAAATAACT TTATCAAAGA TGTTAAATAA TACATTTTAC AGAATAATTT CCCATGGGCT TCTCGAG	60 120 180 240 267
(2) INFORMATION FOR SEQ ID NO:1025:	

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 232 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:	
GAATTCGGCC TTCATGGCCT AGCCATCTTA TTTGAACTAT ATTTTCCTT CAAAGAAGCA ATAGGTCTCA ACATAGTGTA GGTAGCATCA GGTGACAGAA AGCCAATTTT ATTTTCAAAT TTAAGTTAAT TATCTTCGTG ATCCTATTTA TCCACAATTT CTTTCAGAAA AGACTGAAAA AACACATTAT ATTCAGGAGA TATAATGAAA TTATTGGAAG GCATCACTCG AG	60 120 180 232
(2) INFORMATION FOR SEQ ID NO:1026:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 153 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:	
GAATTCGGCC TTCATGGCCT AGATTGAATT AGACCTGCCT CGAGCCCCTA AAAATATCCT AAATGCATTT CCTCCTCTGC ATTCTAACTA CTGCTGCCCT TGTTCTAGGA CTCCACTCTC CCACATCAAC CAACTTTTCT CCTTGGCCCC CTC	60 120 153
(2) INFORMATION FOR SEQ ID NO:1027:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 294 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:	
GCGAGGGCCA GGGAGGGAGG AAGCAATAAA TAGGGGGAGA AAATGGCAAT AAGACGTTAT ATAGCCCTTC TAACAAAAAT ACCAGAAGGG AGGGGTGAGG GACAAGGCTG TCTGAGGGAG GGCAGGAGGT GAGGCCATGG CTTGGTCTCT TTTGCGCTTG GATGGCCGTC AGCTCAGCAT GAGGCATCTG AAAGAACTAC CCAGATTGCA GAAGAGAGAG GTCCCAGCCT CCTTGGAAGG ACATGATGGG GGAGGAGTGG AGACAACAGC TGAGTGTTAC CTGTAAAACT CGAG	60 120 180 240 294
(2) INFORMATION FOR SEQ ID NO:1028:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 285 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
,/	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

GAATTCGGCC TTCATGGCCT ACACACATAC CCAACACACA CACAGACACA CACATACACA	60
GAATCAACAC TCAACACGCA AACACCCAAC ACACACATGC ACACACACTT TCTGAAGATG	120
AGTTTTCTCA TTTATGAAAT GAGCTCATCT GGACTTGCCA TGAGGGTCCA ACAGGTGCCA	180
TGCAATCAGG TGTGCACTCA GTATGGGCTG GGTGGAGATG GCCATCTCCT TTCCCGTCCA	
GGCCTGGTTC CTGTGTGCTG GGCCTCTGCT CTTCCCCCCC TCGAG	285
decrease crandidata decrease critected responsibility	205
(2) INFORMATION FOR SEQ ID NO:1029:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 263 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) TOPOLOGI: Tinear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:	
GACAAGCTGA GAAAATGAAA GGAAAACTAG AAGAATTGTC TAATCAGTTA CATCGCAGTC	60
AAGAGGAGGA AGGAACACAA AGAAAGGCCT TGGAAGCCCA AAATGAAATA CATACCAAAG	120
AGAAGGAGAA GCTGATTGAT AAGATTCAAG AAATGCAGGA GGCCAGTGAC CACTTGAAGA	180
AACAATTTGA AACTGAAAGT GAAGTCAAGT GTAACTTCCG GCAGGAAGCA TCCCGGCTCA	240
CTTTGGAAAA CAGGGAACTC GAG	263
	203
(2) INFORMATION FOR SEQ ID NO:1030:	
(1) 0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 243 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:	
GAATTCGGCC TTCATGGCCT ACCTCCTACA AATTTAATTT	60

(2) INFORMATION FOR SEQ ID NO:1031:

GAG

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 base pairs

ACTTGTAAAT TCTTCATGTA TGAGGAGTTG TGTTTATTAA TGCTACTTTT TAAATTTTCC

TGTGCCATGT GGCAGATGTT TATTCTCTTA ATGCACTTCA GGTTTGCTAT CTGTAAAGCC

TTTGACCCAG GCCTACTGAG TCAAATCTAC ATTCAGTGTA ACATTAAAGG CAGAAACCTC

120

180 240

243

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

AATTCGGCCT TCATGGCCTA ATTGAATTCT AGACCTGCCT CGAGATTACA GCCAGAGTCT 60
CCTAACTGCT CTCCATCTAT TCTCTAATCC CAATAGCTAC TCTCCATGCA GCTGTCAGAG 120

TGGGCCTTAT AAAACAT GGGTAAGAGC CGAAGCC CTCGAG					180 240 246
(2) INFORMATION FO	R SEQ ID NO:103	32:			
(A) I (B) 5 (C) 5	E CHARACTERISTI LENGTH: 114 bas TYPE: nucleic a STRANDEDNESS: d TOPOLOGY: linea	e pairs cid ouble			
(ii) MOLECU	LE TYPE: cDNA				
(xi) SEQUEN	CE DESCRIPTION:	SEQ ID NO:	1032:		
GAATTTACAC CTGCCTC					60 114
(2) INFORMATION FO	OR SEQ ID NO:10	33:			
(A) 1 (B) f (C) :	E CHARACTERISTI LENGTH: 302 bas IYPE: nucleic a STRANDEDNESS: d IOPOLOGY: linea	e pairs cid louble			
(ii) MOLECU	LE TYPE: cDNA				
(xi) SEQUEN	CE DESCRIPTION:	SEQ ID NO	:1033:		
GAATTGTTGT TCTTTTG GGATTATAAC CATTTGG GTGGAGAAGT TGCATAT TTGTAATAGC CCCTGTA AACTGTTTGG TGTGTTT AG	GATA TTTGGTTCAC TGGC CAAGTCCTTG ACTT TTGGTGGTTG	TAACAATTTT GAGTTATAGG GATCATTTGA	CTTACTGGCC ATATTCATTA AGTGGTGTCT	AGAGTTCTTG CTTCCTCTCA ACACTTATAA	60 120 180 240 300 302
(2) INFORMATION FO	OR SEQ ID NO:10	34:			
(A) (B) (C)	E CHARACTERIST LENGTH: 262 bas TYPE: nucleic a STRANDEDNESS: c TOPOLOGY: linea	se pairs acid double			
(ii) MOLECT	JLE TYPE: cDNA				
(xi) SEQUE	NCE DESCRIPTION	: SEQ ID NO	:1034:		
GAATTCGGTC TTCATG TATCTATGTG TTGTCT TTTGAGATGG TTCAAA TGTTTGCTTT CATACT TCTCAGGTGT AACATA	CTGA GGAAATGTCC CAAT TTTTTCCTTT TTCA AATGCTGTCT CCTC GG	TTTAATGTCI TCCCTTCACI TTTTATTTTI	TCCTCAGGCT GGAAGCTTTG	TGATACCTAA TTACTCATTC	60 120 180 240 262
(2) INFORMATION F	OR SEQ ID NO:10	J35:			

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 388 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:	
GAATTCGGCC TTCATGGCCT ACCTACTAGG CATGTTTAT GACACAGATG ATGCGAGTTT CAAGTGGTTT GATAATTCAA ATATGACATT TGATAAGTGG ACAGACCAAG ATGATGATGA GGATTTAGTT GACACCTGTG CTTTTCTGCA CATCAAGACA GGTGAATGGA AAAAAGGAAA TTGTGAAGTT TCTTCTGTGG AAGGAACACT ATGCAAAACA GCTATCCCAT ACAAAAGGAA ATATTTATCA GATAACCACA TTTTAATATC AGCATTGGTG ATTGCTAGCA CGGTAATTTT GACAGTTTTT GGAGCAATCA TTTGGTTCCT GTACAAAAAA CATTCTGATT CTCGTTTCAC CACAGTTTTT TCAACCGCAA CCCTCGAG	60 120 180 240 300 360 388
(2) INFORMATION FOR SEQ ID NO:1036:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 258 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:	
GAATTCGGCC TTCATGGCCT ACTTTTAGT AAAGAGCAAA CTCATAAATT TTGGCATCAG AGTTTGAGCT TTATTTTCT TAAATGAGTT TGAAATCAAT TTAATATTTC TCTCCAATTC CCTAATGTCT CAGAAGTGAA TTTACAGTAT ACCTTTGTTT TTTCGTATTC TTAAGTAGTA TTTGGATTTT ATTTAGTAGT TGCAGTACTA AATAAGGAGT GGGGAGTTAA TTACAAAACG AATCAGGTGA CTCTCGAG	60 120 180 240 258
(2) INFORMATION FOR SEQ ID NO:1037:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 85 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:	
GCGATTGAAT TCTAGACCTG CCTCGAGTGA TTTGGCCTGC ATGGTTTTCC TCCTACCCCT TTTTCTTTGC CTGGGTCAGC TCGAG	60 85
(2) INFORMATION FOR SEQ ID NO:1038:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 248 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
424	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

GCGATT	GAAT	TCTAGACCTG	CCTCGAGGGG	TTTGGAGCTC	TGTTGGGTGG	TGACCTCAGT	60
CCTGTT	TACC	CCTGCAGAAG	AAGGACCCAG	CCCAGTTCCT	GCAGGTACAT	GGCCGAGCTT	120
GCAAGG	TGCA	CCTGGATTCT	GCAGTCGCCC	TGGCCGCTGA	GAGCCCTGTT	AATATGATGC	180
CCTGGC	AGGG	GGACACCAAC	AACATGATTG	ACCGATTCGA	TGTCCGTGCT	TAGGCCATGA	240
AGGTCG	AG						248

- (2) INFORMATION FOR SEQ ID NO:1039:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

GAATTCGGCC	TTCATGGCCT	AGTCACTTAA	ATAGATTTGG	TGTGAAATTT	TATGATAAAA	60
GGTGACTTTT	GTTCTAGTAA	GTATTCTCAA	AGAAAAGAGA	GTGAGTAGCT	ATTTTGGGAT	120
GAAGATAGTT	ATAACTGAGA	TAGCGGTTTT	TGTTTTTGTT	TTTTGTTTTT	GGCCCAGGCG	180
GAGTGCTGTG	GTGCGGTCAT	GGCTCACTGT	AACCTCAGCC	TGGGGTCAAG	GTCTGCCCAT	240
CTCAACCCTC	GAG					253

- (2) INFORMATION FOR SEQ ID NO:1040:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

GAATTCGGCC	TTCATGGCCT	AGTTCAAAAA	TAAAGCAAAT	ATTTATTTTG	GTATTGTTTT	60
GAGCACAGCT	GATTTTTAAC	ATTTTCTTTC	ATAACACTCA	GAAATCATTA	ACAATTGTTT	120
GCTCATTTGG	TATGGGTTTT	TTGTTCTCTT	TTTTTTTTTG	GGTTCTTTTA	GGTGCTTTCT	180
TTTAACATTG	GTCATGTTTC	ACCCTTTTTT	TTTTCATCCC	CCCAGTCTCG	AG	232

- (2) INFORMATION FOR SEQ ID NO:1041:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

GAATTCGGCC	TTCATGGCCT	ACAAGGACGT	TAAAGGCATT	TTATTCCAGC	GTCTTCTAGA	60
GAGCTTAGTG	TATACAGATG	AGGGTGTCCG	CTGCTGCTTT	CCTTCGGAAT	CCAGTGCTTC	120
CACAGAGATT	AGCCTGTAGC	TTATATTTGA	CATTCTTCAC	TGTCTGTTGT	TTACCTACCG	180

TAGCTTTTTA CCGTTCACTT CCCCTTCCAA CTATGTCCAG ATGTGCAGGC TCCTCCTCTC

240

TGGACTTTCT CCAAAGGCAC TGGACCCTCG AG	272
(2) INFORMATION FOR SEQ ID NO:1042:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 286 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:	
GAATTCGGCC TTCAGGGCCT AGATTAAATC TCAAGGTGGA CTAGGAGAGA ACAAGCAGAC TTCTATAGAA CAGTGTCTTC CTTTGGTGTT GTTTACGATC AAGAAAAGAA	60 120 180 240 286
(2) INFORMATION FOR SEQ ID NO:1043:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 230 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:	
GAATTCGGCC TTCATGGCCT AGTGTAATCT TATTGGGAAC CTAAAACTGC TCTTAAAGTC TTTTTGAAAA CTCAGACATA TTTTTGGCAT TACCTTTTT TTATTGGAAA GGAAAAATGA AAACCTTTCA TTTTATTAAT AATTCTATAI TCCACTCCTG TATTTTCTTC TCTTGGATGA TGATGGTGAT ATTATTCTC ACTTTTCAAA ATAATACCCT GGGACTCGAG	60 120 180 230
(2) INFORMATION FOR SEQ ID NO:1044: .	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 238 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:	
GATTCGGCCT TCATGGCCTA GGGAAAATAA AAATGTATTC AGTAGCACGT GGGTTATGGT TTCTCATAGA CCAGGGGATA AGATTAAAAG TCACTGAAGA GTGGGAAAAT GCATGTTGAG AAGATGAGAA TGGCCTGTAT TTTCTCCAGG GGAATCTGTG TAATGTGCCT TTTCCCTCTC CAAATGCCTA GAACCATGGC ACTGTGTCTT ATTTATTTAA CCGTTGGGCC GTCTCGAG	60 120 180 238
(2) INFORMATION FOR SEQ ID NO:1045:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs	

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:	
TAATTCATCT AAGTTGTTGA ATTAGCATAA AGTTTTTAAT AAAATTTTAT GTAATTCCTT TTTAGAGAAC TAACTTTTGA AATTGCTGAT TTTCTGTTTT CCGTTTCAAC ATTTTACACA CTGGTAGTTA ATAGTTTTTT CTCTCCAGCT TACTTCGTGT TTGATTTACT TTTCCTTTTC TGTCTTCTTG AGGTGGAAGC TTAGAGGATT AATGATTCCA TTTCTTTCTA ACGAAATCAC TTAAAACTAT AAATTTCACT CCAACTACTT CTTTAGCTAA ATTCCATAAA TTTTACTATG TTGTGTTTCC CTTTTTCACT CCGTCTCCTC GAG	60 120 180 240 300 333
(2) INFORMATION FOR SEQ ID NO:1046:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 429 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:	
GAATTCTAGA CCTGCCATTG TGGGGAGTGG AAGTGGCATG ACCTCAGGAG CCAGTTCTGA GTCCAGGTGA ACCAAAGCTC AGTTTCTTC ATCTTTGAAC CTGAACCTCT TACCTCCAAG AAAAAGGGCC CAGGAATTTG GGCCTTCTTG TTTATTTGTC CTTCTGCCCC TCTCCCTATC TAACCCCTGG GTAAGGGTGA GCTTGAAGGT GATGGTGACA GTGGCTTCTG TGTGTGTCAG TCCACCCTCC AAGCAATGCT TAGAAACCAG TCCATAAGCC AATTAACACA TCATTTTTAG GGCAGATTTG CAAGTTCTCA GTTGTTTACA TGTTTCGTTA AGTACTAACC TCCAAATTAA TAAAGCATGA CACATGACAT CACACATTTC ACAATTTGTA CCCAAGCAAA GTTCATGGAG GTACTCGAG	60 120 180 240 300 360 420 429
(2) INFORMATION FOR SEQ ID NO:1047:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:	
GCTTGGTAGA CCACATCCAA GGGACGATGA GGTTTCCCAG AGGAGGAGTG GTCACCATGA	60

(2) INFORMATION FOR SEQ ID NO:1048:

TCGAG

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 base pairs (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

65

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

GAATTCGGCC	AAAGAGGCCT	AAATTTGGTT	TAATGTGTCA	TCAAACTTTG	TATTCAGCTA	60
TCTAGAGCCA	TTTTCTGGAT	TCATGCAATA	CATTTTCCCC	AAACCCTTTT	TATTTTGAAA	120
AAGCTCAAAC	ACAGAAAAGT	TGAAAGAATA	GCGTAAAGAA	CATCTGGATG	TGGTGCAGGG	180
TCTCATGTTC	ATAATCCCAG	CACTTCGGAA	GGATTATTTC	AGACCAACCT	GGGCAACATA	240
GTAAGACCCA	ATGTCTACAA	AAATGTTTAC	GGATAAACCA	GGCGTGGTGG	TGAGGTAGTC	300
CCAGCTACTC	AGGAGGCTGA	GGTGGGAGGA	TTGCTTGAGC	CCAGGAGTTC	AAGGCTGTAG	360
TGAGCAATAA	TCACATCACT	GCATTCCAGC	CTTGAGTAAC	AGTGAGACCT	GTCTCAAAAA	420
ааааааааа	AACACCAAAA	ACAACCAACT	GTGTATATCT	TGCACTGATA	ATCCCCCGAA	480
TTCTAGACCT	GCCTCGAG					498

- (2) INFORMATION FOR SEQ ID NO:1049:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

GAATTCGGCC	AAAGAGGCCT	AAGCTGAGAT	GGGTGTTAAA	AGTTAAGACA	CAGCTTAAGA	60
CAGAAGCATT	GTAAAACAGG	AACAAATACT	GGCTTAAACC	TGATGTCTCT	AACTATATTC	120
CTCTATTTTA	AGAATGTTTT	AGTATCTGAT	AGTTTCATCA	GCCTTTCCAT	TTTCCAATAT	180
GTGACCTTTA	TTCCCACCAT	GTCCCAAATA	AACGAGTCCT	AGGATTTCCT	AGAAGGTGGA	240
CCTCAATTAT	TGTGTCCCTT	TTATATATAA	GGCAAACATT	GCTTTTAAGT	TCTGTTGGAA	300
CATGGGAACT	TTCACTAGAA	TGCTTAGAAT	GTTCAGAAAA	AATGTCCCAA	AGCTCTCTTC	360
TGGTCCATAC	AAGACAATCA	GAATGTAACA	CAGTAGCAGA	GGGTGTGGAA	CATACACTAG	420
TCATATTTGA	TTCTCTCTGT	CAG				443

- (2) INFORMATION FOR SEQ ID NO:1050:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

GAATTCGGCT AAAGAGGCCT ACTTCTGGCT ATTTTCAAAT ATATAATATG TTATTGTTAA 60 CTATACTC 68

- (2) INFORMATION FOR SEQ ID NO:1051:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

GAATTCGGCC	AAAGAGGCCG	GAATTTGGCC	CTCGAAGCCA	AGAATTCGGC	ACGAGGGCAA	60
GACTCTGTCT	CCAAAAAAAA	AAAAATTTAA	AAAAAAAAA	ATTTTTTAAA	AAATTTTANT	120
TAANGTAAAT	TTAAAAATGT	TCAGTGAAAT	GGTAAAAAAA	AAAAAAAGAC	GCACAAAATA	180
CCTTCATGTT	TCTCATCTCT	TTTTCCCTTC	AGATTCTGCC	TTTCTTCCAA	TTCAGCTCTT	240
CTTTTCCAGT	CTTTCAACCA	ACCACCACGA	CTCTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:1052:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

CTCGAGGACC	AAGGATGAAG	AGCATAAGAA	GATGAAGATT	GTAAACTTGT	TATTAAAATTA	60
CTTGGTGAGA	AGACAAATTG	TAAAGTAGAT	ATTTGTAATC	TTTTACCACT	TTGGGGTTGC	120
TTTTTTCCCG	GAATTCATCA	GAACTTTGAA	TTTTTTTTT	AAATGGGCTG	TTTTTAATGC	180
AGGGGCTTTT	CTTCCCTAGA	AACCCAATTC	TAAGCAGAAA	AAGNAAAAAN	ACACCAAAAA	240
TAAAAAACCC	CCCTCGTGCC	GAATTNTNGG	CTTCGGGGGC	CAAATTCCGG	CCTCTTTGGC	300
CGAATTC						307

- (2) INFORMATION FOR SEQ ID NO:1053:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

GAATTCGGCC	AAAGAGGCCG	GAATTTGGCC	CTCGAAGCCA	AGAATTCGGC	ACGAGGGCAG	60
TTAAGATCTG	GGTGATTCTT	TAGGGAAACG	GCTGGTTGAG	AGGCTTTGAT	GGAATCCCAT	120
TCTCTGCTGT	GGCCAGAAGG	TGGTGCTAGA	GGCCAGTCCC	ACTTGGATGT	GACCCTGGCC	180
TCTGCCAGGA	TTCAAACCAC	AAAGAACATT	TGGAACTGGG	ATGTTTGCTT	TGAAGCAGCC	240
TGAAAACAAG	TGAAAAGGAA	ACCAAGATAA	CTCTCTCTCC	CTCCGCTGGC	AAGGATCAAA	300
AATACCTTGT	GCAGGGAAGC	CCGAGCCTCG	AG			332

- (2) INFORMATION FOR SEQ ID NO:1054:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

GAATTCGGCC	AAAGAGGCCG	GAATTCGGCC	TCGAAGCCAA	GAATTCGGCA	CGAGGCCTCG	60
TGCCGCGCCG	TTTTTTTTTT	TTTTTTTCAC	AGGGGGCAG	TCGGGATTAT	AATACACTGT	120
AGCAGTTGGC	TGGGGAAAAG	TCTATCAAAT	TCCATGACCA	ATTGGACTTT	TCTCCCACCT	180
GTAATATAAA	TAAAATATGT	ACTGTTTCAT	ACTGAATTTT	TTCAATGCAT	TGGGGTTCAA	240
CATAAAAGGC	ACAAATAAAT	AAAAATATCA	TTAAATAAAC	GGAAATTACA	ATTTCAAGTT	300
TCATGTGGAG	TTGTATCTCA	CTGTTTGGTT	ACTTTTTCCA	ATTTAATTTG	ACAGACTTAG	360
TAATAGCACA	CAACTGTCCT	ACCCTCGAG				389

- (2) INFORMATION FOR SEQ ID NO:1055:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

GAATTCGGCT	AAAGGGTCTA	CGAGGTCAGC	AAGGACGCCC	AAGGAGACTC	AGTCATGAAA	60
GGTGAACTGC	TCCTGTTTTC	CAGTGTGATT	GTCCTGCTCC	AGGTGGTATG	CAGCTGCCCG	120
GACAAGTGTT	ACTGTCAGTC	ATCTACAAAT	TTTGTAGACT	GCAGCCAGCA	GGGTCTGGCC	180
GAAATCCCTT	CCCATTCCCC	TCCGTCGCTC	GAG			213

- (2) INFORMATION FOR SEQ ID NO:1056:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

GAATTCGGCC	TTCATGGCCT	AGCGATTCCA	GGTTTTAAAT	AGTTTGTAAA	TTTTCAGTTT	60
CTACACACTT	TATCATCCAC	TCGTGATTTT	TTAATTAAAG	CGTTTTAATT	CCTTTCTCTG	120
TTCAGCTGTT	GATGCTGAGA	TCCATATTTA	GTTTTATAAG	CTTCCCCCTC	GAG	173

- (2) INFORMATION FOR SEQ ID NO:1057:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

GGTCATACTC	TCTCATCCAG	ACTGGAGTGC	ATGGAGTGCA	GTGGCACCAT	CTCGGCTCAC	60
TGCAACCCCT	GCCTCCCAGG	TTTAAGCAAT	TCCCCTGCCT	CAGCCTCCCG	AGTAGCTGAG	120
ATTACAGGCA	CATGCCACCA	TGCCTGGCTA	ATTTTTGTAT	TTTTAGTAGA	GACGGGGTTT	180
CACCATGTTG	${\tt GCCAGGCTGG}$	TCTCGAACTC	CTGACCTCAA	GTGATCTGCT	CACCTCAGCC	240
TCCCAAAGTG	CTGGGATCAC	AGGTGTGAGC	CACTGCACCC	GGCCTAGTTT	CCATTTTTCT	300
GTTGATATTT	ACTTCTATTC	ACTCATTAAG	ACTATATTTT	ATTTCTTTAA	TATATTTTCC	360

CTTAGTTCTT	TGAACATATT	TATAAGAGCT	ATTTTTAAGT	ATTTGTCAGT	TGAATCTAAC	420
ATCTTTTGGG	GCCATTTTCT	ATTGACTGCT	TTTTTCTTGA	TGATGAGTCG	CATTTTCCTT	480
TTTGCCTATC	TAGTAATTTT	TAAATTATAT	ACTGTACCTT	GTGGATGTAT	GGTAGAGACT	540
CTGGGGTCTC	TCGAG					555

- (2) INFORMATION FOR SEQ ID NO:1058:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

GAATTCGGCC	TTCATGGCCT	AGAATGTTAG	AAGGTGCCTG	CCGAGGCGGG	ACAGAGTGTT	60
CGCTCGCGCT	GGAGAAGGCT	CTGCTCAGCC	CTGAGAGTCC	CTTCCTGCCC	CACCGATACT	120
GGCACTTTAA	CAAGGAAGCT	GACCGCACAG	TGTCCAGACG	AATTGGCCCC	CAGAAGATGG	180
GGAGTTCTGT	CCTGCCCTTC	TGTGTCTGCG	TGACCTCACC	CAGCCTAGGA	GGGAGGTGCA	240
TTCAGGGTAG	ATTTGCCTCT	CATTCAAAGT	TCTGGGGCTT	TGGGTGGAAA	ACAGCCAGCT	300
TTGGCGCTGC	TGGGGAGACT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:1059:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

GAATTCGGCC T	TCATGGCCT	ACTTGATGCT	GCAAAGAACA	AGATGCGAGT	GAAGATCAGC	60
TATCTAATGA T	TGCCCTGAC	GGTGGTAGGA	TGCATCTTCA	TGGTTATTGA	GGGCAAGAAG	120
GCTGCCCAAA G	BACACGAGAC	TTTAACAAGC	TTGAACTTAG	AAAAGAAAGC	TCGTCTGAAA	180
GAGGAAGCAG C	TATGAAGGC	CAAAACAGAG	CAGCTCGAG			219

- (2) INFORMATION FOR SEQ ID NO:1060:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

GAATTCGGGC	CTTCATGGCC	TAGTATTTAT	AGCCAAGGAA	ACAGGGCTAT	GAGTTTGTAC	60
TGTAGGCAGC	AGTAGGGAGG	GGGAATTGGA	AGCAGGGGGG	AGGGCTCTGC	AGTAGTTCAG	120
TTGATGCATA	CATAAGGCCT	GAATTAGGGA	ATTAGGAGAG	TGATCATAGG	TGTGGAAAGG	180
AGGGGAGGC	TTCCAGGCAC	ATTTGGTGTA	AAATGGATAC	AACTTGGTAA	CCTGTACATT	240
CCTACCTTTC	CACATTTGGT	TTCCCCTGTC	TCAAAGGCTC	CCTCTTCTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:1061:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

GAATTCGGCC	TTCATGGCCT	AAAGAAAACA	AACAAACAAA	GAGAAAACCC	ATGAGCATTT	60
TAATTCTGAC	TTTTTTACTT	TTCTCCCTAC	ATTTAGAATA	CTGTGGCACT	TTCTGTTATC	120
CAAATGTGTC	TCAGTCTCCA	TATTTAAGGA	CTGTGGGTGA	AAAGCTTCTA	CCTGGAATTG	180
AAGTGCTTTG	GACAGGTCCC	AAAGTTGTTT	CTAAAGAAAT	TCCAGTAGAG	TCCATCGAAG	240
AGGTTTCTAA	GATTATTAAG	AGAGCTCCAG	TAATCTGGGA	TAACATTCAT	GCTAATGATT	300
ATGATCAGAA	GAGACTGTTT	CTGGGCCCGT	ACAAAGGAAG	ATCCACAGAA	CTCATCCCAC	360
GGTTAAAAGG	AGTCCTCACT	CTCGAG				386

- (2) INFORMATION FOR SEQ ID NO:1062:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

GAATTCGGCC	TTCATGGCCT	ACATGAAGCT	GAATTACTCT	CATCTTATAT	CTCTCTGCAG	60
TGGCATATCC	TGATGGTGAT	TTCCTCTTTT	TGTGCCTCAG	TTTCACCCCC	TATGGAATGG	120
GGATAAACAC	TTGCGGCTGG	GCATGGTGGC	ATGTGCCTGT	AGTCCCAGCA	CTTTGGGAGG	180
CTGAAGTGGG	AAGATTGCTT	GAGGCCAGGA	ATTTGAGACC	AGCCTGGGCA	ACATAGTGAG	240
ACACTCTCTC	TACAAAAAA	AAAAAGAAAA	AAAAAATCAG	ATGTGGTTGG	TGCATGCTAC	300
TGAGGCGAAA	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:1063:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

GAATTCGGCC	TTCATGGCCT	ACTAGACCTG	CCAAGCTTTC	TTCCTTCATA	CTACATATTT	60
CACAAAATTT	GCTCGTCAGG	TCTGCAAAAA	TACCCTCCGG	CTGCGGCAGG	CAGCAAGACG	120
GCCGTTTGTT	GCTATTAATT	ATGCTGCCAT	TAGGGCAGAA	TGTAAGATGC	TTTTAAATTC	180
TTAACCTTAT	ATGTTGTGCT	TCTGACCATT	TTCTCTTTTC	CTCTCTTTCC	TTTTTTTTT	240
GTTTGTTTGT	TTGCAATAAA	CATAAGTTCT	TGTGTACAGC	CCACTCGAG		289

(2) INFORMATION FOR SEQ ID NO:1064:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

GAATTCGGCC	TTCATGGCCT	ACAGAGCTGA	GAAATAATTC	CCTTGTGTGT	TTATAAGTAA	60
GAGTTAAATC	CCTCCCATTG	TAATGTAGCA	CCAGATCGAA	GTAAACAGAC	TATGATTTCA	120
GTGCTAGACA	CAGCCTTAAG	GCAGAAGAAA	TTACACTGTC	ATGCAAAGGA	TATGTAGCTG	180
CTGCTATTTT	GGTGCTTGAA	TTCTTCGTTG	TCACATAGTT	GAAGGCAATC	CAGATGAGGA	240
AGAGTGTTAA	CCAACAAAAA	GAGAAAATTC	CCTGCACATG	GTCTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:1065:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

GAATTCGGCT	TTCATGGCCT	ACTGGGAGCT	ATCTTGTCTA	CCTTGAGGTT	CCTGAACAAT	60
GAATTCCCAT	TAATGAGCAG	TCTTCAGTAT	TAAAACCACT	GTCTTGTCAC	CTCATTTTGC	120
ATTACTGTCT	TCCGTGGATG	TTTCAGTTAC	AACTGTAATG	TTATTTATAG	AACAACATTA	180
ATCCATTAAA	GCTAACCTAT	TTTTCAATAT	TTATGATAAT	CTATGTACAT	ATATTGTCTG	240
TCCATATGTA	TTTGTAAATA	GGTTGTATAT	AATGTCAGGT	TTGGGTCTTG	GGTTCAAGTG	300
TATATATTCC	TGTAAGTTTC	TTAACTGCAT	TTTGATGAAT	TCACATTATG	TAACTATAAG	360
AATTGTCCCA	AAAGTACCTG	TACAGAAAAT	TGAATATTGA	AAAATTGACA	AATTGTGTAC	420
AAACACTAAA	AAAAACTTGT	TTAAATTGTA	TTTGCAATAA	ACAACATCAA	ATTTTTTCAT	480
GAAATCTGCC	TCGAG					495

- (2) INFORMATION FOR SEQ ID NO:1066:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 507 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

GAATTCGGCC TTCATGGCCT	AAAGATTATA	AAGGAAAGGG	GGGTAGTTAA	GATTTAGAAT	60
TCAAGTTAAA TTTCAGAAAT	TGGGGCAGTC	AGGCATTTGT	ATCTTTTAGG	GCAACAAGTA	120
AAACATGTAG AGTGCTTGCT	ATCCCACTTC	ATAAAGCTTT	TACCCAATCT	TATTTCTAAA	180
CCTCTGTGCA TTCTTAGTGT	CTTCTCATTC	TGAAACAGAA	AATAAGGAAA	AACATTTAAC	240
TTAGTTTTCT AAAATCAGAT	AATCCTAAAC	AAAAATGTTA	GTCAGGGTCA	CTAAAAAGTA	300
TTGCACATTT ATATAAATAC	AGTCCTTTTA	AAATTTGACT	TTTAAAAAAC	AAAAGACTTT	360
GTACGATATT GTGTTTTTAT	TGCGTTTGCA	ATATTTTTAT	AGTAGCCTTT	ATGAACTCAG	420
TATAAGTGCA AGTTGTTTGA	AAAGGTGTTT	TTATTAGTGC	ACAATAGAAT	TGTGAGGTTT	480
TCAATAGATG TCATGAGATT	CCTCGAG				507

- (2) INFORMATION FOR SEQ ID NO:1067:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

GAATTCGGCC	TTCATGGCCT	ACTTATTTTT	TTCTTTTAAA	CAAATAAGCA	CACATTCTTT	60
TTAAATAAAG	TTTCTCTTCC	CCAACCTAAA	AGTAGTAATG	CTAGAATTTG	AGCATAGCAG	120
AAAAATATTT	AGGAAAATTA	AATCCCAAAC	AAGAGAGACC	ATCTTGGACT	GTGCTCACTC	180
GGGTGGAAAG	TCGACCCAGG	TGCCTGTGTG	CTTGACAGAG	GCGTGGCTGC	ATCCGCGTAG	240
CTGACCTTCA	GATGGACTGG	AGTTAGCACA	TTTGTAGTCA	TTTTTCCAAC	CATTCTTTCG	300
TATCTGAGGT	ACGTTTTTGA	CCTGTTTTAG	TATGTCACTC	GCGATCTTGA	AGCACACTCT	360
TTCATTTACT	TAAATATTTC	CTGAGCACTC	GAG			393

- (2) INFORMATION FOR SEQ ID NO:1068:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

GAATTCGGCC	TTCATGGCCT	AAGGTAATGT	GTCAGTGGAT	GGAAAAGTTT	AGAAAAGATC	60
TGTGTAGGTT	CTGGAGCAAC	GTTTTCCCAG	TATTCTTTCA	GTTTTTGAAC	ATCATGGTGG	120
TTGGAATTAC	AGGAGCAGCT	GTGGTAATAA	CCATCTTAAA	GGTGTTTTTC	CCAGTTTCTG	180
AATACAAAGG	AATTCTTCAG	TTGGATAAAG	TGGACGTCAT	ACCTGTGACA	GCTATCAACT	240
TATATCCAGA	TGGTCCAGAG	AAAAGAGCTG	AAAACCTTGA	TACACTCGAG		290

- (2) INFORMATION FOR SEQ ID NO:1069:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

GAATTCGGCC	TTCATGGCCT	ACTCGACTCA	TATTTTTATC	ATACATTTCA	AAGTCAGTTG	60
CTGATGTTAA	TCCCATTTCA	ATGTGGGGCA	GACTCTCGGG	GTAATTTCAA	AAAGATGTCT	120
CAAACATGTT	TGTGTGTGTG	TGTGTGTGTG	TGTGTGTGTG	TGTGTGTGTG	TGTGTGTGTG	180
TGTGGAGACA	GGGTCTCACT	CTATTGCCCA	GGCTGGAGTG	CAGTGGTGCC	ATCATGGCTC	240
ACTGCAGTCT	CGACCTCCCA	GACTTAAGCA	ATCCTTCCCA	AATAGCTGGG	ACTCCAGGGG	300
CACCCCACTA	CAACTCGAG					319

(2) INFORMATION FOR SEQ ID NO:1070:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

GAATTCGGCC	TTCATGGCCT	ACTTCTAAAT	GGCAAACAGT	TGTCTTGAAG	GCACTGTCTT	60
TTTCTACCTA	GATGTTGGGT	GGAAAAAAA	AAAAAAAAGC	TGCCTTTTAT	ATAGAAGTTC	120
TTGGGAATAT	TTCTCATATA	GTGAGATGAA	CAGAATGCAA	AAGTTTTCTT	CCTGCAGGAT	180
CTCCCAAAAT	CCTTCTTGGC	TTGAATTTTT	CTTCTCACTT	TTTCTTTTGA	AAAGCTTTGT	240
TCCTTTTGCA	CCTTGGAAAA	ATAAGTCTTG	TTTGTCCTGA	CAGCAGAGTG	CAAGCATCTA	300
TTGCATCAAA	ATTCCCAAGT	GGAATAGAAA	ACCAATGGTC	CTTTTCTGAA	TTTCGTTAGC	360
AGTAGCAACA	AACATTTCAT	TATAACCTCG	AG			392

- (2) INFORMATION FOR SEQ ID NO:1071:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

GAATTCGGCC	TTCATGGCCT	ACACAATGGG	AATCCAAGGA	GGGTCTGTCC	TGTTCGGGCT	60
GCTGCTCGTC	CTGGCTGTCT	TCTGCCATTC	AGGTCATAGC	CTGCAGTGCT	ACAACTGTCC	120
TAACCCAACT	GCTGACTGCA	AAACAGCCGT	CAATTGTTCA	TCTGATTTTG	ATGCGTGTCT	180
CATTACCAAA	GCTGGGTTAC	AAGTGTATAA	CAAGTGTTGG	AAGTTTGAGC	ATTGCAATTT	240
CAACGACGTC	ACAACCCGCT	TGAGGGAAAA	TGAGCTAACG	TACTACTGCT	GCAAGAAGGA	300
CCTGTGTAAC	TTTAACGAAC	AGCTTGAAAA	TGGTGGGACA	TCCTTATCAG	AGAAAACAGT	360
TCTTCTGCTG	GTGACTCCAT	TTCTGGCAGC	AGCCTGGAGC	CTTCATCCCT	ATACGCTCGA	420
G						421

- (2) INFORMATION FOR SEQ ID NO:1072:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

GAATTCGGCC	TTCATGGCCT	AATCGGTCAC	TGATAGTATG	TATTTCTTTA	GTAAGAATGT	60
GTTAAAATTA	CAATGATCTT	TTAAAAAGAT	GATGCAGTTC	TGTATTTATT	GTGCTGTGTC	120
TGGTCCTAAG	TGGAGCCAAT	TAAACAAGTT	TCATATGTAT	TTTTCCAGTG	TTGAATCTCA	180
CACACTGTAC	TTTGAAAATT	TCCTTCCATC	CTGAATAACG	AATAGAAGAG	GCCATATATA	240
TTGCCTCCTT	ATCCTTGAGA	TTTCACTACC	TTTATGTTAA	AAGTTGTGTA	TAATTGTTAA	300
AATCTGTGAA	AGAATAAAAA	GTGGATCCCC	TCGAG			335

(2) INFORMATION FOR SEQ ID NO:1073:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

GAATTCGGCC	TTCATGGCCT	ACAAAAATAG	GCACAGTTTC	AGATGCTTCA	GCATATGAGG	60
CATGGATACT	TCAATCATTT	GCAAAGGGTT	CTGCTCAGTA	GACTGAATGG	AAAAGATGGT	120
CATTGCTCTT	TAATGTAATT	TTGCAGCTCT	CATCAAAGAA	AATATCTCCA	TGAAATTTAT	180
TGGTAACTGT	TTATCTTTGA	TCAGTGCAAA	CTGAAGTCAA	ATATACAAGG	TAAACACACA	240
TAAAGATAAG	TTCACACATT	TCTGTGAATT	TTCTAAATGT	ACACACTTCT	GCAAATTCTC	300
TAAATTCACA	AATAACAAAT	TTGCATGCAT	GCAAGCATAT	GTGCACATGT	GCACACCTCG	360
AG						362

- (2) INFORMATION FOR SEQ ID NO:1074:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 612 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

GAATTCGGCC	TTCATGGCCT	ACCCAGGTGA	TCAATGTTTT	CAATGCGATC	AGTAATAACC	60
ATGTGCTCAT	GAATCAGATA	GGACTGAGGC	AAATAGGTTC	CAGCCTTGAT	GTTAATAAGT	120
AACTCCAGTA	GGTTTCTGGG	TGGCATAACA	ATGGAAGTGT	TCAGAGGGAT	CACATAGCAC	180
TTATCCAGGT	TAAGATCTAA	ATAGGCTGTA	AGTTTCTTGT	TAAAGTCATG	AACAATGTTG	240
GCAGGATCAC	TATCTGCAAA	CTCTGGGACA	GGCACACTGA	TAAATTCAAC	TTCTCTTCTT	300
CAAAGATTTT	AATATTTTCT	TCAATTGTCT	GGTAGAGAGC	AGCTGGGGCA	TCTGCAGAGG	360
GCTCATTTAA	GATGACATCA	TCTTTGATGT	ACTTTATTCC	ACAGTAGTAC	ACGTCATCTG	420
GTTGAAGTGC	AAAATATTTG	TACAAGTATG	CTCCTCCTAG	AATAACACCT	GCAAGCATAA	480
ATGCTAGTCC	AAAGCACATG	CACCACCACC	ACCCGGCTAA	TTTTTGTACT	TTTAGTAGAG	540
ATGAGATTTC	ACCCTGTTGG	CCAAGATGGT	CTTGAACTCC	TGACCTCAAG	TGATCCGCCC	600
ACACCACTCG	AG					612

- (2) INFORMATION FOR SEQ ID NO:1075:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

GAATTCGGC	C TTCATGGCCT	AAGTTTGTGG	TCCTCTGAGA	ATTCTCTGAA	GGAGGAAATG	60
GGTTGACCT	A TTTGGTTGCT	ATGAAGTAAA	AACAATCTTG	TTTTCATTTT	TTAGTGAACA	120
TCTGGGTTG	C ATTTATTATT	TCACATTCTG	GAGATTCTGT	AAAACCACAA	TTTGATAATA	180
TGAGGGTTC	A TCAAAGCGGT	AATTATTGAG	CTATTTTTAT	AGTTGATTCA	AGAATTAGGG	240
TGGCGACTC	G AG					252

- (2) INFORMATION FOR SEQ ID NO:1076:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

GAATTCTAGA	CCTGCCTCGA	GTGTGATACC	AGCAGCTATG	AAGCAAACTG	TATTAACCAA	60
GTCTTTTATT	TTCTGTGTTC	TGATGCATGA	CTTTCATGGC	CTTGTCAACC	CTAGAGACCC	120
TGCCCCTCCC	ATAGCTAGCG	AACGTCTCGA	G			151

- (2) INFORMATION FOR SEQ ID NO:1077:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 542 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEO ID NO:1077:

GAATTCGGCC	TTCATGGCCT	AGGAAGTAGT	CTAAAAAATT	AACAGTTATG	GTTTTAATAG	60
GATCTGAAAG	ACAATCTTTA	AAGAAATGGG	AGAAATTGGG	GGTATCAGTG	AACCTATACC	120
AACCTCTCTT	TGTACATAAA	TATGGTGATG	TAGCTAGATA	TAAAAATCAG	TGTCTTACTG	180
GCACCATTTA	CAGTTTAGAA	AACAATCTTT	TTCTTAAAAA	TGCCCATCTG	ATTTCTATTT	240
TTAGGAGCTA	CTTGGATTTG	TATGTATTTT	TTCTACGTGA	AAATATATGT	ACTCTTCACT	300
TTTGTTCCAG	TACTATAATT	GCTCATGCAC	TCTTTCTCCC	CTTTGAGAAC	ATTCAGTGAA	360
ATACAACTTC	ATCAAAGATT	TGCTCAAAGG	AGAAGAATCG	CATGAGTGTG	AAAAGTAGAT	420
GCTCGTAGCC	AGAACAGAAA	AGGTTACACA	TGATCATGGC	ACAGAAGATA	GGAGGTTTGA	480
CTTGGTGGGC	CATAATGTTT	ATTATCCTTT	TTGAAATAAC	AGGGACCAGC	AGCACTCTCG	540
AG						542

- (2) INFORMATION FOR SEQ ID NO:1078:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

GAATTCGGCC	TTCATGGCCT	AGGTTGCCAT	TACTTGTGAT	GCCTCTGAAT	GTGGAGGCTG	60
ACTCTCCCGT	CTCTCTGTCC	CTCCTACCCC	ACGGGGCCGC	AGCAAAAGCC	ATCCTGGGCC	120
TTCGACTGGG	CCATGTCTTC	AGGAAGATTC	CTGAAGAGGA	GGGCCCGAAA	TACCTGCCTT	180
TATAGGTTCC	CAGAGTGCCC	TAGAACATTC	TTAGATACAT	ATTTTTTAAA	CAAGTAGGAC	240
TCCACCTTAT	TTTCTCCAAT	AGTCCCCAAG	CAGTACAGGT	CACTTGAAGA	CATAAACATT	300
CTTCTTGGTT	GAGGGATCCA	CGCCCTTGTT	TCAGAAATGA	CACCACAGAA	GGCTGTGAGC	360
TCCAGGAGCA	TGCGTTGGGA	TGTCCGGATG	ACCGGGGTTT	AAAGGTTTTC	CTATTCTCGA	420
TAAAGCCTGT	GCGCACTGTA	CGGGGAGTGG	GGGTGAAGCG	TGTTCTCTAC	ATAGGCAACA	480

(2) INFORMATION FOR SEQ ID NO:1079: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 284 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(A) LENGTH: 284 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:	
GAATTCGGCC TTCATGGCCT AGGGGCCAGG CGGCCGCCG GAGTCTGGTA TCCTGAGCTT CGTGAGTTGA GCGCTGCTGC TCCGCGGTGG AGTCACCGCA CCGCTCCCGG GATCATGGTG TTCTACTTCA CCAGCAGCAG CGTTAATTCA TCTGCCTACA CTATTTACAT GGGAAAAGAT AAATATGAAA ATGAAGATCT GATCAAGCAT GGCTGGCCTG AAGATATCTG GGAGAGAATA TAGAAGACAT CCCCAAAGGAA GTGCTGATGG ACTGTGCGCT CGAG 28	20 80 40
(2) INFORMATION FOR SEQ ID NO:1080:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 359 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	٠
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:	
TGGAAACACA GAAACTTGGT TCAGTTTTGT CTCCAGAATC GCCAAAACCT ACTCCTCTTA CTCCCCTGGA GCCTCAGAAA CCTGGCTCTG TTGTTTCTCA TGAGCTACAG ACACCTCTTC CTTNTCCTGA GCCTTCAAAA CCTGCCTCTG TTTCTTCTCC TGAACCTCCA AAATCAGTCC CTGTTTGTGA GTCTCAGAAA CTTGCCCCTG TTCCTTCTCC AGAACCACAG AAACCTGCCC 30	60 20 80 40 00
(2) INFORMATION FOR SEQ ID NO:1081:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 474 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:	
GGGGTTTTCA CCTGTGAGCC TTGGTCTGTC TCGGTAGGGT GGTCAACTTC AGTGGACTGT GGTTGGTTTC AGAGCGCCTG GCTGAGGAGT TCCACTGAGG GGAGCACTGG AGCAGCCCTT TGGCAGAGGC TGAGGAGGA GATGGACCAG CCCACGCCTG GCACCTGGCT CCATGGCATA AGGAAAGGGA GATGCTGGCC TCTGTGCTCC TGCTGTCTTT TCCTGTTTCT GTTTGCGTTT GACTTAGTAG CAACCGACAG AGTGGCAAGG GATTTGGTCT TCAGCAGTAG ACATCCTTCC 3	60 120 180 240 300 360 420

CGGCCCAAGA GTGTCCAGCG GTGGCCCACT TTTTCCTCCC ACCACAACCT CGAG 474 (2) INFORMATION FOR SEO ID NO:1082: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 505 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEO ID NO:1082: GAATTCGGCC TTCATGGCCT AATGTGTGTG GCACAAAGAA GAAAGTGGAC TCTACACTGT GTTAGTTAGG AAAACCAGAA ATTGGGCCAA ATTGCCTGTT TAGTGGGAGA GATANCTTTT GAGAGCTGTG ATCCCGCTGG TGTGGCTGGC TCTGGGCAGA TATTTGTATC TGAAATGACT 180 CATGCTGTGG GACCCTTCCT GAGATCTAAC ACTTACAGTG GTTTGATCAG AAATTGCACC 240 ATGCTTGCCA AGCAACTTTT GGACTAAAAG TTGCTGCCCA CGTATATCAG GGGAAGAATA 300 TATATATAT TATATAGT ACCTATCTTA GCATCTGATT TGTATGACCA TTACTTCAAT 360 GTAAAATAAT AAATTGGCTT TCCAGCTTAA ACTTCAATTT CTTGTATATT ATATGATCAT 420 GAGACAACCT CCCTGGGCTG ATCAACAGCA GGACGCTAAA AAGATTGAGT ATCTGAGTCA 480 GGAAGGTAGA GGGCCAAACC TCGAG 505 (2) INFORMATION FOR SEQ ID NO:1083: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 481 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083: GAATTCGGCC TTCATGGCCT ACTACTATTC AGAGACAACA GTGACACGGA CCTATGTGAT 60 GCTGGCCTTA GTGTGGGGAG GTGCCCTGGG CCTGGGGCTG CTGCCTGTGC TGGCCTGGAA CTGCCTGGAT GGCCTGACCA CATGTGGCGT GGTTTATCCA CTCTCCAAGA ACCATCTGGT 180 AGTTCTGGCC ATTGCCTTCT TCATGGTGTT TGGCATCATG CTGCAGCTCT ACGCCCAAAT 240 CTGCCGCATC GTCTGCCGCC ATGCCCAGCA GATTGCCCTT CAGCGGCACC TGCTGCCTGC 300 CTCCCACTAT GTGGCCACCC GCAAGGGCAT TGCCACACTG GCCGTGGTGC TTGGAGCCTT 360 TGCCGCCTGC TGGTTGCCCT TCACTGTCTA CTGCCTGCTG GGTGATGCCC ACTCTCCACC 420 TCTCTACACC TATCTTACCT TGCTCCCTGC CACCTACAAC TCCATGATCA ACCCTCTCGA 480 481 (2) INFORMATION FOR SEQ ID NO:1084: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 389 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

GAATTCGGCC TTCATGGCCT ACCATTTTA TTAAACCCAA ATCCATGGAA AATATCATGG

60

AAATGAATAA	GCGTCTAACA	GAAGAACAAG	CCAGAAAAAC	ATTTGAGAGA	GCCATGAAAC	120
TGGAACAGGA	GTTTACTGAA	CATTTCACAG	CTATTGTACA	GGGGGATACG	CTGGAAGACA	180
TTTACAACCA	AGTGAAACAG	ATCATAGAAG	AACAATCTGG	TTCTTACATC	TGGGTTCCGG	240
CAAAAGAAAA	GCTATGAAAA	CTCATGTTTC	TCTGTTTCTC	TTTTCCACAA	TTCCATTTTC	300
TTTGGCATCT	CTTTGCCCTT	TCCTCTGGAG	TCTTTCTTGA	GTACTGATTT	CATGTTGAAT	360
TGTATCCCAC	ACATCATGGT	CATCTCGAG				389

- (2) INFORMATION FOR SEQ ID NO:1085:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 base pairs

 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

GCGATTGAAT	TCTAGACCTG	CCTCGAGACC	GCCTACGAAT	GGAAATCCAT	AAGAATGAGG	60
CTTGGCTCTC	TGAAGTCGAA	GGCAAAACAG	GTGGGAGAGG	AGACAGAAGA	CATAGCAGTG	120
ACATAAATCA	TCTTGTAACA	CAGGGACGAG	AAAGTCCTGA	GGGAAGTTAC	ACTGATGATG	180
CAAACCAGGA	AGTCCGTGGG	CCACCCCAGC	AGCATGGTCA	CCACAATGAG	TTTGATGATG	240
AATTTGAGGA	TGATGATCCC	TTGCCTGCTA	TTGGACACTG	CAAAGCTATC	TACCCTTTTG	300
ATGGACATAA	TGAAGGTACT	CTAGCAATGA	AAGAAGGTGA	AGTACTCGAG		350

- (2) INFORMATION FOR SEQ ID NO:1086:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

GCTCCACCAG	CTACTGAGAA	AATGGCCTGT	AAAGATCCAG	AAAAACCCAT	GGAGGCCTGT	60
GCCTCAGCAC	ATGTGCAACC	CAAGCCTGCC	CCTGAAGCCA	GTAGCCTAGA	GGAGCCCCAT	120
AGCCCAGAAA	CAGGGGAGAA	GGTAGTAGCA	GGAGAGGTAA	ACCCACCCAA	TGGCCCTGTG	180
GGGGACCCAC	TGAGCCTCTT	GTTTGGGGAT	GTGACATCCC	TGAAAAGCTT	TGATTCATTG	240
ACAGGTTGTG	GTGACATAAT	AGCAGAACAA	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:1087:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

GCAGAGACTT	AAAGGGTTAA	TAAAAATTGT	AAAGCCAGCA	GAGATTCCAG	AACTAAAAAA	60
GACTGAAACT	CAGACTACAG	GTGCAGAAAA	CAAAGCTAAA	AAGCTTACAT	TGCCTCTATT	120
TGGTGCCATG	AAAGGAGGAA	GCAAATTCAA	ATTAAAAACT	GGAACAGTAG	GGAAGTTACC	180

CCCCAAGCGT CCAGAACTCC CTCCAACTCT AATGAGAATG AAAGATGAGC CTGAAGTAGA AGAGGAGGAG GAAGAGGAAG AGGAAGAAGA GAAGAAAAG GAGGAG	240 295
(2) INFORMATION FOR SEQ ID NO:1088:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 339 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:	
GAAATGAGGG TCCCTGAAGA AGCTCTTAAG CATGAGAAGT TTACCATTCA GCTTCAGTTG TCCCAAAAAT CTTCAGAATC AGAATTATCC AAATCTGCAA GTGCCAAAAG CATAGATTCA AAGGTAGCAG ACGCTGCTAC TGAAGTGCAG CACAAAACTA CTGAAGCACT GAAATCCGAG GAAAAAGCCA TGGATATTTC TGCTATGCCC CGTGGTACTC CATTATATGG GCAGCCGTCA TGGTGGGGGG ATGATGAGGT GGATGAAAAA AGAGCTTTCA AGACAAATGG CAAACCTGAA GAAAAAAACC ATGAAGCTGG AACATCAGGG TGCCTCGAG	60 120 180 240 300 339
(2) INFORMATION FOR SEQ ID NO:1089:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 433 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:	
GAATTCGGCC TTCATGGCCT ACTCAAGAAT ACAGGTCTTA CTCGTATAGT CTTTGAACAA TAGGCTGTGT GACTAAAAGA GAGACACAAT CAATTGCTTC CCAGTCAAGA AGCCAGAAAA GCTTCAAAAC CTTTCCCCCT CCCTACTCCT TGCCACCGCA CCTAAAAAAA AGAGAAATCT TTTAAGTGTT TAAAATCTGT AGGAGTCTTA TGAAGAAGCA GCTTTATGTG TATTCTTTAT GGCATAATAT TAATGCATGA AAATCTGTTG CTTTTTAAA AATTGTGGCA AAATATACAT AACATAAAAT TTATCATTTT AGCTATTTTT AATATACAAT TCACTAGCAT TAAGTATTAA TACATTCACA GCACCATTGC AACCATGGCC ACCATCATCT CCAGAACTTG ATCTTCTTCA ACGCCCCACTC GAG	60 120 180 240 300 360 420 433
(2) INFORMATION FOR SEQ ID NO:1090:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 319 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:	
GACTGGGTCC ATGGGAGCAA GATTAGTGGC TGCTAAACTT GAACCGAAAA GCTTCAAACA TACCCATATA GATAAACCAG ACTGCTCAGG GCCCCCCATG GACATAAGTA ACAAGGCTTC	60 120

180

240

TGGGGAGATA AAAATTGCCT ATACTTACTC TGTTAGCTTC GAGGAAGATG ATAAGATCAG

ATGGGCGTCT AGATGGGACT ATATTCTGGA GTCTATGCCT CATACCCACA TTCAGTGGTT

TAGCATTATG AATTCCCTGG TCATTGTTCT CTTCTTATCT GGAATGGTAG CTATGATTAT GTTACGGACA CCACTCGAG	300 319
(2) INFORMATION FOR SEQ ID NO:1091:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 328 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:	
GTGCAAATTG AGCACATCAT TGAAAACATT GTTGCTGTCA CCAAAGGACT TTCAGAAAAA TTGCCAGAGA AGTGGGAGAG CGTGAAACTC CTGTTTGTGA AAACTGAGAA ATCGGCTGCA CTTCCCATCT TTTCCTCGTT TGTCAGCAAT TGGGATGAAG CCACCAAAAG ATCTTTGCTT AATAAGAAGA AAAAAGAGGC AAGGAGAAAA CGAAGAGAAA GAAATTTTGA AAAACAAAAG GAGAGGAAGA AGAAGAGGCA GCAGGCTAGG AAGACTGCAT CAGTTCTTAG TAAAGATGAT GTGGCACCTG AAAGCGGTGA TACTCGAG	60 120 180 240 300 328
(2) INFORMATION FOR SEQ ID NO:1092:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:	
GATCATGAAG TCCATCATCC CAGTGGTCAT GGCTGGCATC ATCGCCATCT ACGGCCTGGT GGTGGCAGTC CTCATCGCCA ACTCCCTGAA TGACGACATC AACCTCGAG	60 109
(2) INFORMATION FOR SEQ ID NO:1093:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 388 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:	
GAATTCGGCC TTCATGGCCT ACTGGAATTC ATAAGTCTAA ATGGTTCTAT GAGTCTAAAA TTAAAGTGTT AGCAGGGCTG GGCTTCCTTT GGAAGCTCTA GAGAATGATC TGTTTTCATA CCTTTTCCAG CTTGTATGAG CTGACTACAT TCCTTAGCTC ATGGCCCTGC TGCCCACAGC TTCAAATGAG ACAACACCAA GTTGAGTCCT CTTTAGATCA CATCAATTTA AATCTCCTAC TATTCATATT TCCTTGTGAC TCTCCTATGC ATCCTTCCTT CTCTTCAAAG GATCTTTGTG ATTATACTGG GCCCTCTGAA GAATCCATGA TAATCTTATC TCAAGGTGCT TAAGTTAATC ACATTTACAA GATCTCCTTT TCCTCGAG	60 120 180 240 300 360 388
(2) INFORMATION FOR SEQ ID NO:1094:	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

GAATTCGGCC	TTCATGGCCT	AGGTGGCACA	TGCCTGTGGT	CCCAGTTACT	CGGGAGGCTG	60
AGGTGGGAGG	ATTGCTTGGG	CCCGGGAGGT	CAAGGCTGCA	GTGAGCCGTG	ATCTTGCCGC	120
TGTACTCCAG	CCTGGTGATA	GCGAGACCCT	GTCTCAAAAA	AATGCTTTTA	GGGAAATTAA	180
TATGTCCTGT	GCCTGTTTAA	TCATTGAAAA	CATTTTAATA	TTTTCAGAGC	CATAGAGGGC	240
AGTGAAAAAC	AGAGTAGCAG	AATTGATTAT	ACCAGTACTA	TTTATCCAAT	GGCTAATACA	300
AATAAGACTC	TCAGGGATAA	TTCACACGTG	CTTCCAAGAA	CACTAGATGG	CACCAATTAT	360
TTAGGATTCA	GACTACCTCA	GGGAACAGCT	GTCTTCATTC	AACAAATATT	TATTAAATAA	420
TGAACAAAAC	AAAAATATCT	GTCATTGTGG	AGCAGCTCGA	G		461

- (2) INFORMATION FOR SEQ ID NO:1095:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

GAATTCCCCC	TTCATGGCCT	AAACCTATGC	AGATGCCTGT	GATGAGTTCC	TEGATECEAT	60
TATGAGCACA	CTGATGTGTG	ACCCTGTGGT	GCTGCCATCT	TCCAGAGTCA	CTGTGGATAG	120
ATCCACCATT	GCAAGACATT	TGCTCAGTGA	CCAAACAGAT	CCCTTTAACC	GTAGTCCCCT	180
CACCATGGAC	CAGATCCGGC	CAAACACAGA	ACTAAAAGAA	AAAATCCAAC	GGTGGCTTGC	240
AGAGAGGAAA	CAACAAAAGG	AGCAACTTGA	ATAGATACTG	TGAACTAACC	AAACCAAAAC	300
CAACCCCAGA	TCTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:1096:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

GCTGCAGCCA	ACGCGCAGCT	CCACTGGAAG	AGGATGGAGA	ACCTCAAGGA	GGAGGAAGAT	60
GACGACTCCT	CCACAGCCTC	AGACAGCGAT	GTTCTCATCC	GGGACAACTA	CGAGCGGGCA	120
GAGAAGCGGC	CCATCCTGTC	TGTGCAGAGA	CGTGGATCTC	CCAACCCGTT	TGAAATCACA	180
GACCGGGTGG	AAATGGGACA	AATGGCCTCC	ATGTTCTTCA	ATAAAGTGGG	GGTCAACTTG	240
TTCTATTTCT	GCATCATCGT	TTACCTGTAT	GGAGACCTCG	CCATCTATGC	TGCTGCCGTG	300
CCCTTCTCCC	TCATGCAGGT	GACCTGCAGC	GCCACTGGCA	ATGACTCCTG	GCGGCTCGAG	360

(2) INFORMATION FOR SEQ ID NO:1097:

70/43430	PC1/US98/06955	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 311 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:		
GAATTCGGCC TTCATGGCCT AGTGAGCCAC CGCACGGGGC CTAACGATGA ATGTGACATC TGCAGGATCC CCAGCTAGTC AGCAGCATCT AGAGGGCTAG AGCTGACTGG GCCTTTTGCT AACTGTTTTC TGTCCCCTCT GTGCCGGGGT TTTGCGGGAC AGGCTGGTCT GTCGTGCCTT CAGCTCAGGG AATGTGGCTC GGCTGGACTG AGAGGCGTTA GGTGAGCCAG AGAAGGCCTC AGACACAGGG GCTCCCTCGA G	AACTCTGGCC GTCACTGAGC CCGAGCATAG	60 120 180 240 300 311
(2) INFORMATION FOR SEQ ID NO:1098:		
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 436 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	·	
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:		
GAATTCGGCC TTCATGGCCT ACCTGCAGCT CTACAATATA TTTTCAAACT GAGAACAAAG GATACCTGAA TGTCTTTTCA CTTAATTATT TCTTTAGGGC CTAATGAAAA TCCATGGACA AGATCCTGTT TCATTTCAAG ATGTCAAGGA GACATGGTAA AACCAAAGGA TCCTTTGAAA ATCTCTCTTC AGGATTTAAT CAAGGAGACA CAGTAACCAC CATTCTAATC GATTTGAATG GCTTCTGGAC AGAGAGGCTC TTGTTGCAAA TGACAGTGAA AACTCTGCAG ACCTTGATGA CTGAAAGACT AGACTGTCTT ATATTATGAG ATACTTGAAT GCTGCATGTA AGCAAAAAAC CTCGAG	CATACAGGAA TGAAATCTTT CAACAGTAAT TTACGAGAAC TACATGATCT	60 120 180 240 300 360 420 436
(2) INFORMATION FOR SEQ ID NO:1099:		
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 291 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:		
GAGAAGATGC AAGTGGACCA GGAGGAACCA CATGTTGAAG AGCAACAGCA GCAGAAAATA AGGCAGAGTC TGAAGAAATG GAGACCTCTC AAGCTGGATC		60 120

- (2) INFORMATION FOR SEQ ID NO:1100:
 - (i) SEQUENCE CHARACTERISTICS:

180

240

291

AAGATGGACC TACCACCCCA AGCCAAGAAG GCAAAAGTGA AGACCAGTAC TGTGGACCTG

CCAATCGAGA ATCAGCTATT ATGGCAGATA GACAGAGAGA TGCTCAACTT GTACATTGAA

AATGAGGGTA AGATGATCAT GCAGGATAAA CTGGAGAAGG AGCGGCTCGA G

(A) LENGTH: 101 base pairs

	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) Mo	OLECULE TYPE: cDNA	
(xi) S	EQUENCE DESCRIPTION: SEQ ID NO:1100:	
	CATGGCCT AGTCATTTTA TAGGTTAAAA AAAGGTCAAA TTGTGACAAT CAATATAAA ATTATATTAA ATATACTCGA G	60 101
(2) INFORMATI	TON FOR SEQ ID NO:1101:	
(i) SE	QUENCE CHARACTERISTICS: (A) LENGTH: 492 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) M	OLECULE TYPE: CDNA	
(xi) S	SEQUENCE DESCRIPTION: SEQ ID NO:1101:	
GGAATTTGTA AA TACAGTTTAT TC AGTGTCTTAT TC AATAGAACTA AA TATACATTGG GG GGTAACCGAA TC	CTGTAAGTT GGGAAGTAAA ATAGAGAAAA TAATAAATCT AGATGTTCTC CAGGAACTT TTTATCCCTC CTCACTAAGG AATTCCCACT GTGACTTTAA ATTACTTGT GTGCATGTAT ATGTCTGTAT TTTTTACACA CATGCAAAAA GGCACGTGT GTGAGAGATA TGAATGTGTG CTTATATAAA AATAGATAAA GTATTGTAG AAACATGATT TATTTAGTTG AGGGTATTGG AGTTACTTTC GTTGTATAA ATACACCAAA TTAATCATTA TGTTATCTTA TGTTAAAAGG	60 120 180 240 300 360 420 480 492
(2) INFORMATI	ION FOR SEQ ID NO:1102:	
(i) SE	EQUENCE CHARACTERISTICS: (A) LENGTH: 343 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) M	MOLECULE TYPE: cDNA	
(xi) S	SEQUENCE DESCRIPTION: SEQ ID NO:1102:	
ATTAATAAAC AAATTCTGTTTT TCTCTCACTCT GCACTCACCCTC C	TCATGGCCT AGGCCTGCGT TAATACTCTT AATTATAGAA ACAATCCTTA AGTCCTTTC ATTGGAAAAA GAACTAATAC ATTTTGTTCT CTCAGTCAAA GTGGTTAGA GTAATAAAAT GGTAACACCT AGGGTCTGCC ACGATCATGG GATTCATTC CCTACCACAT CCTTATTTCC CTCCTCTTCC CCATTCCCTC TCCTTTCCT TCCCTCACTC ACCCTCCTCT TCCCCATTCC CTCACTCA	60 120 180 240 300 343
(2) INFORMAT	ION FOR SEQ ID NO:1103:	
(i) SE	EQUENCE CHARACTERISTICS: (A) LENGTH: 282 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

GAATTCGGCC	TTCATGGCCT	AACCGGGCAA	ААААААААА	AAATCTTAAA	AGCACTAACT	60
TACTATCAAA	TCTCAAGAAA	CAGAAGCAAT	TTCAAAAAAT	CAATACTATC	CTTTTGGTCA	120
GTAACACTTT	CTTCATTCCT	AATGTATGAG	AACAATAAGG	ACATTTTAGC	TCCTTTACTC	180
TTCCTTCATT	TAGTGACTTC	CACATTTCTC	TCACCATTTT	TCCAGCCTCT	GGGTGTGGTT	240
CTGATGAACC	TTAAACTTGA	AAGGCACAGG	CCAGAACTCG	AG		282

- (2) INFORMATION FOR SEQ ID NO:1104:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

GCGATTGAAT	TCTAGACCTG	TCTTACGCTT	CCCTTCCTAA	GCCTTTGTCT	ACTCTGCTTT	60
GTCTGCTTTT	ATGCTTCTCT	CTCTTTTGTC	TGAACTGGTC	TCTGTCCTCG	TCCATGCTTC	120
AAGTCCTAAT	TCAAATGCCA	CTGTCTTTAT	GAAGGGCTCC	CTGATTGTTC	CAACCAAAAT	180
AAGCTTTTAT	TCCTTTGAAC	TCGAG				205

- (2) INFORMATION FOR SEQ ID NO:1105:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

GAATTCGGAC	TTCATGGCCT	ACGTTTTTAT	TACAAATATT	ACATTAAACT	AAAGCTCACA	60
ACTGTTACTA	TGCATCAGGA	ATTAACAGTC	ATTTCTCATT	TGTGTTATTC	TCCTATTTGA	120
TCACATATAG	TGACTATCTC	TTTATGGGTT	AAATATCAGT	TTCTTGGCCA	GAATTCAAGA	180
TCTGCCCCTA	ACNAATCCTA	CTTCTCCCAG	TACCCTTACA	GCACTCCTAC	CCTACTAGTA	240
ACCCTCGAG						249

- (2) INFORMATION FOR SEQ ID NO:1106:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

AATTCTAGAC CTGCCTCGAG ATTGTCTGCC AGTTTAATTC TTTAAAACTC AGTTTAGCTG	60
TCCTTTTCTT TGGAACACTT TCCCTAATCT TCCCCACCAC CTGTTCATCA ACATATATAG	120
AAGCACATTT ACTCTCTCAT TCTCTCTCTT TCTCTCTCCA AGTCTATGTT AGGTGTTTTA	180
GCGTTTATCA TAGGTTTATG TTTACTTATC TCCCCACTAG TCTATGAAAT CCTCGAG	237
(2) INFORMATION FOR SEQ ID NO:1107:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 313 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(wi) CRAHENCE DECCRIPATION, CRAITE NO. 1107.	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:	
GATTTATTAT AAAGCTGCAA AGAAGCTGTT GCACTCAGGA ATGAAAATTC TTAGCCAGGA	60
AAGAATTCAG AGCCTGAAGC AGAGCATAGA CTTCATGGCT GACTTGCAGA AAACTCGAAA	120
GCAGAAAGAT GGAACAGACA CCTCACAGAG TGGGGAGGAC GGAGGCTGCT GGCAGAGAGA	180
GAGAGAGGAC TCTGGAGATG CCGAAGCACA CGCCTTCAAG AGTCCCAGCA AAGAAAATAA AAAGAAAGAC AAAGATATGC TTGAAGATAA GTTTAAAAGC AATAATTTAG AGAGAGAGCA	240 300
GGAGAGCCTC GAG	313
(2) INFORMATION FOR SEQ ID NO:1108:	
/i\ CHOUDNED GUADAGEDIGETGG	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 467 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:	
GCGAGAACAC CATCACCATG ACAACCAGTC ACCAGCCTCA GGACAGATAC AAAGCTGTCT	60
GGCTTATCTT CTTCATGCTG GGTCTGGGAA CGCTGCTCCC GTGGAATTTT TTCATGACGG	120
CCACTCAGTA TTTCACAAAC CGCCTGGACA TGTCCCAGAA TGTGTCCTTG GTCACTGCTG	180
AACTGAGCAA GGACGCCCAG GCGTCAGCCG CCCCTGCAGC ACCCTTGCCT GAGCGGAACT CTCTCAGTGC CATCTTCAAC AATGTCATGA CCCTATGTGC CATGCTGCCC CTGCTGTTAT	240 300
TCACCTACCT CAACTCCTTC CTGCATCAGA GGATCCCCCA GTCCGTACGG ATCCTGGGCA	360
GCCTGGTGGC CATCCTGCTG GTGTTTCTGA TCACTGCCAT CCTGGTGAAG GTGCAGCTGG	420
ATGCTCTGCC CTTCTTTGTC ATCACCATGA TCAAGATCGC GCTCGAG	467
(2) INFORMATION FOR SEQ ID NO:1109:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 74 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:	
GAATTGCGGA AACGGTCGTT CCACTCGCTC CAATGTGGCC CCCAGGCACC TACCTGATAG	60 74
CONTRACOR COMO	, ,

- (2) INFORMATION FOR SEQ ID NO:1110:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

GAATTCGGCC	TTCATGGCCT	AGGAATTTAG	GAACCAAGAT	ACTGGGGTGT	TATTGTTTCT	60
AAGCTCTTTC	AGTGAACAGA	TCTAGGAAAT	ACATGTGTGT	CCTAATCCAT	GAATACACAC	120
TAAAATATAA	TTATTTCTGT	ATCTATGTCA	AGCTAAACCT	AAGTTCACAT	TGAGGTTTCT	180
GACTTTAATA	CAGTCCCACA	AGGTTCGTTC	TAGCTTTCCT	TCCTTGCATA	CCTTTGACTT	240
TCCTCTCCAG	CTGTGGGAAA	CTTGGCTCTC	TCCATCCACC	ACCCCTTCAC	TATTTGTTTA	300
ACCCTTGTAC	DAAATATATA	CAGCGTTGGA	ACTGTCAACC	TGTGTCCCAT	GAGAAACTTT	360
ACCCACTAGA	GTACAGCGTT	TATGCAGTTC	TTTTTGTAGT	TTTTATAGAT	TATAGCCAAA	420
ACTCGAG						427

- (2) INFORMATION FOR SEQ ID NO:1111:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

GGTGAACCCG	AATCACCGAT	GGATGTGGAT	AATTCTAAAA	ATAGTTGTCA	AGACTCAGAA	60
GCAGATGAGG	AGACAAGTCC	AGGTTTTGAT	GAACAAGAAG	ATGGTAGTTC	CTCCCAAACA	120
GCAAATAAAC	CTTCAAGGTT	CCAAGCAAGA	GACGCTGACA	TTGAATTTAG	GAAACGGTAC	180
TCTACTAAGG	GCGGTGAAGT	TAGATTACAT	TTCCAATTTG	AAGGAGGAGA	GAGTCACACT	240
GGAATGAATG	ATTTAAATGC	TAAACTACCT	GGAAATATTT	CTAGCCTGAA	TGTAGAATGC	300
AGAAATTCTA	AGCAACATGG	AAAAAAGGAT	TCTAAAATCA	CAGATCATTT	CATGAGACAG	360
CCCAAACTCG	AG					372

- (2) INFORMATION FOR SEQ ID NO:1112:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

GAATTCTAGA CCTGCCTCGA GCTATACCTG TATCCAGTCT TGATGCACAC CAGGCTGGGC 60 ACTTTCCAGA AACTACCTCT AACCTCCAGG GTTCCCTCAT CACTCGAG 108

- (2) INFORMATION FOR SEQ ID NO:1113:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 base pairs

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:	
GAATTCGGCC TTCATGAAGA TTGAGAAGAA GGAGGAAAAA AAGCCTGAAG ACATTAAGAA	60
GGAAGAAAA GACCAGGATG AGCTGAAACC CGGACCTACA AATCGGTCTA GAGTCACCAA	120
ATCAGGAAGC AGAGGAATGG AGCGGACGGT CGTGATGGAT AAATCGAAAG GAGAGCCCGT	180
CATTAGCGTG AAAACCACAA GCAGGTCCAA AGAGAGAAGC TCCAAGAGTC AGGATCGCAA	240
GTCAGAAAGC AAAGAAAAGA GAGACATCTT GTCGTTTGAT AAAATCAAAG AACAAAGGGA GAGAGAGCGC CAGAGGCAGC GGGAACGGGA GATCCGCGAA ACGGAGAGGC GGCGGGAGCG	300 360
CGAGCAGCGC CAGAGGCAGC GGGAACGGGA GATCCGCGAA ACGGAGAGGC GGCGGGAACGGGA	382
(2) INFORMATION FOR SEQ ID NO:1114:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 253 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D). TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:	
GAATTAGCAA AGGAAATCTC AGATTGCATT TCCAAAGATG GTTGCTAGCT GCTGCCGTTT CCTTTGCTAT TTCTGTCGAA TTAGCCGGCA AAATCAGAAG GCCATGTTTG AGCATCTGAG TTATCTTCTG GAGAATAGCA GTGTTGGCCT AGCCTCCCCG TCGATGAGGG GATCCACCCC GCTGGATGTG GCAGCTTCCT CTGTGATGGA CAACAATGAG TTAGCGCTGA GCTTAGAGGA ACCAGACCTC GAG	60 120 180 240 253
(2) INFORMATION FOR SEQ ID NO:1115:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 76 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:	
GAATTTTTT TTTTTTAAA GAAAGAAAAC TAGGGCGATG CAATGTCCAG ACAGAAGCCG GGGGCCGGGG CTCGAG	60 76
(2) INFORMATION FOR SEQ ID NO:1116:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 70 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
449	

(vi)	CECTIENCE	DESCRIPTION:	CEO TI	NO.1116.
1 X 1 1	SEQUENCE	DESCRIPTION:	SEC II	J N(): 6:

GAATTCGGCC	TTCATGACGA	CCGCGTCCAC	CTCGCAGGTG	CGCCAGAACT	ACCACCAGGA	60
CACCCTCGAG						70

- (2) INFORMATION FOR SEQ ID NO:1117:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 526 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

GAAAATGAAA	AGTTCTGTCT	TTGATGAAGA	CAAAACTTTT	GTAGCAGAAA	CATTGGAAAT	60
GGGTGAGGTT	GTTGAAAAGG	ATACAACAGA	ACTCATGGAA	AAACTTGAGG	TAACCAAGCG	120
AGAGAAATTA	GAGCTGTCAC	AGAGACTGTC	TGATCTTTCT	GAACAATTGA	AACAGAAACA	180
TGGTGAGATT	AGTTTTCTAA	ATGAAGAAGT	TAAATCTTTA	AAGCAAGAGA	AAGAACAAGT	240
TTCATTGAGA	TGTAGAGAGC	TAGAAATCAT	TATTAACCAC	AACAGGGCAG	AAAATGTACA	300
GTCATGTGAT	ACTCAAGTAA	GCTCTTTATT	AGATGGAGTT	GTGACTATGA	CAAGCAGGGG	360
TGCTGAAGGA	TCAGTTTCTA	AAGTAAATAA	AAGTTTTGGT	GAAGAATCAA	AAATAATGGT	420
GGAAGATAAA	GTTTCTTTTG	AAAATATGAC	TGTTGGAGAA	GAAAGTAAGC	AAGAACAGTT	480
GATTTTGGAT	CACTTACCAT	CTGTAACAAA	GGAATCTTCA	CTCGAG		526

- (2) INFORMATION FOR SEQ ID NO:1118:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

CGATTGAATT	CTAGACCTGC	CTCGAGCCGA	CCTACTCCAC	AGCTGTCCTG	ACTGTGTAAG	60
CGAGATGATG	ATTAGTGATC	AGACGAAAGG	ATTCCTGTCA	TTGGTAACCC	TCTCAAAGTA	120
TTTGGAAAAC	AGTTCAATTT	TCATCTATTT	CAGAAGCACG	CCGTGGTGTC	TATTGAGGCT	180
CACCCTCGAG						190

- (2) INFORMATION FOR SEQ ID NO:1119:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

GAATTCGGCC	TTCATGGCCT	ACCATCCTGC	ACTCAACCAA	TCATCTGATG	CTGACTCAGA	60
AGCTCTGTTT	GGAGTACCTA	ATGATAAGAA	TTTACTGTGG	GCTTATGCTG	TTATCGGTAC	120

						100
TTACATGTTC	TTAGTTTCTG	TCATTTTTT	TTGTCTGTTT	TTAAAGAATA	GCTCAAAGCA	180
					ACGCCCTTCT	240
						200
TTGTCTCCTT	TTTCTGTTCT	TCTTTTTTTA	TGTTGGAGCT	GAGGTAACAT	ATGGCTCTTA	300
	mmmaca a aca	CCCATCTCGA	C			331
TOTAL TOTAL	TITICAALLA	CCCMICICOM	G			

- (2) INFORMATION FOR SEQ ID NO:1120:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

GAATTCGGCC TTCATGGCC	T ACAGATTTGC	ATCTTTACAA	CCAGAAGCTC	AGGGAGAAGT	60
TGAAGGAGGA GGAGAACAC	A GTGGGTATGT	TCAGATTGCT	TTTGGGTACC	CTTGATCCAG	120
CCACATTGTC TACCCTAGA					180
TTGAGTTGTA TACCGTCTG					240
TTTTGATGTA GCTGATAAG					300
					352
CTGTCTGGTG TGCTTGAGG	T AATAATAACC	CCTTTTATAC	CCAAACCTCG	AG	332

- (2) INFORMATION FOR SEQ ID NO:1121:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

GAATTCGGCC	TTCATGGCCT	ACCAATCTCT	TTTACTGAGC	ACAATGTGGG	TAAAACTGCT	60
		GTTTTTCCCC				120
		CTCTATCCTC				180
		GTACATCGGA				240
		CCGAAGCAAA				300
		CGCTGGTGTC				360
		TGAGGAAAGC				420
		GTTACAGATC				480
CGAG		•				484
-0.10						

- (2) INFORMATION FOR SEQ ID NO:1122:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

GAATTCGGCC TTCATGGCCT ACTTATGTTT TTCTCATTTG TTGACCTAAA TGATCTTTAT 60

CCAAACTATT CCAAAATCTG AATTTCTGGG TCCTTCTTTC TTTAAAATAT TCTGTTCAAT ATTAAACAAA CAAACGTTTG AGAACATGAG TAACCTTTTG ACTTTATCCC GTATCTGTTT GCTAATGTTC TGTTCCATGT CTTTCTTGTC AGAACACACT GTTGCAGCAG CTAGGAGTGC ACTCGAG	120 180 240 247
(2) INFORMATION FOR SEQ ID NO:1123:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 276 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:	
GAATTCGGCC TTCATGGCCT AGGAGGAAGC TAATAAGAGA CTGTCAAGAT TGTATACCTT CTTGGTTTCT TTTAAGAATT TGTTGCCTTT CTACTATTAC AGCAAAGCAG CATTTTGTTA CTGACTGCCT AAAATCACTT AATCTCAGGT GAACGCATCA CTTGCCAAAC TGTTGGAATG CTATTTGTGT TTTGTTGCAC TGTTTTTTTC GTTTGTTTGT TTGTTTATTT GGTTGGCTTT TTGGAGAGGG AAATTTGGAA ACGGGACACA CTCGAG	60 120 180 240 276
(2) INFORMATION FOR SEQ ID NO:1124:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 252 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:	
GAATTACTAG CAGAGATCAG TGCTATAAGG GAAAAGGAGA TTGATTTGAA AGAAACTGGA AAAAGAGACA TTCCCATGAT GGAGAAAGTA TCAGGAAAGA TGGCTGTTGT TGAAGAAATG GAGGCAGATT TGAAAGAAAC TGGAAAAGAA AATTTTAGAG AGAGAGGATC TGAAGAGATC TGTGTTACTG AGGAAAAGGT GGCAGAATTG AAACAAACTG GAAAAACAGA CATTTCTCCA AGGGCCCTCG AG	60 120 180 240 252
(2) INFORMATION FOR SEQ ID NO:1125:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 317 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:	
GAATTCGGCC TTCATGGCCT AAACAGAATA TTCTGAGGCT AAAAGAAAAT ACACCCCGC AAAAATCAAT ATAACTATGA TTAAGTACAC AAAACATGCA GCCCATAAAA CATATTTCAC CTATGAAACT GAGACTGAGG AATTTAACAG TAAACAGTCA TTTGTTAAAG AAATATTTTT ACAATTTATT GCCTATGTAT AAGGCAGCAG GCCTGTACTC TCTTGTATTT TCAATCTCTT	60 120 180 240

317

ATTCCCCATC CCTCGAG

- (2) INFORMATION FOR SEQ ID NO:1126:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

GAATTCGGCC TTCATGGCCT	ACTTTGTAAC	TGTGAAATAC	TCTCCAGGAT	TTAAAAGGCT	60
GTGGAGCTCC AGATAAAGAA	TCGTTTATCT	TTCTTCTGAA	GAAATTCCTT	TGGTTACAAG	120
TTTACCCCAT AAACGGCAAC	ACACTCACCT	CCATCCAAGA	CAGACTCAAG	GTGGAGGAAG	180
CGTGGAAATG TGCTTCCGGA	CAAAGCTCTC	AGTATCCTGG	GTGCCATTGT	TTCTTCTACT	240
CAGCCGTGTT TTTTCTACTG	AGACAGACAA	ACCCTCAGCC	CAGGACAGCA	GAAGCCGTGG	300
GAGTTCAGGC CAACCGGCAG	ACCTGCTACA	GGTTCTCTCT	GCTGGTGACC	ACCCACCCCA	360
CAACCACTCA AGAAGCCACT	CG				382

- (2) INFORMATION FOR SEQ ID NO:1127:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

GAATTCGGCC	TTCATGGCCT	ACAGACTTCT	GTGTGTGGGA	CTGAAGCACC	TGTTGTGCAA	60
TCTGAAGAAG	CTCTGGTTGG	TCAGCTGCTG	CCTCACATCA	GCATGTTGTC	AGGATCTTGC	120
ATCAGTATTG	AGCACCAGCC	ATTCCCTGAC	CAGACTCTAT	GTGGGGGAGA	ATGCCTTGGG	180
AGACTCAGGA	GTCGCAATTT	TATGTGAAAA	AGCCAAGAAT	CCACAGTGTA	ACCTGCAGAA	240
ACTGGGGTTG	GTGAATTCTG	GCCTTACGTC	AGTCTGTTGT	TCAGCTTTGT	CCTCGGTACT	300
CAGCACTAAT	CAGAATCTCA	CGCACCATCT	CGAG			334

- (2) INFORMATION FOR SEQ ID NO:1128:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

GAATTCGGCC	TTCATGGCCT	AGTCTGTCCA	TCTGCTTTCT	CTGGACCTCC	TTCTCATACT	60
TTGAATTTTT	TAAGTAGTTT	GTCCCTCATA	TGATTTTTTT	TCTATTCCTT	TTTCCCTTCC	120
TGTCCTTCCT	TCACTCCTTT	CCCTCCCACC	TCCCTCCCTC	CCTTCCTCTC	TCCCTTCCTT	180
CCTTCCTTCC	ATCCAACCAT	CCATCCATCC	ATCCATCCAT	CCATCCATCC	ATCCATCTAT	240
CCACTCTCGA	G					251

(2) INFORMATION FOR SEQ ID NO:1129:

(i) S	SEQUENC	E CHARA	CTERIST	ICS:			
	(A) I	LENGTH:	372 bas	se pai	rs		
	(B) 1	rype: n	ucleic a	acid			
	(C)	STRANDE	DNESS:	double	:		
	(D)	ropolog	Y: line	ar			
(ii)	MOLECU	LE TYPE	E: cDNA				
(xi)	SEQUEN	CE DESC	CRIPTION	: SEQ	ID	NO:112	9 :

GAATTCGGCC	TTCATGGCCT	AATTTCATGT	NCCTTTGAGC	TATCTTTCCA	TTTTGTAGGA	60
ACACCGTCAC	AGGAGACAAT	TTCATGGACC	TTTGAGCTGT	CTTTCCATTT	TGTGGGAACG	120
CCGTCACAGG	AGACAATTTC	ATGTGCCTTT	GAGCTGTCTT	TCTATTTTGT	AGGAACGCTC	180
TCAGAGGGGA	CAATTTCATG	TGCCTTTGAG	CTGTCTTTCC	ATTTTGTAGG	AACACTCACA	240
GCAGTGCTTG	GGGTTCACTG	TTACCTAAAT	CCCATGATGG	GTGAGAAGAC	TGAATGGGAC	300
GTTTATTTTT	TGTGTTAAAA	AGCCCACGCA	AATAGAGTTT	AAAATAGTCT	CAGTGAGCTG	360
GGCATTCTCG	AG					372

- (2) INFORMATION FOR SEQ ID NO:1130:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

GAATTCGGCC	TTCATGGCCT	AGTGCCTAGT	TACAAGGTTT	TATTACAGCA	GTATTTCTAA	60
ACATTTGGTT	AGTCTGTCTC	TGCTTTTCCC	ACCATAATTT	TCTAGCACTT	GTAGCTCACC	120
TTATCTCCCA	CTTCCCTTTT	TAAATAGAAA	ACAGGCTTGT	TCTGTTTTGA	CCAGGTATAA	180
CTCTTTGCTC	AGACTGTCTC	TAAAGCCCAG	AAAACTATTC	CTCTAGTGGT	CCAATGAAGT	240
GTTCCCCATT	GAAAGTTTGC	CTCATGTCAC	TCGAG			275

- (2) INFORMATION FOR SEQ ID NO:1131:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

GAAAATTGAG (CCTATGTTGG	AGACACTGGA	GAATCTTTCC	TCTCGCCTGC	GTATGCCACC	60
ACTGATCCCT C	CTGAAGTAG	ACAAGATCAG	AGAGTGCATC	AGTGACAATA	AGAGTGCCAC	120
CGTGGAGCTA C	SAAAAACTGC	AGCCATCCTT	TGAGGCCTTG	AAGCGCCGTG	GAGAGGAGCT	180
TATTGGACGA 1	CTCAGGGAG	CAGACAAGGA	TCTGGCTGCA	AAAGAAATCC	AGGATAAATT	240
GGATCAAATG (STATTCTTCT	GGGAGGACAT	CAAAGCTCGG	GCTGAAGAAC	GAGAAATCAA	300
ATTTCTTGAT	STCCTTGAAT	TAGCAGAGAA	GTTCTGGTAT	GACATGGCAG	CTCTCCTGAC	360
CACCATCAAA (GACACCCCAG	GACTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:1132:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

GAATTCGGCC	TTCATGGCCT	AAAGTTATAC	CAGCTAAAGT	GCAGTAGTGT	CACTTTTTTC	60
CTGTCAATAT	ATAGAGACTT	CTAAATCATA	ATCATCCTTT	TTTAAAAAAA	AGAATTTTAA	120
AAAAGATGGA	TTTGACACAC	TCACCATTTA	ATCATTTCCA	GCAAAATATA	TGTTTGGCTG	180
AAATTATGTC	AAATGGATGT	AATATAGGGT	TTGTTTGCTG	CTTTTGATGG	CTACGTTTTG	240
GAGAGAGCAA	TCTTGCTGTG	AAACAGTGTG	GACTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:1133:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

GAATTCGGCC	TTCATGGCCT	AATCATTATA	ATTTAGTTTG	AATTCTTAAA	ACCCCGTTAC	60
TAGAACTTAT	GTTTAAATTT	ATAAATTATA	AATAGTTATA	TAAATTAAA	AAATTGAGAC	120
TGAGGCAGGA	AAATCACTTG	AACCCAGGAG	GCAGAGGTTG	CACTGAGCCA	AGATCACGCC	180
ACTGCACTCC	AGCCTGGGTG	ACAGTGAGAC	TCCATCTCAA	AAAAAAAAA	AAATTATATA	240
TAAATTCTGG	TAAGTAAGTT	TGAAGAAAAA	CCGATTCAAA	TAGTATATAT	TCAGCTTTAT	300
AAATTCTGTT	AAGCATATTT	GAATGAGAAT	TTATTAAAAT	${\tt GGTTTATATT}$	AAGTCTACGG	360
TTCTCGAG						368

- (2) INFORMATION FOR SEQ ID NO:1134:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

GAATTCGGCC	TTCATGGCCT	ACGTCTGATT	CTCTAAGTTC	ATTTCTTGGT	GGTGGAGGCT	60
CATTTCTTCT	GGAGTCACTG	AAATTTTTGG	GATATCTTTC	GAAGCTTGGA	TCTTCCCTTC	120
GTGCAGTAGG	TCGTGCTTTT	TTCCCCTCAC	TTTGACCAAC	AAAGCGATCC	CGCCTTTCAA	180
AAGATGAAGA	CTGTACTGCT	GAACTCTCAG	GAAACCTGCC	CCTCTCTCGG	TGATCAAAGT	240
CATTAAATCT	GTTCTGTTGG	CGAGAGTAGT	CGGATCCATG	GCCAAATCGT	GCATCTGTAT	300
CTAGAGACAA	CTTTTTATTC	TCGCTCCAGT	AAGGATCATC	TCGCCTATGA	TCTACATCAC	360
GTGGGCGTTT	CAAGGAATTC	CTTTTTTCTT	GTTCATAACG	AAGCTGCTGT	TGTTGCCTTC	420
TGAGTTCCTC	TCTTTCTCGA	G				441

- (2) INFORMATION FOR SEQ ID NO:1135:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:	
GCGATTGAAT TCTAGACCTG CCTCGAGCAA GAAACGTTTT CTAAGTCAAA GGAATAAATC CAAAGCCTCT AAGACTGGGT GAGAGAGAG AAAAGAAATG ACGGAAGCAC TCGAG	60 115
(2) INFORMATION FOR SEQ ID NO:1136:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 253 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:	
GAATTCTGGT TTTACTGAAG CTATGTTAGA AACGTCATGT AGAAACTCTT TAGATACTGA GCTTCAGTTT GCTGAAAATA AGCCAGGCAT GTCTTTGTTG CAGGAAAACG TAAGCACAAA GGGTGACGAT ACAGATGTCA TGCTCACAGG TGACACTTTG AGCACCTCAT TGCAGTCTTC CCCAGAAGTG CAGGTACCTC CTACCTCCTT CGAAACAGAA GAAACGCCCC GTCGGGTACC CCCAGATCTC GAG	60 120 180 240 253
(2) INFORMATION FOR SEQ ID NO:1137:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 339 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:	
GAATTCGGCT TCATGGACGA GGAGATCGTG TCCGAGAAGC AAGCCGAGGA GAGCCACCGG CAGGACAGCG CCAACCTGCT CATCTTCATC CTGCTGCTCA CCCTCACCAT TCTCACAATC TGGCTCTTCA AGCACCGCCG GGCCCGCTTC CTGCACGAAA CCGGCCTGGC TATGATTTAT GGTCTTTTGG TGGGCCTTGT GCTCCGGTAT GGCATTCATG TTCCGAGTGA TGTAAATAAT GTGACCCTGA GCTGTGAAGT GCAGTCAAGT CCAACTACCT TACTGGTAAA TGTTAGTGGA AAATTTTATG AGTATATGCT GAAAGGAGAG ATACTCGAG	60 120 180 240 300 339
(2) INFORMATION FOR SEQ ID NO:1138:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 363 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
·	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

GAATTCGGCC TTCATGGCCT	AATTCAGAGG	TGGTGGGACC	TTGGCTATGA	TTCTGTTCAA	60
GCCCCCTAAT TTTACAGATT					120
TCATAAACAG GAAAAAAGGA	GAGCCAGGAA	AGAACTCAAT	TGTTGTAAAC	TGCTGTCTTG	180
TCTTGATGTT CTGTCTTCAT	TCATCATCCA	GCCTTTCCTA	GGAGTGTCAG	AGATAGACCC	240
AGGTAGAAGT GGGCTGCCCA	TGGGGGGCTT	AGCACAACAG	AAATTTATTC	TTTTACTGTT	300
CTGGAGGCCA GACATCTAAA	ATAAAGGTGT	TGATGGGGTC	ATTCTTCCTC	TTGAGGGCTC	360
GAG					363

- (2) INFORMATION FOR SEQ ID NO:1139:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

GAATTCGGCC	TTCATGGCCT	ACTTGTAGAA	TATTGAGCAA	TTTGTGTGAA	GTGGGGAAGA	60
				AAATAAAAT		120
				CCCGTTCTGC		180
				CTGCAAGGTC		240
				CTGAATCTAG		300
				GCTCCCGCTC		360
	CCCGAAGGCA	IIMINCCCOO	10.0001010			367
TCTCGAG						

- (2) INFORMATION FOR SEQ ID NO:1140:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

GAATTCGGCC	TTCATGGCCT	ACACCCTCAC	CACCCAAGGG	GTCATCATCT	CTGGCCACCA	60
				CCTCCCGCTC		120
CGGAGCCTCC	GCATTGCCCC	CACCCCCATT	TTCCAGGGGG	GTTGTAATTT	ATAAGCTGAC	180
GAAGGTAGCC	AGACTTCCGG	AGGACTGACC	ATCTCTCACT	GTCCTCCCCA	CCTTCTTCCT	240
				TTCTGTTTAT		300
TGTCTCTCTC	TATTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGG	360
TGCAGGAGTG	CCACCCCCAG	GGCCTCGAG				389

- (2) INFORMATION FOR SEQ ID NO:1141:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

GAATTCGGCC	TTCATGGCCT	AGCAGCACTA	ATCTTGATGG	GACAGAAAAT	TTCAAATGAA	60
GAGCTTTCCC	TCTTTTTTTC	TTCCTTGGGG	GCATGCCAGC	TTGTGCTTCT	ATGTCAGTAG	120
CCTTGTAGTT	GCCATTCCTG	GCCCAGACAC	TTGCATGCAG	TTTGGTTTGT	CCTCCACCAC	180
TTTGATCATG	TTGCCCATGG	TCTAGACACC	TCCGTGTCCT	TGTTATCATG	GCATATAGTC	240
TGTATGCCTC	TGCTGGATTT	ATAAGCGGCC	CCATAATAGC	CTTCCTTTCT	GGTTACCCCC	300
TTGATCTCGA	G					311

- (2) INFORMATION FOR SEQ ID NO:1142:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 530 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

GAATTCGGCC	TTCATGGCCT	AAAAGATCAG	ATTTTGTCAT	TTAAGACACA	TATTTTACAT	60
TCAAAAATGT	AAAGTCAGGG	TGTGTCTTAA	AATCCATTGG	TGTTTTAATC	ATGCTTAAAC	120
ATGTGACTGC	TGTTGGCCAG	GATACAGTTG	TGGTGGTGTC	GTCAGTATCT	GAGCACATGT	180
GAACTTNGCC	ATGACTATTC	ATATTGTCTT	CTCTTAAACT	GAATTATGTC	CATGGTTGCC	240
AACATGTACT	GTCCATAGTT	GCCACCATGT	ATTTAGGTTG	TCATTTAAAA	TGTCCTCAAA	300
AAGATTTCAC	CATGATTCTC	CATCAAAATA	GAAAGCTATT	TTGTATGAAG	AAGAACTCAG	360
ACCAGAAAAG	TCTGATAAAA	ATAATCTCTT	AAATAAGTCT	ACATTAGGTC	TTTCAATTTG	420
TATAAAATGT	AAATTTTGAA	TTATAAGAAA	ACAATTTGTT	ATACTGTAAT	TGGTAGCATT	480
TTTTCTTAGT	AGTGTACAAA	ATAATGTGTA	CCTTACATTC	AAATCTCGAG		530

- (2) INFORMATION FOR SEQ ID NO:1143:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

GAATTCGGCC	NNCATGGCCN	ACCTATGTNA	NGNATTTCNN	CTCCATTINC	CCNAGGGTTC	60
TTTCCTGTTC	TTAGAAATGT	TTTGTGATTT	TGCTTCAGAC	ACAGTTTGTC	TACTTCTNGT	120
AAGCATTGTT	CTTAGATNGC	TGGCTTTATA	TCTATCACTC	CCTTGCTCAT	CTGCCCATCC	180
ATCTATCCAT	CCATCCATCC	ATCCATCCAT	CATCCCTCCA	TCCACTTGCT	CATCTGCCCA	240
TCCATCCATC	CATCTATCCA	TTCATCCAGT	CCATTCACCA	CCCACCATCT	ATTATCCATC	300
CATCCATCCA	TCCATCCATC	CATTCATCCA	CTCACCCATT	CATCCATCAT	CCATCCACTC	360
ANCCATCCAT	TCATTCAGTC	ACCCTTCATC	CATTCACTCA	CCCATCCTTC	CATCCACTCA	420
TCCAATCACC	CATCCATCCA	TACATCCACT	CATCCATTCA	CCATCCATAC	ATCCACTCAT	480
CCATTCATCC	ATCCATCCAC	CCACCCAGAC	GTCCGTCCAT	CNATCCATCC	ATCCATNCAT	540
CCTTCTATNN	NNTCTGCCAA	CAATCCANAC	ACNTGTCCNT	CNATCCCTTC	CAACCACTCA	600
CCCAGCACAC	TCGAG					615

- (2) INFORMATION FOR SEQ ID NO:1144:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

57 GAATTCGGCC AAAGAGGCCT AACCGCGGCC GCTACTTCGG CCTCTTTGGC CCTCGAG

- (2) INFORMATION FOR SEQ ID NO:1145:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 227 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

GAATTCGGCC	TTCATGGCCT	AGGTTTTCTT	TTATTTAAAA	GATCATTCAC	AAAATACCAT	60
ATCCATAGAT	TTACTTTCTG	TCATATAGCT	GAATGTGTTA	AGTGTTTGGA	ATTCCATTCT	120
TACATTTAAA	GGTCAACTGG	ATTGCCCAGC	AGTTTAGATG	CATGTGTTTT	GTTCTTTATC	180
TTATCCACAT	TGAAGATGTA	AGTATTGAAT	TCTAGACCTG	CCTCGAG		227

- (2) INFORMATION FOR SEQ ID NO:1146:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

CTCGAGTATC	TCCTCCTTTC	TGATATCCAG	TTTAGGTGGT	CCAATTTTTC	CATCTCGGCA	60
TACAGCAAAT	TCTTCTGACT	TTGCATAGGC	AGATTCTTTT	TGTCCAACCC	TGGCTTTAAC	120
TCTGACCCAA	AGAGAATTTG	ATGGATCACC	AACATGATCA	GAAATATTAC	AATAATGATG	180
AGAAATATTG	ATGCAGGCAT	CAATCCATTC	TGAATTCTTA	ACACCATAGT	TCTTTACCTC	240
TACGGTAAAA	ACAGGGACCT	GTGGCATGAT	CTGGTACTCC	CAATATACGA	TAGGGTTCAT	300
GTTATAGGAT	TCAATTGTAA	CATTAGTTGG	TGTAGGCACT	GAGGACGGCC	CCAGATCCGC	360
GGTGCCCATC	TCAGCCCTGC	TCACACCCTG	CATGACAAGG	GGTAGGAGAA	AGAGGAGAGC	420
CATGCTGCTA	CCGACGGTCG	CTGGCTC				447

- (2) INFORMATION FOR SEQ ID NO:1147:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 271 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

GGGCGCCATG TTTGCCATCT CAGGTCCAGG TTTCTCCCGG ACTTCGAAGA GCTCATTATC GGGTCTGATT TTCAGCTCCT TCTGCAGAGT CTTCCGGAGC TCCAGCATC GCTGCTGCAT CTGCTTTATG GTCTTATTTT TCTCCAGAAG TTGCTGCTC AAGTCCTGTT TCTCCTTCTG TAGCTGTGT AGATCCATGG CCCCAACCTC ACCATTTGGT GTTCTTCCTG CAGTTGGAAG CTGGAACACA GGGTCCTGCA TGGCCCTCGA G	60 120 180 240 271
(2) INFORMATION FOR SEQ ID NO:1148:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 298 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:	
GGATTGGGGA GGGAGTGTGC GAATAGGTGT GGGTGACAGA CATCAAGTAC TTAACAGGGT AATAGAATAT CACAAGGCAA GTGGAGGCAG GGCGAGATCA CAGGACCACA GGACCAAGGC AAAATTAAAA TTGCTAATGA AGTTTTGGGC ACCATTGTCA TTGATAACAT CTTATCAGGA GACAGGGTTT GAGAGCAACC GGTCTGACCA AAATTTATTA GGCGGGAATT TCCTCCTCCT AATAAGCCTG GGAGCGCTAT GGGAGACTGG AGTTTATTTC ATCTCTGCCT GCCTCGAG	60 120 180 240 298
(2) INFORMATION FOR SEQ ID NO:1149:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 332 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:	
GAATTCGGCC TTCATGGCCT ACGGCATTTC AGCGTCAAGT GCACTTAGCG GGGTACCCGG CTCCCCCAGC CCCCACACCC GTCCTGGGTC TCAGGGTGGT TCCAGCTTCT CCTTGGGCAG CCAGAAGTTG GAGTCCCATC CCCCANNGNA NATTTTTTTT TTTTTTTTT TGTGATCAGG GAGTGTGTCC AACGTAGCCC CCTGGCCTGT GCAAGCCCTG ACTCCCTCAT GGTGCCTCGG AGAGTGGGGA GCATATTGGG CTGGGGTAAG CACTAGACCC AAGTAGACTG GACACAAAGG GCTCGCCCAG GGCCCTGGCG CCACCCCTCG AG	60 120 180 240 300 332
(2) INFORMATION FOR SEQ ID NO:1150:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:	
GCGAGGCAGG GAAACTCACT TCACGTCTCT TTCCTTGTAG AGCATCATGC TTATTTCTGG CTCACTCACA TCTTTGTCTC GGGAGTTCTC TGCCGAGCCA TTGCCCCCTA CAGCAGAGAG	60 120
CACAGCTGGC TGCACTAGTG CTGAAGGAGC CAGCCCCAGA GCAGGGCATT TCCAGGGGCT	180

CTTGTCCCAG	AGCGGCAGGC	GTTGTGTGCA	GAGAACGCCC	CTCCCACGCA	GCACAGAGAA	240
					CACCGCCGAC	300
					TGTTTTGTTG	360
	GACGGGCTTG					400

- (2) INFORMATION FOR SEQ ID NO:1151:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

GAATTCGGCC	TTCATGGCCT	ACCCAGACAA	ATACCAAGTT	TATTTCACAA	ACACTAGGAA	60
GATGGGTTGA	GGGTGGAGGT	GGGGGACACA	GGTGCGCAGC	TGCACAGAGT	CAGCAGCAGC	120
	CCGCACTGAG					180
	GTGCAGGGAG					240
	CCCAGGAAAA					300
	TCACCCATCT		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			329
TATCATCIAG	TUACCUMICI	ICACICIOG				

- (2) INFORMATION FOR SEQ ID NO:1152:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

GAATTCGGCC	TTCATGGCCT	ACCCATAGCC	ATGAGCATGA	CTGGCTGCCA	GCTCTTAGTC	60
ACCAAATGCC	ATTCTCCGCT	GAAAGAAGCA	AGGGCTTTTC	AGAGAATAGA	CTGAGCACAA	120
AAATGACAAT	GGTAATGGAG	TAGAACACCT	TGACTTTTAA	AAGTCCACGA	GTCCACAGTG	180
	GAAGTAGGGA					240
AAAAGGAATG	ACAAAATGAA	AAATCACCAT	ATTGCAACTC	TCAATAAAGT	AACTGATTCA	300
GGCATATCTC						313
GGCWINICIC	CAC					

- (2) INFORMATION FOR SEQ ID NO:1153:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

GGGCTCCTCG	CCAAGGAACT	CGTGGCAGAA	GAGGGCAGCA	GTTGGCAGTA	GCTGCCGATG	60
	GCTCCACCAT					120
	GTGTCTGCCC					
	CTCTCCCCTG					

TGGGATGGGC CCCCATGAAC TGCAGCAGCA TGCTGAGGTG TCCATGTTGT CTGCCTTTGT ATAAAGAAAC AGCCTCTACT CGAG	300 324
(2) INFORMATION FOR SEQ ID NO:1154:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 327 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:	
GCGAGTTCAG CGGAGAAAAG AAAAAGCAAC GTTTAATTCT AGAAGGCCTC CTGTCCCTGC CTGCTCTGGG TGCTCATGGA ATCAGCTGCT GCCCTGCACT TCTCCCGGCC AGCCTCCCTC CTCCTCCTCC TCCTCAGCCT GTGTGCACTG GTCTCAGCCC AGTTTATTGT CGTGGGGCCC ACTGATCCCA TCTTGGCCAC GGTTGGAGAA AACACTACGT TACGCTGCCA TCTGTCACCT GAGAAAAATG CTGAGGACAT GGAGGTGCGG TGGTTCCGGT CTCAGTTCTC CCCCGCAGTG TTTGTGTATA AAGGTGGCGC ACTCGAG	60 120 180 240 300 327
(2) INFORMATION FOR SEQ ID NO:1155:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 504 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:	
GAATTCGGCC TTCATGGCCT ACGAGCCCTT TGCCTCAGT AGTCCCACCT TTCTGGACTG AACTGATATT CACCTTACAC AAATGGATTG ATGTCTCATG TCTCCCTAAA ATGTACAAAA CCAAGCTGTG CCCCACCACC TTGGGCACAT GTCATCAGAC CTTCTGAGGC TGTGTCACGG GTGCACGTC TCAACCTTGG CAAAATAAAC TTTCTAAGTT ATCTGAGACC TGTCTCAGAT TTTTGGGGTT CACACACCAT ATGTCTGAAT ACTGTCTTTT CCTATCTCTG GCTCCATCCC ACATTGTAAG GGGCCTTGCA CACACAAATG TGGACATTCC AGCCTGCACA CCTAAGCATC GCCTCCACTC CCACCCTTCC AGCGGATGGG TGTGAAAACT GGCAGTGTTG TTCATCTTCA AGATGATGTA TACAGGAAAG TGGTCCAGGC AGATCCTGTG AGCAGGCTTG GGCCCACTTG GGAAGAGTAA CCCAGGATCT CGAG	60 120 180 240 300 360 420 480 504
(2) INFORMATION FOR SEQ ID NO:1156:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 686 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:	
GNNNNNNNN NNNNNNNNN TTCCCCCTTN TNNCATGTTT TGTTCCTTTN TCCTTGTTTN TTTTTTCGGC AAAATATTTC AAGNTATACC CAGGCAACAT NAANTCCAGT TCGGATTTTA ATTAGTCGAG TATGCAGCGT CTTTTCATTT TTATTACTCA AAAAAGTTTC ATTTTTTTAT	60 120 180

TTAGCTTTCT GACTCTGTGC TTGTGCCTTC AACACTTTCA CAACGATTTT CTGCTCCTCG ATAAGGAAAG CACGCTTGAT CCTGTCACGA ACACATTTAG CACACATTGG ACCACATAG GCCCTGCTGA CATGTTTCTT TGTTTTGGAC AATCTCATAA GAACTTTAGG TCTTACAGCA CGAACCCCTC GAAGTCTGCC TGGGCACACA CCACATGCAG ATTTTGGTGC TTTCCCAACC TTCTTGGTAT AAAGGTAAAC AATTCTATTA CCAGGGGTTC GGGACAGCCT AGTTTTGTTA GAGGCTGTAT TGTAGGAAAG CCTACGTCGG TATGTCAAAC GCTGGACCAT TCTGAGTGCC TGCAGACAAC CAAGGGTGAC TATAATGACA GCGTGCAAGT TGTGGACTGT GGACTAAGTC TGAATGATAC TGCTTTTGAG AAAATGATCA TTTCAGAATT AGTGCACAAC AACTTACGGG GCAGCAGCAA GACTCACAAC CTCGAG	240 300 360 420 480 540 600 686
(2) INFORMATION FOR SEQ ID NO:1157:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 274 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:	
GCAATTTGCT TTTTTAAAAA TACATTTTCA TACACTAAGT TTTCTGTTAG CCTAAGTAAT TATATTTCTA ATTAACTTCA AAGTAATTGA TAGGTGGCAA AGGATATCAA TCAAAACCAG TCCAAGTAAA AAATGTACAC TAATTTAATA ACAATATTAT TCTATATTAC TTTTTTTT	60 120 180 240 274
(2) INFORMATION FOR SEQ ID NO:1158:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 196 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:	
GAAGATGGAC AACCGGGATG TTGCAGGAAA GGCTAACCGG TGGTTTGGGG TTGCTCCCCC TAAATCTGGA AAAATGAACA TGAACATCCT TCACCAGGAA GAGCTCATCG CTCAGAAGAA ACGGGAAATT GAAGCCAAAA TGGAACAGAA AGCCAAGCAG AATCAGGTGG CCAGCCCTCA GTCCCCACAT CTCGAG	60 120 180 196
(2) INFORMATION FOR SEQ ID NO:1159:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:	

60

120

GAATTCGGCC TTCATGGCCT AGAGGTGAAA TACAGAAAGC CTTTTTTCT TGATCTTTTC

CCGAGATTCA AATCTCCAAT TCCCATTTGG GGGCAAGTTT TTTTCTTCAC CTTCAATATG

•	AGAATTCAGC GAACCCTCGA G	141
	(2) INFORMATION FOR SEQ ID NO:1160:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 355 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:	
	GAATTCGGCC TTCATGGCCT AGTAATATAT ATAATTTATA AGTAAATATA AATTAGGGAG GTGTACTCAA CATTTTCATA GAATACATAG TCAAAAATGG TTTGCAACCT CTGCCTAACA AAAATAAAAC ACCCTACATC TTTGGTTCAA GATTGTCACC CCCAACAGTT GTGTGAAATG TGGGGCAGGA ATTATCACTA TTTTCCTTTG GAAATTAAGG TTCCAAAGAT AATGAGACCA GAGCCAAAGG TCAGAGTCCA CTGTCTTCTC TCTGAGGCCT CAATGTGAAG ACCTGAACTG TGGCAGCAGA TAATTCTGGA GACCTGTTAA TCAGCTGTAT GCACCACAAC TCGAG	60 120 180 240 300 355
	(2) INFORMATION FOR SEQ ID NO:1161:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 257 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:	
	GTATTTCATC ATATAATTT CTTCGAATTG GGAATTTAGG CAGTATGTTA TGGGATTTTT TTTTTAATTT ATTTTTTTT TTTTTAGGAA GCTTGTTTCT CTTTTGCATT TATAGAGAGC ATGTTTATAT TAAAGAGTAC CTTCCATACT ATAGAACACA TTTGTGGGTG GATTCGGTCC TTTTCTTTCT ACCCTCCTG ATTGCTGCTA ACAATCCAGA AAGACAGAAA TTTTGTTTTC ATTCAGGCAC ACTCGAG	60 120 180 240 257
	(2) INFORMATION FOR SEQ ID NO:1162:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 220 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:	
	GAATTCGGCC TTCATGGCCT ACTGTTTCCT TGCCCTTTTC ACCGTCTGGT GGTTCCCTGC AGCCCTTGGC TTGTGGCCCT CTCATCCATC TTCCGAGCCT AGCACTCCAG TCTCTGCTTC TGTCATCACA TCGCCTTCTC TTGAGAAAGA TCCCAGGCTG GTATTTAAAT TGCCTGTTGG CAGGAACTTT GCCTGTCTC CCCTACCCCC ACAGCTCGAG	60 120 180 220
	(2) INFORMATION FOR SEQ ID NO:1163:	
	(i) CENTENCE CUMPACTEDICTICS.	

(A) LENGTH: 405 base pair	's
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ 1	ID NO:1163:
(MI) Dagodina Dabonitilion. Dag 1	10.1100.
GAATTCGGCC TTCATGGCCT AATCACTTGA GGTCA	GGAGT TCATGACCAG CCTGGCCAAC 60
ATGTTGAAAC CCCATCTCTA CTAAAAATAC AAAAA	
TGTAGTCCCA GCTGCTAGGG AGGCTGAGAC AGGAG	
GTTGCAGTGA GCGGAGATCG TGCCACTGCA GTCCA	
TCTCCAAAAA AAAATTAAAA ATAGAAATAC ATTTT	
TAAGGGACAA TTGCAGTTTG GAAGGTACTT CCACA	
AATGAATCTC ATTTGGTTGT CATGAAATTT GGCAA	GCTTC TCGAG 405
(2) INFORMATION FOR SEQ ID NO:1164:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 259 base pair	^ s
(B) TYPE: nucleic acid	.•
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) ToPoLogi: Timear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ :	ID NO:1164:
GAATTCGGCC TTCATGGCCT AGCAGAAGCG AGAGG	AGGAG GAGAAGAAAG CGGAGTTCGA 60
GCGGCAGCGA AAAATTCGAC AGCAAGAAAT AGAAG	AAAAA CTCATCGAGG AAGAAACAGC 120
ACGAAGAGTA GAAGAATTGG TAGCAAAAAG GGTGG	AGGAA GAACTGGAGA AAAGGAAGGA 180
TGAAATTGAA CGAGAAGTTC TCCGAAGGGT GGAGG	AAGCC AAACGCATCA TGGAAAAGCA 240
GTTGCTCGAA GAACTCGAG	259
3.200.000.00	
(2) INFORMATION FOR SEQ ID NO:1165:	
(2) Information for day 15 no.1105.	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 114 base pair	LS
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ	ID NO:1165:
GAATTCGGCC TTCATGGCCT AAATTTCAGC AATAC	CAGCTC TCACATACAT AAATTATAAA 60
ATAATTTAT TTAAGGTGAT GAAATTTATA AGCAG	GGTTCA AAAATATAAT AAAA 114
(2) INFORMATION FOR SEQ ID NO:1166:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 316 base pai	rs
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(11) MOLECULE TYPE: CDNA	

(xi) SEQUENCE	DESCRIPTION:	SEO	ID	NO:1166
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GAATTCGGCC	TTCATGGCCT	AGTCAGCAAC	ACCCAACACT	GTCTGTTTTC	CATTTGTTGG	60
TTTTAATCAT	AAAATTGTCA	AGTGATTCGT	GTTTGTACTT	TATTTTTTTG	TGCCTTCTGA	120
AAGGATCTAA	AACAAAAATA	TTTTGCCTTT	TTTTCCCCAC	GTGTATCTGA	ACATTAAGCA	180
GATTGGCTCA	GACACAATGA	AAAGGATAAT	CCAATGTACG	TGCTGGTGCA	CTCTGCTAGT	240
TGTTATCTCT	GTAGGGCTCA	GGAAGCTGGA	AGGAGGAAGG	GAGGGTAAGT	GGCCTGGTGA	300
GTGGAGGTGG	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:1167:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

GAATTCGGCC	TTCATGGCCT	AGGTACCAAT	AATTTCTTCA	CTTCTTCAAC	TGCTCTCTTC	60
AATTTGATTT	CTGCTCTGTT	CTGAGCATCT	TCCACAGTGA	TTAGTACATG	TAAATCTTCA	120
TTTAGATGCT	CCCAATTGGG	CTTGCCTCTA	TTTTGCTCCT	CCTTTTTTTT	ATCCCTCATT	180
GAGCCTTTGC	CTCGGACCAT	GATTTTACAT	CCGGTTTCTG	CTTCAAGTTG	TTTGGCTGTA	240
AGTCCTCTAG	GTCCAAGGAT	TCTCCCAACA	AAATTAAACT	TCGTCCAGCA	GCCGCTCGAG	300

- (2) INFORMATION FOR SEQ ID NO:1168:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

GAATTCGGCC	TTCATGGCCT	ACCTTCACAG	AAAAATGCAT	AGCTGGATGC	TGCAGACTCT	60
AGCGTTTGCT	GTAACATCTC	TCGTCCTTTC	GTGTGCAGAA	ACCATCGATT	ATTATGGGGA	120
AATCTGTGAC	AATGCATGTC	CTTGTGAGGA	AAAGGACGGC	ATTTTAACTG	TGAGCTGTGA	180
AAACCGGGGG	ATCATCAGTC	TCTCTGAAAT	TAGCCCCCCC	GATCTCGAG		229

- (2) INFORMATION FOR SEQ ID NO:1169:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

GAATTCGGCC TTCATGGCCT AGTGCTGGGA GCGCAGCCGG CGGGCGAGGC TGCCTGGAAC
GTGGAGCTGC TGGAGCTGTC CGGCTGACCT GGAAAGTTCT TTGGCCTCTA GGCTTTACCT
120

GGAGGCCTCT	TCCTTCAGCT CCTTGTTTTT CCGCACCTCC TCGGCGTG	CT TGTCCTTCTC	180 240
TTGCAGCCGT	TCCAACATGG CGGCGAGGTG GGCCTCCCTG TTCTCCTT AGTTTTTCCT TAGCCATCTT GATGAAGTTG TTGTTTTC	CT TGGATICCAT	300
TTGGATCACC	TCTCTCTCAT GTTCCCGGAA TTCTAGACCT GCCTCGAG	;	348
	ATION FOR SEQ ID NO:1170:		
(i)	SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 81 base pairs(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: double		
	(D) TOPOLOGY: linear		
(ii)) MOLECULE TYPE: cDNA		
(xi)) SEQUENCE DESCRIPTION: SEQ ID NO:1170:		
GGCTTTTTCC	C AAATTGCTCT GGCTACCATA TAGAAAATTG ACTGAAGG	EAG GGCCAAGATG	60
GAAACAGAGA	A GGACGCTCGA G		81
(2) INFORM	MATION FOR SEQ ID NO:1171:		
(i)	SEQUENCE CHARACTERISTICS:		
. ,	(A) LENGTH: 418 base pairs		
	(B) TYPE: nucleic acid		
	<pre>(C) STRANDEDNESS: double (D) TOPOLOGY: linear</pre>		
	(2) 10102011 111021		
(ii	.) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:		
ar remanda r	G GGACTAACTA CGACCATGAG ATTGGCAGTG ATTTGCT	TTT GCCTATTTGG	60
CATTGCCTC	C TCCCTCCGG TGAAAGTGAC TGATTCTGGC AGCTCAG	AGG AGAAGAAGCT	120
TTACAGCCTC	G CACCCAGATC CTATAGCCAC ATGGCTGGTG CCTGACC	CAT CTCAGAAGCA	180
GAATCTCCTT	T GCGCCACAGA ATGCTGTGTC CTCTGAAGAA AAGGATG	ACT TTAAGCAAGA	240 300
AACTCTTCC/	A AGCAATTCCA ATGAAAGCCA TGACCACATG GACGACG T GGAGACCATG CAGAGAACGA GGATTCTGTG GACTCGG	ATG ATGACGATGA	360
TGATGACGA:	T GGAGACCATG CAGAGAACGA GGATTCTGTG GACTCGG T TCCGATGAGT CTGATGAGAC CTTCACTGCT AGTACAC	CAAG CAGTCGAG	418
(2) INFOR	MATION FOR SEQ ID NO:1172:		
(i)) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 431 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: double (D) TOPOLOGY: linear		
	(b) Topologi: Timear		
(i:	i) MOLECULE TYPE: cDNA		
(x.	i) SEQUENCE DESCRIPTION: SEQ ID NO:1172:		
GAAAACAGC	CA CTGCATGTCT TTGGCAAGCC ACAAGTTTCA TAGATA	CAGC TGTGCTCACT	60
GCAGAAAGC	CC TTTTCATAAG ATAGAAACAT TGTACCGACA TTGCCA	AGAT GAGCATGACA	120 180
ATGAGATAA	AA GATTAAATAC TTCTGTGGGC TTTGTGATCT TATCTT AG TCATTATGAG GAGCACCACA GCATAGATTA TGTATT	TGTG TCAGAAAAAA	240
CTGAAACTI	AG TCATTATGAG GAGCACCACA GCATAGATTA TGTATT TC AATTAAAACC GAAGATGATT TTCCAGTAAT AGAGAC	CAGT AACCAGTTAA	300
CTTGTGGTT	TG CCGTGAGAGT TACATCTGTA AAGTCAACAG AAAAGA	AGAT TATAGCAGAT	360

420

GTCTCCAAAT CATGCTGGAT AAAGGAAAAC TGTGGTTTCG CTGCAGTTTA TGTTCGGCAA

431

CAGCACTCGA G

(2) INFORMATION FOR SEQ ID NO:1173:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 319 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:	
GAATTCGGCC TTCATGGCCT ACCCCTTAAA GGAAAGAATG GCTGCTCTAG AAGAAAAGAA	60
TGTTTTAATT CAAGAATCAG AAACTTTCAG AAAGAATCTT GAAGAATCTT TACATGATAA	120
GGAAAGATTA GCAGAAGAAA TTGAAAAGCT GAGATCTGAA CTTGACCAAT TGAAAATGAG	180
AACTGGCTCT TTAAT.GAAC CCACAATACC AAGAACTCAT CTAGACACCT CAGCTGAGTT	240
GCGGTACTCA GTGGGATCCC TAGTGGACAG CCAGTCTGAT TACAGAACAA CTAAAGTAAT	300
AAGAAAACCA AAACTCGAG	319
(2) INFORMATION FOR SEQ ID NO:1174:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 171 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:	
GAATTCGGCC TTCATGGCCT ACTTAATATA TTTGTGAGAT AATTATTGAG ACATTTTATT	60
AATATTTTAT TTAGTCTTAG AATTTCAGAG AAAAGTGAAC CTAGAGAGGT ACTTCTCCTG	120
GTTCAAACTG TGAACATGAA AATTCTGAAT TTAAGTAACT GGATCCTCGA G	171
(2) INFORMATION FOR SEQ ID NO:1175:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 366 base pairs	*
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:	•
GAATTCGGCC TTCATGGCCT AAGGAAACAA AAAGCTAAGG GCAAAATGTA CAAACTTAGA	60
AGAATTGGAA GATAGAAACA AGATAGAAAA TGAAAATATT GTCAAGAGTT TCAGATAGAA	120
AATGAAAAAC AAGCTAAGAC AAGTATTGGA GAAGTATAGA AGATAGAAAA ATATAAAGCC	180
AAAAATTGGA TAAAATAGCA CTGAAAAAAT GAGGAAATTA TTGGTAACCA ATTTATTTTA	240
AAAGCCCATC AATTTAATTT CTGGTGGTGC AGAAGTTAGA AGGTAAAGCT TGAGAAGATG	300
AGGGTGTTTA CGTAGACCAG AACCAATTTA GAAGAATACT TGAAGCTAGA AGGGGAAGGA	360
CTCGAG	366
(2) INFORMATION FOR SEQ ID NO:1176:	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

GAATTCGGCC	TTCAGGCCTA	CAAGAATTTT	ATGCCATCCA	AGAGTATTAG	CACAAATAAA	60
TAAAGGCAAT	TTGTAAATTT	TTTCCCTGAA	AATCTAAAAA	ACAAGAAAAC	TATCTCTTCA	120
					AGAATCTATA	180
GTTGGAAATA	CTTATTTTAA	AATGTTCAGG	CAGTTGCTCG	AG		222

- (2) INFORMATION FOR SEQ ID NO:1177:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

GAATTGTCCA	CAGCCTGTCA	TGCCGCACAA	CTGTCCACGC	TCGGTTCTCT	CGGATATCAC	60
		AGGGGGCCAC				120
		TAAGCCTCAC				180
TOTOTITIES	GTAGCCCGTC	AGTTCGCAGT	AGCAAATGAA	GTCATCCCAA	GACTGGTAGC	240
ACCOMOCATO	ATCCTCACAC	ATGTTAGGGC	TGCACCTATC	AGTGATGCCA	CATGTATCAA	300
					TTGACCAGTT	360
	AGCATAGAAT	CCAAGCCGCC	GGCCCICCAC	Choholado	110	367
GACCGAG						3 0.

- (2) INFORMATION FOR SEQ ID NO:1178:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

- (2) INFORMATION FOR SEQ ID NO:1179:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:	
GAAACCGAAA GTGGAAATGT ACTCTGGGAG TGATGATGAT GATGATTTTA ACAAACTTCC TAAAAAAGCT AAAGGGAAAG CTCAAAAATC AAATAAGAAG TGGGATGGGT CAGAGGAGGA TGAGGATAAC AGTAAAAAAA TTAAAGAGCG TTCAAGAATA AATTCTTCTG GTGAAAGTGG TGATGAATCA GATGAATTTT TGCAATCTAG AAAAGGACAG AAAAAAAATC AGAAAAAACAA GCTCGAG	60 120 180 240 247
(2) INFORMATION FOR SEQ ID NO:1180:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 149 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:	
GAATTCGGCC TTCATGGCCT ACGAGTTCTT CATGCTTGTT GTTGAGATTT GAGATGTTTA TTGGTAACAT TGTCTTTTTT CCATCCTTTT TTTTCTTTCC TAACCTGGTT TCTTCCAGTG CAACTGCAGA TAGAAGACCT GACCTCGAG (2) INFORMATION FOR SEQ ID NO:1181:	60 120 149
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 251 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:	
GAATTCGGCC TTCATGGCCT AGAAAATTAA ACTGTTTTTT AAACCAGGTG TTCACTTTTC ATTGATTTTT GCATAGTACT TGGTGAACCC TATTGATTTT TAGATTCAGG TAATTTTTCA GTGTGAAAGA GTTTTTCTGT TATATCTTCA CTGTGATATC CATTCCATTC	60 120 180 240 251
(2) INFORMATION FOR SEQ ID NO:1182:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 176 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:1182:	

PCT/US98/06955 WO 98/45436

GAATTCTAGA CCTGCCTAGA GTGCTCTGTG TATGCGGATG ATTTAGAATT GTCATTTCTC TTTACTGGAT GTTTATTTAT AAAGATCTGG CCTGTTCCTG CGTCTGCGGA GCGGCCCTTG TCTCCCAGCT ATCTATAACC TTAGCTAGAG TGTCGCCTTG TGGGTTCCCT CTCGAG (2) INFORMATION FOR SEQ ID NO:1183: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 410 base pairs (B) TYPE: nucleic acid	60 120 176
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:	
GAATTTAGAA TTCTTGACGG GTTCTCGGGG GTTCCTGTTG TATAAAGGCC TTCATTACTT TAGTTATACC CAAGTGAAAG GGGCATTTAC CTCGTGACAA GTGGATTATA GGAGAAAAAG AGGAGATGGT AGGTCAGAGT GTGCTTAGAA GTCATGCCCA GTGTTCTCAT CAATGCCAGA CATTACGGGC TGCCCTTCCA TCAGCCATTC TACCTTTCTT CCTGCTAACA ATATCCCAAT TTTGTTCAGG TATCAGGCCA CTTAATATGT TTCAGGGAAA ACTGGTTCCA GCCCAGAGCA GTGTGGACCT TGATTACATC AAACTAATCA TGGTGAGTCC ATTTTCCTTG CCAGAAATTC GTTTAGGAGT GGACATGTAT TTCACTTGTG AGTACACAAG ACGACTCGAG	60 120 180 240 300 360 410
(2) INFORMATION FOR SEQ ID NO:1184:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 286 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:	
GGAAACAGAC AGTACCAAGG AAGAAGCAGC TAAGATGGAA AAGGAATATG GAAGCTTGAA GGATTCCACA AAAGATGATA ACTCCAACCC AGGAGGAAAG ACAGATGAAC CCAAAGGAAA AACAGAAGCC TATTTGGAAG CCATCAGAAA AAATATTGAA TGGTTGAAGA AACATGACAA AAAGGGAAAT AAAGAAGATT ATGACCTTTC AAAGATGAGA GACTTCATCA ATAAACAAGC TGATGCTTAT GTGGAGAAAG GCATCCTTGA CAAGGAAGGG CTCGAG	60 120 180 240 286
(2) INFORMATION FOR SEQ ID NO:1185:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 417 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:	
GCGATTGAAT TCTAGACCTG CCTCACCTTA CCCCAGGACT CCGCTATGAC ACCGCCTCTG CCCCTACAAG ACACAGATCT CTCGTCAGCC CCAAAGCCTG TGGCTGCAGC CACGATTGTG TCCCAGCAGG CTGAAGAGGG CCTCACCTTA CCCCAGGACT CCGCTATGAC ACCGCCTCTG	60 120 180
CCCCTACAAG ACACAGATCT CTCGTCAGCC CCAAAGCCTG TGGCTGCAGC CACGCCTGTG	240

240

TCCCAGCAGG CTGAAGAGGG CCTCACCTTA CCCCAGGACT CCGCTATGAC ACCGCCTCTG CCCCTACAAG ACACAGATCT CTCGTCAGCC CCAAAGCCTG TGGCTGCAGC CACGCTTGTG TCCCAGCAGG CTGAAGAGGG CCTCACCTTA CCCCAGGACT CCGCTATGAC ACTCGAG	300 360 417
(2) INFORMATION FOR SEQ ID NO:1186:	
(i) SEOUENCE CHARACTERISTICS:	
(A) LENGTH: 260 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:	
GGAAGGGGCT TTTACAACTT CCTTTTGTTT CCAGGCGTTA GTATCTCTGC TTGGTATAAG	60
ATACCAGTAT TCCTAGGAAA GGCCTTGAAA AGAGGGACAG ATACAAGCCT CTTCTGAAAA	120
ATCTATGCTT TTCTTACCTC TACCAAGTAA TAGCAAACAT GAAAATGGTA AAGATCTTTA CAACATTTGT CTCTGTACAT ATAAAACGTT TAAACACATG CGCAAAGATG GAGCAAAATA	180
TCATAGAAAA TAATCTCGAG	240 260
	200
(2) INFORMATION FOR SEQ ID NO:1187:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 337 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:	
GAATTCGGCC TTCATGGCCT ACAAGGAAAT GCCCAAGGAA AAACGTGAGC TTCAGTTTCG	60
GCGAAAGGTC TTAGCAGTCA CAGACTCACC TGCCAGGAAG GGCAAGGACT CTCCCTCTAA	120
GCAGAGCCCT GGGGAGTCCA CGAAGAAGCA GGATGGCCTA GTCCAGATTG CACCAAACCT	180
GACTGTGATC CAGTTCATTA AAGTCTTCCC CAGGGTGCTG CTGCAGACCC TACGCCACCC CATCTTCCTG CTGGTGGTCC TGTCCCAGGT ATGCTTGTCA TCCATGGCTG CGGGCATGGC	240 300
CARCTTCCTG CCCAAGTTCC TGGAGCGCCA GCTCGAG	337
CACCITECIO CCCAABITCC TOUAGEGCCA GETCGAG	33,
(2) INFORMATION FOR SEQ ID NO:1188:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 537 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:	
(AI) SEQUENCE DESCRIPTION: SEQ ID NO:1100:	
GAATTGGCCT TCATGGCCTA CGAGGCGTCA CTGATCTTAA CGAGACTTCC AAATCGTCTC	60
AGCAGGGGCT CCAGACTTCC CCAGCAGGCG GCAGGTTTCC TGTCATGCTT TCGCCTTCCT	120
TCTCATATAC ACCAGTGCTA GAGTTCATCA TGTGTCAAAA TTGTATCTTG CTTCTTGTTT	180
TCAAGATGAT CTAATAGTTG TCTTATCTCA GCATCATACT CCACCCATTC TGGGACAATT	240
CTGGCAGCAG CTTTTAGTTT GGATTCTTTT GTTTTGGGAT TATTGCACAG ATCAATTGTT	300

360

TTGGCCCTCC TTGGACTAAC CACATACAAA TATGAATCTG GCTGCAAGAA CAGGATATCC

AGGTAACTAG AGAGTGGGCA TTGATAAAAA TATCTGGTGG AGAAGCCTAG GATTTCAACT TTTTGTCAGA GGATTCCTGT TGGGACAGCT TTACCAGAAA AGAATAATAG CGGATATGTT CATCCAAACT AAGAACTTTC ATGCATCTTG CATTGTTACA TAGCCTGTGG ACTCGAG	420 480 537
(2) INFORMATION FOR SEQ ID NO:1189:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:	
GAATTCGGCC TTCGTGGCCT AATTGAATTC TAGACCTGCC TCGAGGATTC AATTAGGCCA TCGAG	60 65
(2) INFORMATION FOR SEQ ID NO:1190:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 398 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:	
GAATTCGGCT TCATGGCCTA ACTTTATGTC ATAAAACTGA TTTAAATAAT CTTGAAATGG CCATTAAGGA AGATCAGATT GCAGATAACT TTCAAGGAAT ATCAGGTCCT AAAGAAGACA GCACAAGTAT AAAAGGTAAT TCAGACCAGG ATTCTTTCT TCATGAGAAT TCGTTACACC AAGAAGAGAG TCAAAAAGAA AATATGCCTT GTGGGGAAAC AGCAGAATTT AAACAAAAGC AAAGTGTTAA CAAAGGAAAA CAAGGAAAGG AGCAAAATCA GGACTCACAG ACAGAGGCAG AAGAGCTACG CAAACTTTGG AAAACCCATA CTATGCAACA AACTAAACAG CAAAGGGAAA ATATTCAACA AGTGTCACAA AAAGAAGCTA AACTCGAG	60 120 180 240 300 360 398
(2) INFORMATION FOR SEQ ID NO:1191:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 231 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:	
GAATTCGGCC TTCATGGCCT AGCCATTGTT TATACATTAT TGCTGTCAGT ATTCACCAAG ATGGTGCTAT TACCTGTTGT GGGGCAATTT TCCTTGTCAT TTCTACATAT CTTGGAACAG CTTTTGTCCT TATATTTTCA AGAATGTTCT AAAGCAGACA GCCTTGGAGG AGAGACAGAT AGTGACTCCC TCCAGGGAAA AAGTCGGATT TGTGTGCTCC CCTGCCTCGA G	60 120 180 231

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(2) INFORMATION FOR SEQ ID NO:1192:

(i) SEQUENCE CHARACTERISTICS:

PCT/US98/06955 WO 98/45436

(A) LENGTH: 262 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:	
GAATTCGGCC TTCATGGCCT ACACTAACCG CAGCATGGCG GATCTGAAGC ACAGCAGCTT	60
GCGGTACGAG CTCCGAGCAG ATCTGGAGGA AGAAAGAATG CGGCAGAAAA TAGCAGAAAG	120
GACCTCAGAA GAAACAATAC GCATTTACTC TTTGAGACTG TTTTTGAACT GTATTGTTCT	180
GGCTGTTTTA GGGGCATGCT TTTATGCAAT ATACGTAGCA ACTGTCTTCT CGCAAGAGCA	240
CATGAAAAAG GAAATCCTCG AG	262
(2) INFORMATION FOR SEQ ID NO:1193:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 381 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:	
GAATTCGGCC TTCATGGCCT AGAGGAAATT GCTAATGTAA CAGAGACATC AGATCCAGAA	60
TTCCAACGAA CCTGAATGAG CCCTGGTGTG GAACAGCCGT GAGCCTGTCC ACGTTTTTCT	120
CCTGATCTCT GCTTTTCATT AGTAATGAAT TTCCACTCCT TCTCCCCTTT CATGACAAAT	180
CAGTACAGTG AATGTAATTG CCACATCCAG CGATGCATCA TCTTCCCACT TTTCTAGGCT	240
GCAGAGAAGG AAGCAGCCCT TGTGCAGCAA GAAGAAGAAA AGGCTGAACA ACGGAAAAGA	300
GCTCGGCTG AGAAGAAAGC GTTAAAAAAG AAGAAAAAGA TCAGAGGCCC AGAGAAGCGC	360
GGAGCAGATG ATGGACTCGA G	381
(2) INFORMATION FOR SEQ ID NO:1194:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 294 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:	
GCGATTGAAT TCTAGACCTG CCTCTCTTAC CCTTGGCTTA CTAATATATT CTTAGTGGCA	60
TTTCATTTGG TGGTACTGGT GGCGCATTCA AACAGGACAC TTGTATCTGA GTGAGCAGCT	120
GGAGCAGTAA GAATGACAAC ACTTGGTCTC TGCAGATTGG CTGGACCCAC CACTCTGGTG	180
CTAGTGCTGG CTTGGTGGCT GAGGGAACAA GCAGGAAGTA GAAGAGGAAA TGAGATGTGG	
GTGGAGTGGG AAGAGGGACAA GCAGGAAGTA GAAGAGGAAA TGAGATGTGG GTGGAGTGTGG AAGAGGGACAA AGTGCAAACT CGAG	240 294
GIGGAGIGGG ANGAGGGAC AGAIIGGGAA GGGGAGGAAACI CGAG	234
(2) INFORMATION FOR SEQ ID NO:1195:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

GCGATTGAAG	TCATTGCCAC	GCCTACTAGT	TTGCACTAAA	GGAAAGTCAG	TTTGGTATGA	60
ATTACAATGG	CCAACGTTAC	ATTCTCCTCC	GTTTTGTTTT	TTTTTTTAA	TCTCAATTTC	120
				TTCTTTTGGG		180
				CCTCTCTTTA		240
CCCAGAAACC	CAGGAGCTCG	AG				262
CCCAGAAACC	CAGGAGCTCG	AG				202

- (2) INFORMATION FOR SEQ ID NO:1196:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

GAATTCGGCT TCATGGCCTA	GACCGTCTCA	AAGAAAACAC	ATATACCTTT	TGCTCAGATT	60
ATTGTTAAAT TTTACCTCAT	TTACTTTATC	AATTGCTCTT	TCTCTATTTA	TGTGTATCAG	120
ATTATTGTTA AATGTTACCT					180
GTACTGTTGC ACATGCAAAT	GCACACAAAT	ATATGTTTCT	GAATTTTTTG	AGAGTAGATT	240
GCATACATTA TGGGACCTGC					266

- (2) INFORMATION FOR SEQ ID NO:1197:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

GAATTCGGCC	TTCATGGCCT	AAGAAACACT	TTTAAAAAATC	TTTCACTAGT	TATTTTGTAC	60
				TGTCATAATT		120
				TGTGTGCGGA		180
				GGGATGCTCG		232

- (2) INFORMATION FOR SEQ ID NO:1198:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

GACCTTTACC ACTAAGTGGA GCCAACTTTA GCACCTTGCT AATGAATCTG GGTCCTGAGA ATTGTGCAAC ACTGCTGCTC TTTGTTTTAC TTGAGAGTAA AATTCTGCTG CATTCTCTTA GGCCAGCTGT CTTGACTGGG GTAGCTGAAG CTGTTGTAGC TATGATCTTT CCATTTCAGT GGCAATGCCC ATATATTCCC CTTTGTCCTC TTTCACTGGC TGCAGTGCTT AGTGCACCTT TACCATTTAT AGTTGGAGTT GACTCAAGGT ATTTTGATCT TCATGACCCA CCAAGGCTCG AG	60 120 180 240 300 302
(2) INFORMATION FOR SEQ ID NO:1199:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 231 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:	
GCCACTGCTC CTGGCCAGGA CTCTCTTATT AGGTTTGACA TTTCAAGAGT TTAGAAATTA CCTTCCAGAA TTCACAGGTA AAAGCCAGAC CTCTCCTTGG TGAAGATACA ATTCTTTACA ATTTTACAAT AGTTAAGTAT ATTTTATCAG TCTATATTGG CTGTTTAGTT GACAAACCGT TAAAAAATTGG TGACAGTCCA GATGTGGTCA CTCATGCCTC TAATCCTCGA G	60 120 180 231
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 235 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xì) SEQUENCE DESCRIPTION: SEQ ID NO:1200:	
GAATTCTAGÇ CCTGACCCAG CCCCCATGGC TTCAGAAGAG CTACAGAAAG ATCTAGAAGA GGTAAAGGTG TTGCTGGAAA AGGCTACTAG GAAAAGAGTA CGTGATGCCC TTACAGCTGA AAAATCCAAG ATTGAGACAG AAATCAAGAA CAAGATGCAA CAGAAATCAC AGAAGAAAGC AGAACTTCTT GATAATGAAA AACCAGCTGC TGTGGTTGCT CCCATCACTC TCGAG	60 120 180 235
(2) INFORMATION FOR SEQ ID NO:1201:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 119 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:	
GAATGAGAGG TCAGAGTATT CCATTGCACA CGCACCCTGG GGCTGACAGA CTTGTGCCCC	60

(i) SEQUENCE CHARACTERISTICS:

476

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CTAGCCTTCA TGCATGCCCA AGCACTGGCA GCTTTGCAGC CCCTGCCCCA CGACTCGAG

(2) INFORMATION FOR SEQ ID NO:1202:

(A) LENGTH: 366 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

GATTGAATTC	TAGACCTGCC	TCGAGATTCT	TTGAGCACTT	TCCCCCATCC	CCAGGGCCAC	60
AGATCCCCTT	CCTTACTTGT	TGGGGGGAGG	TCTGGAGCAC	CTCGCCAATG	CCCTTCCCCC	120
ATCCGGCTGG	GTCCTTCCAG	TTATTTATTT	GTGTATTTAT	TTATTTATCT	TTATTATTA	180
CTATTTAATC	TCTTGGCCTC	ACCCAGGGAC	CGTCTGGCTT	CCCCAGCTGG	ACTGGGAGGT	240
CAGGAAGCCA	GGCAAGGAGA	GGGACAGCAC	AGGCCACAGA	GGGCTGCCCC	CACCACACAC	300
ACCCCCGCGT	CTCGGGAGAA	ACCCACCCTC	TTCAGAGCCT	GCACTCGCTA	AGGAAGGGGA	360
CTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:1203:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs(B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

GGTGAGATGG	AAAAGGAGTT	TCCTGAGCTT	ATCCGAAGTG	TTGGTTTACT	TACGGTAGCT	60
GCTGACTCTA	TCTCTACCAA	TGGCAGTGAA	GCAGTTACTG	AGGAGGTATC	TCAAGTATCT	120
CTCTCAGTAG	ACGACAAAGG	TGGATGTGAG	GAAGACAATG	CTTCTGCAGT	CGAAGAGCAA	180
CCAGGCTTAA	CACTGGGGGT	GTCATCATCT	TCAGGAGAAG	CTCTGACAAA	TGCTGTTCAA	240
CCCTCCTCTG	AGACTGTGCA	GCAAGAATCC	AGTTCCTCCT	CCCATCATGA	TGCAAAGAAT	300
CAGCAGCCTG	TTCCTTGTGA	AAATGCAACC	CCCAAACTCG	AG		342

- (2) INFORMATION FOR SEQ ID NO:1204:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 645 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

GAATTCGGCT	TCATGGCCTA	CGTCTTTCTA	ACTATCTATG	GGGTGGAGCT	GTTCCTGAAG	60
GTTGCCGGCC	TGGGCCCTGT	GGAGTACTTG	TCTTCCGGAT	GGAACTTGTT	TGACTTCTCC	120
	TCGCCTTCCT					180
TTCATCGTGG	TCCTGCGCCC	CCTCCAGCTG	CTGAGGTTGT	TTAAGTTGAA	GGAGCGCTAC	240
	TGGACACCAT					300
CTGCTCATCT	TTTACTACTC	CTTCGCCATC	GTGGGCATGG	AGTTCTTCTG	CGGGATCGTC	360
TTCCCCAACT	GCTGCAACAC	GAGTACAGTG	GCAGATGCCT	ACCGCTGGCG	CAACCACACC	420
GTGGGCAACA	GGACCGTGGT	GGAGGAAGGC	TACTATTATC	TCAATAATTT	TGACAACATC	480
CTCAACAGCT	TTGTGACCCT	GTTTGAGCTC	ACAGTTGTCA	ACAACTGGTA	CATCATCATG	540
GAAGGCGTCA	CCTCTCAGAC	CTCCCACTGG	AGCCGCCTCT	ACTTCATGAC	CTTTTACATT	600
	TGGTGATGAC					645

- (2) INFORMATION FOR SEQ ID NO:1205:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

GAATTCGGCC TTCATG	GCCT ACAGTACACA	AGTGCTAGCC	CTAGCAGCTC	GCGATGTGCT	60
TCAGCAGAGC AGACGC	TGCG GATAACTACC	CTTTTGGAAC	ATGTCAACAG	AGGAAACTTT	120
TTCCTCACTT CCATCO	CCCG AATTTGATTG	GGAACAAGTT	TGTCCCTCTT	AGGGGATCAC	180
CCCACAGAGG GCCTGG	GTGT TATTTTTCAG	ATGGATATGG	CTTGGCATAC	GACTTATCTA	240
AGATCCCAAC CAGTAT	AAAA GGATATACTT	TGGGAGCCAG	AACAGCTGTG	AGGTTTAAGC	300
CAATACAGAA GGAAAT	GACA CCTCATGCAG	GCAGGT			336

- (2) INFORMATION FOR SEQ ID NO:1206:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

GGAAAATCTG AACAAACAAC CGAATAAGCA GTGGA	AGAAA TCACAAACAT CTACAAATCC 60
AAAAGCTGCT CTCAAGTCTA AGATAGTTGC TGAAT	TTTCGA TCTCAGGCCC TAATTGAAGA 120
GCTGTTGCTA TACAAGCGCT CAGAAGATCA GATAC	BAACTG AAGGAAAAGC AGTTGTCAAC 180
TATGAGGGTG GATGTGTGCA GCACAGAAAC TCTC	AAATGC TTAAAAGATA AAACAGGTGG 240
GAAGAAGTTC TCCAAAGAAT TTGAAGAGGC AAGCT	CCAAG CTGGAAGAAT TTGTGAATGG 300
ATCACTCGA	309

- (2) INFORMATION FOR SEQ ID NO:1207:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

GAATTCGGCC	TTCATGGCCT	ACAGCTTTTG	AGCGGAAACC	TGAAAGAAGG	TTTGCAGTAT	60
CTTCAGAGTC	TGAATTTTGA	GCGGATAGTG	ATGAGCCAGC	TAAATCCCCT	GAAGATTTGC	120
CTGCCCTCAG	TGGTTAACTT	TTTTGCTGCA	ATCACAAATA	AGTACCAGCT	CGTCTTCTGC	180
TACACCATCA	TTGAGAGGAA	CAATCGCCAG	ATGCTGCCAG	TCATTAGGAG	TACCGCTGGA	240
GGAGACTCAG	TGCAGATCTG	CACAAACCCG	CTGGACACCT	TCTTCCCCTT	TGATCCCTGT	300
GTGCTGAAGA	GGTAGGTACT	TTTAAACGTT	GACATCTCGA	G		341

(2) INFORMATION FOR SEQ ID NO:1208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

GAATTCGGCC	TTCATGGCCT	ANCGAGCGGC	AGGTGTGCAC	AGAGGTNCTC	CACTTTGTNT	60
TCTGAACTCG	CGGTCAGGAT	GGTTTTCTCT	GTCAGGCAGT	GTGGCCATGT	TGGCAGAACT	120
GAAGAAGTTT	TACTGACGTT	CAAGATATTC	CTTGTCATCA	TTTGTCTTCA	TGTCNTNCTG	180
GTAACATCCC	TGGAAGAAGA	TACTGATAAT	TCCAGTTTGT	CACCACCACC	TGCTAAATTA	240
TCTGTTGTCA	GTTTTGCCCC	CTCCTCCAAT	GGTACTCCAG	AGGTTGAAAC	AACAAGCCTC	300
AATGATGTTA	CTTTAAGCTT	ACTCCCTTCA	AACGAAACAG	AAAAAACTAA	AATCACTATA	360
GTAAAAACCT	TCAATGCATC	AGGCGTCAAA	CCCCAGAGAA	ATATCTGCAA	TTTGTCATCT	420
ATTTGCAATG	ACTCAGCATT	TTTTAGAGGT	GAGATCATGT	TTCAATATGA	TAAAGAAAGC	480
ACTGTTCCCC	AGAATCAACA	TATAACGAAT	GGCACCTTAA	CTGGAGTCCT	GTCTCTAAGT	540
GAATTAAAAC	GCTCAGAGCT	CAACAAAACC	CTGCAAACCC	TACTCGAG		588

- (2) INFORMATION FOR SEQ ID NO:1209:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

GAATTCGGCC	TTCATGGCCT	ACAAGGATAG	AATTCATTCC	ACCTATATGT	ACTTAGCAGG	60
	TTAACAGCTT					120
CTTCATGATG	AGAGGCTCTT	GGGTGACAAT	TGGTGTGACC	TTTGCAGCCA	TGGTTGGAGC	180
TGGAATGCTG	GTACGATCAA	TACCATATGA	CCAGAGCCCA	GGCCCAAAGC	ATCTTGCTTG	240
GTTGCTACAT	TCTGGTGTGA	TGGGTGCAGT	GGTGGCTCCT	CTGACAATAT	TAGGGGGTCC	300
TCTTCTCATC	AGAGCTGCAT	GGTACACAGC	TGGCATTGTG	GGAGGCCTCT	CCACTGTGGC	360
CATGTGTGCG	CCCAGTGAAA	AGTTTCTGAA	CATGGGTGCA	CCCCAGGGAG	TGCTCGAG	418

- (2) INFORMATION FOR SEQ ID NO:1210:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

GAATTCGGCC	TTCATGGCCT	AGGTTGCAAC	TGCCACGCAG	CAACTGCCAC	GCAGAAAAAG	60
GAGGGGTTGA	AAAGGGAGTA	GCTTCTGATA	TTCAGAAGCT	ATTGGAAGAG	ATGCTCAAAG	120
AAGAAAAAAT	TACCATAATC	CAATAAAGAA	GAAGACCTGA	GATCCAGGAA	GCAGATGATC	180
TGAACTGCAG	AGAAAGTTCA	GGAAAGTTCC	CTCATTCATG	ATGATGGGAA	ATAACAGTAA	240
ATTCTGTACA	GCAGTCTTGG	ACAACAACCA	ATCTAAACTG	GCACAGTGCA	GAGGCAATCA	300
ACAGAGAACA	TAATATTGAT	AGAATGCCTG	ACGCTTTTGA	TTGTATTCAC	AGGAAACATA	360

AACAATTGGA A	AAACTCGAG	379
(2) INFORMAT	TION FOR SEQ ID NO:1211:	
(i) S	EQUENCE CHARACTERISTICS: (A) LENGTH: 380 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1211:	
AATGATTCTG AGGATTGGCC AACATTTCTA AGCATGGTCG	TTCATGGCCT AGAAACAGGG TATTATTTAT CCTCTTAGCA TATGTTTTGT TTACATCAGA GCTTCTGTTG ATGAGTGCCA CTAAAGTGAG ATTGTTGATG TTATTTTTTT GTGGTTCTAT TCAATACTTG CCACAGCATT TATTTTCTAA CGGTCTATAC TTATCAGTGT CTGATCACAT GCAGGCACTG GTCAAGGTGG AGGCGTTCTT ACTGATACAA ACTCGTGCCT TCTCTTGGAC ACAAGGAGCC TTAACCTCTGT GTTCATTTAT TTCACTTGTC ATGCATCGCC TCTATCTTCT CGTCCTCGAG	60 120 180 240 300 360 380
(2) INFORMA	TION FOR SEQ ID NO:1212:	
(i) s	EQUENCE CHARACTERISTICS: (A) LENGTH: 430 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1212:	
ATTTGGGCAT AGTGTAGGTT GTTGATAAGT CAGCACCTGC GTTTTAGGGT	TTCATGGCCT AGTGAAGGGT ATTGGTGGTG TTTTTTCCCC TTTACCTCTC TTTAAAATAG GAGGCCAACT TCATTTACTC CTGTTTAGTA AATCTAAATG TTAAAATTAGA TTTTTTCCCA AAACCCTTCA GAAGGTCTAG TATTAGGGCA AAGTGGAAGC ACCTTGGGCA GGACCCAGTG ACCTGTCCTT TTACTTATTA ACGGGAAGCA GATCTGGAGG ATGAAATTTA ACCTGTTACA GTGTGTGTAT GTGTGTTTTC CGAATACTGT GGGGAGTTCC CTTTTTCCTT CTCCCATGAT GTCTTTCTAG AGATACCATA GGAGGATATC TGGATTTTC ACCTAAGGCA	60 120 180 240 300 360 420 430
(2) INFORMA	TION FOR SEQ ID NO:1213:	
(i) :	SEQUENCE CHARACTERISTICS: (A) LENGTH: 437 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1213:	
AAATGGAGAT CCCTACAACC	TCCTGTTAAT CTCCTATTTA TAAAAGGATC ATGAGGCTGC CAAGTGCTAA GGTCTAGTAA CTAGAAAACT CCCCACCCCA GGGAGCACAC CTACGTATGT TAATAATGTG ATGTGTTTTG GAACACAGAC ATTAGAACTT CATGAAGTTT TTCTTTCCCA AGCATCATCA AGTTATGATT TAGGCAATGT ATGATTGAAA	60 120 180 240

TGCATTCATT	CATCACGCAT	AGGCACAATC	ACAGAAATAT	TGCACAAAAT	ATGTCCCTGA	300
CTGAAACTGA	GAGGTACAAA	AACGTATTTC	ACTCTTCGTA	AAGAAGTTTG	TGAGGAAATA	360
CAACTCTGCG	ATCGTATAGA	CATGTTTCCT	GATAATACAC	TGACATTCAC	AAACAGTAGG	420
CCATGAAGGC	CGAATTC					437

- (2) INFORMATION FOR SEQ ID NO:1214:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

GAATTCGGCC	TTCATGGCCT	AAAAAGAAAT	GATGTTTTCT	CTCCAACAGT	GTGTTTTAT	60
TTCTTTCATC	TACCTGTCCA	GTAATCATTT	TAAAAAAGAA	AATAGCATTA	GTTACTGCCT	120
GTGTGATGTG	GCCCCGGCTT	ATCTGCACTC	TCCCTCCTGT	TTACTGTTCC	AGCCACCTCA	180
GCTTTTTCTC	TGTTCCTCTA	GCATGGCAAG	CTTATTCCTG	CCTCATGACT	CTTTCGCATG	240
GTGTTTTCAG	ATTTTCTCTG	TAGCACTCTG	CACGCATTGT	CCACCTAAAC	TCGAG	295

- (2) INFORMATION FOR SEQ ID NO:1215:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

GACCTGCCGC	GAGTGTTGTT	GATAGCTTGC	TCAAGATCAC	ACAGCTAGTA	GGTAGTGAGG	60
		GTTGGTTGTA				120
TGATAACAAT	ATCATTATTA	TTATTATCTT	TTTTTTTTT	TTGATACAAA	GTCTCACTTT	180
GTTGCCCAGG	CTGGAGTGCA	GTGGCATAAT	CATGGCTCAC	TGCAGCCTCG	AACTCCTGGG	240
CTCAAGGGAT	CCCCCCACTC	TCGAG				265

- (2) INFORMATION FOR SEQ ID NO:1216:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:

GAATTCGGCC	TTCATGGCCT	AAAAGAAGGA	GCGCGAGAGA	AAAAAGCGAG	ATGAAGAAAA	60
AGCGAAACTG	CGGAAGCTGA	AAGAAAAAGA	AGAGTTAGAA	ACAGGTAAAA	AGGATCAGAG	120
TAAACAAAAG	GAATCTCAAA	GGAAATTTGA	AGAAGAAACT	GTAAAATCCA	AAGTGACTGT	180
TGATACTGGA	GTAATTCCTG	CCTCTGAAGA	GAAAGCAGAG	ACTCCCACAG	CTGCAGAAGA	240
TGACAATGAA	GGAGACAAAA	AGAAGAAAGA	TAAGAAGAAA	AAGAAAGGAG	AAAAGGAAGA	300
AAAAGAGAAA	GAGAAGAAAA	AAGGACCTAG	CAATGCCACT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:1217:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

GAATTCGGCC	TTCATGGCCT	AGCCATTATT	AAGACCTGTG	ACAAAAACTA	TAGACATGAT	60
GCAGTGAAGA	TTCTGAAACT	CAAGCCTGTG	CTGCAGAGAA	GTCTCACTCA	CCCTCCTACC	120
ATAGCCCCAG	AGGGGTCCAG	ACCCCAGGGT	GGTTTGCCCA	GCAGCAAGCT	AGACAGTGGA	180
TTTGCCAAGA	CATCTGTTGC	TGCTTCTCTA	TACCACACAC	CCTCTGACTC	CAAGGAAATT	240
ACTCTTACTG	TTACTTCAAA	GGACCCTGAA	AGACCTCCTG	TTCATGACCA	ACTTCAGGAC	300
CCACGACTGC	TGAAGAGGAT	GGGCATTGAG	GTCAAAGGAG	GAATATTCCT	TTGGGATCCA	360
CAACCCTCGA	G					371

- (2) INFORMATION FOR SEQ ID NO:1218:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

GAATTCTAGA	CTCCCGCGCG	TACTCGGCCG	CCTGAGCGAT	ACTAAAATGT	CTGATGATGC	60
TGGTGACACC	TTAGCCACTG	GAGACAAAGC	AGAAGTTACT	GAGATGCCTA	ATAGTGATTC	120
TTTACCTGAG	GATGCAGAAG	TGCATTGTGA	TTCAGCTGCA	GTTTCACATG	AGCCAACACC	180
AGCTGACCCC	AGAGGGGAGG	GGCATGAAAA	TGCAGCTGTG	CAGGGTGCAG	GGGCTGCCGC	240
CATTGGGCCC	CCTGTGCAGC	CTCAGGATGC	CAACGCCCTG	GAGCCCCCTC	TCAATGGAGA	300
CGTGACTGAG	GATACACTTG	CTGAATGTAT	TGATTCCTGG	AGCCTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:1219:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

GAATTCTAGA	CCTGCCTCTC	CTGTCACTTC	CTTGTGTTTT	CTCTGTGACC	GGCCTCTGTT	60
CCCACCACCC	TTTTGGAACT	GCTGTCCTGA	TGGTCACCAG	TGCTTTCCTA	ATAGCCAAAT	120
TCAGTGGCCT	GTCCTCAAGC	TCCCCCGAAT	TCTTTGGCCA	CACAGATCAA	CCTCTAAGTC	180
CTGGGAACTC	CCTCCTTTGT	GATTTTGAGG	CGCTGTGTGC	TGCAGGCTCT	GCTTTTCCCT	240
CCCATCACCC	CATGGTTCTT	CCTTCTCCTC	TGACCCCTCC	CTCTTCCATT	TCTCCCACAG	300
CTCTGTCCAC	AGCCACAATG	TCCATAGGAG	CCTGCCACAC	CCTTTATCCA	ACTGCAGCCT	360
CAACCCACCT	GCAAAGGACC	CCTGAACTCG	AG			392

(2) INFORMATION FOR SEQ ID NO:1220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 598 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

GCAAGCTACT	TCTTCAACAG	CTGTATCTGC	TTCAAAGCCG	ACTGCCTCTC	CTTCAAGCAT	60
TGCAGCAAAC	AATTGTACTG	TGAATACGTC	ATCAATTGCA	ACGTCTTCAA	TGAAGGGTCT	120
TACGACTACA	GGAAACTCGT	CTCTTAATAG	CACATCTAAC	ACTAAAGTAT	CAGCAGTGCC	180
TACAAATATG	GCTGCCAAGA	AAAACATCTA	CCCCCAAAAT	AAATTTTGTT	GGTGGTAATA	240
AGCTGCAGTC	NACAGGAAAT	AAAGCAGGAG	ACCTTAAAAG	GGACCCGAAT	GTGTTAAAAG	300
TAATCCTGTC	ATTTCTGCTG	TGCAGATTCC	TGAAGTAAAG	CAAGACACAG	TGTCAGAACC	360
AGTCACACCT	GCATCTCTTG	CTGCTTTACA	GAGTGATGTG	CAGCCAGTGG	GCCATGATTA	420
TGTGGAAGAG	GTACGAAATG	ATGAAGGAAA	AGTAATTCGG	TTCCATTGTA	AATTATGCGA	480
GTGCAGCTTT	AATGATCCCA	ATGCTAAGGA	GATGCACTTA	AAAGGGCGAA	GACACAGACT	540
TCAATATAAA	AAAAAAGTAA	ATCCAGATTT	GCAAGTAGAA	GTAAAGCCAA	TACTCGAG	598

- (2) INFORMATION FOR SEQ ID NO:1221:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

GAATTCGGCC	TTCATGGCCT	AGAGGAGTCC	TGTCAGTTCG	Treference	TGTCCCCAAG	80
ACCATGAATC	ATGGCTGGCA	TGTAGTAGGC	ATTTAATAAT	ATATGTTCAA	CAAGTATTTG	120
GCAGTCTTGG	AGGGCAGAAA	AGGAGGTGGG	GAAGATTTTT	AAATAACATT	TTTTAAAAAG	180
TCACATTGTC	CTACAATACC	GATTTTTCTT	GCATATTTAG	GAAATTGAGG	GTTTTTTTCT	240
AAAACATGCG	GACATATGGG	AAATAGGATG	CAACATTTGC	ACTAATGTTT	CAGACACAGT	300
TAGAGGTTTC	CAAGAGATTT	TGCGCTGGGT	CACTCGAG			338

- (2) INFORMATION FOR SEQ ID NO:1222:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

GCTCGAGTGA	CATGGAAACT	GAGGTCTTAG	AGACACGTGT	AATGGAGAGG	AGAGGAATGG	60
AGACCTGTG	GATGGAAACC	AGAGGGATGG	AAGCAAGGGG	CATGGATGCA	AGAGGATTGG	120
	CCCTGTCCCC					180
GTCCCATTA	TATAGGGGCA	GGTGGCCCTC	CTCAGGGACC	CAGACAGGTC	CCAGGCATTT	240
CAGGGGTGG	GAATCCTGGA	GCTGGTATGC	AGGGTACAGG	CATACAAGGA	ACAGGCATGC	300

335

AGGGAGCAGG CATACAAGGA GGAAAAATGC TCGAG

(2) INFORMATION FOR SEQ ID NO:1223:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 534 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:	
GAATTCGGCC TTCATGGCCT AGGTACAGAC TGAACCCAGG AACCCGGGTA TCTGCGTCCT GAGTCCCAGC GCCCACCAGG ACTGGGGCCT CCTCACATCT ACTCTGAGGA CAGAATCTAT TGGCAGAGTC TTCCTTTTTG TTTGGGATGC TGGGTTTGAG AACATGCCGG GAACCAAGAG TCGTGACTAA TCCAATTTTG AGCGCTTGAG GACCAAGTGG AAAGAAACCC AAGCAGATTT AAAGTGACCA ATGTCTGGTT ATGCCCTTGA GCCCCTGCAG AAGCAAACAA TAATTTTGTG TGTGTGTGGA CAAATACATT TGTATTCCAG ATCTCACAGA ATTTCCTACA CAAAGAAATT TGCAAGGAAA ATGGACATTG CACCCTAAAA ATTAACAAGG AAAGAAAGGTA CCAGGAGCAA CAACTCATTA ACAGGAACAG AAACAATATT GCAAATATTT CAGATGCAAA GTGTATCCGA CTTATAAATAC AACTGTCCCT ACTGTGTCTA AAGAAATGAA AGGCAATCCT CGAG	60 120 180 240 300 360 420 480 534
(2) INFORMATION FOR SEQ ID NO:1224:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 354 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:	
TCACGAATGG CCCACAGGGA TCAGGAATGG TATGATGCTG AAATTGCCAG AAAACTGCAA GAAGAAGAAC TTTTGGCTAC CCAGGTGGAC ATGAGAGCCG CTCAAGTAGC TCAAGATGAA GAAATCGCTC GACTTCTAAT GGCTGAAGAA AAGAAAGCTT ACAAAAAAAGC CAAGGAGCGG GAGAAATCAT CTTTGGACAA AAGAAAGCAA GACCCCGAGT GGAAGCCAAA AACAGCTAAA GCAGCAAAATT CCAAGTCAAA AGAGAGTGAT GAACCTCACC ATTCTAAGAA TGAAAGGCCA GCACGGCCAC CACCACCTAT CATGACAGAT GGTGAAGATG CGGATTCTCT CGAG	60 120 180 240 300 354
(2) INFORMATION FOR SEQ ID NO:1225:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 488 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:	
GCAACAAAAC AAAACAAAAC ACACTTATGG TAACCCATTC TGTTGAGGAG TCCAAAACTC GAATAAAGCG CCTCATTGCC TTTAACTGGT TCTGTGGCAG TGAGATCATC ATCCTTATGC TGGCTCACCT AGTGTCTCTC TCTCTCTCCC GTTTTCTCTC TCCCTCTCTT ATCCCCTTGA CTCTCCCCAC TTCTCATCTT CTCTTTAGAT TATGTGGTAG CTATCCTCAA GAGCTCATAG	60 120 180 240

TGCCTGCCTG	GATCACTGAC	AAAGAACTGG	AAAGTGTATC	AAGTTTCAGG	TCCTGGAAGC	300
GCATCCCTGC	CGTCATCTAC	AGGCACCAGA	GCAATGGAGC	TGTCATTGCC	CGCTGTGGAC	360
AGCCAGAGGT	TAGCTGGTGG	GGCTGGCGAA	ATGCAGATGA	TGAGCATCTG	GTACAGTCAG	420
TAGCCAAAGC	TTGTGCCTCT	GACTCCCGAT	CGAGTGGCAG	CAAGCTGTCA	ACTAGGAAAC	480
GACTCGAG						488

- (2) INFORMATION FOR SEQ ID NO:1226:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

GATCCCCACC	AAAACAGGAA	AAGAAGTGCT	CTCGTGCAGG	GCTTGTTCAC	AGTGAGCCTG	60
GCTGGCTCCT	CATGATCTCT	GAGTTTAAAA	TGTGCCAGCA	GATGATTTTA	ACGATCCCAT	120
CAAAAATTGT	TGTCTGGATC	AGTTTCGAGC	TAGCGTTTCC	TTGCAGAGGC	CATTCTTCCT	180
TTTTTGACAA	AAGTTGGGTC	GGCCAGGTGC	AGTGGCTCAT	ACTTGTGATC	CACCTGCCTT	240
GGCCTCCCAA	AGTGCGGGGA	TTCTAGGCAT	GAGCCACCAC	ACCCTGCCAG	AAAAATGGAT	300
TTAAAAAGAG	AATTACAAAG	TACTCGAG				328

- (2) INFORMATION FOR SEQ ID NO:1227:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

GAATTCGGCC	TTCATGGCCT	AAAATTTTTA	TTTATAAAAA	ATAATGATAG	TTAGAGAACT	60
GTTTATATGA	GGATCAGACA	TTGTTTCAGC	ACTGGATCTC	CTCTGTCCCC	TCTCTTGCTA	120
CAGCATACAG	CCCAGAGACA	CACATGTAAA	AGTAGATGAT	CTCTGTAAAC	TTCAGCTGCA	180
	TGTAGGATTG					240
ATGGAAGGAA	GCATATTCCT	GACCTCCCCC	CTTTTTAGCT	AAAGATACAA	ATTCAGAGCT	300
	GGCTTAGAAT					360
ΤΤΤΤΤΤΑΑΑΑ	TACATTTATT	TTTCTTTCTT	TTTTAGCAGG	CATTTCTGAC	AGAAAATCTT	420
	TAGAGTTTCT					480
1.10000	CTGGAAAAA					527

- (2) INFORMATION FOR SEQ ID NO:1228:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

GAATTCGGCC	TTCATGGCCT	AAGAAAACAG	CCTAGAATTA	AACCTCCAAG	ATGAGTGTGA	60
GATGAAGCCT	TTCCACCTAT	CCCAACAAGG	AAAAAATTT	ATAAAAACTA	GAATGGGGCT	120
ACTACACAAC	AGCCCTTTGC	CCCACCCAAG	GCTCATTCCC	TAGAGGCAAG	TGTACGAGTT	180
TATTTCTCCT	TGAAATTATT	TCCATATCTC	CAAATAGTGT	TTATACCACT	CAAGGCAGAG	240
ATAGCAATTT	GCCTACCCAG	TATACATTTC	CCCTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:1229:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 603 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

GAATTCGGCC	TTCATGGCCT	AGCCACCTTG	AAGCTCTCAA	ATATCACTGT	TGTGAATACA	60
GAGAGGGAAA	ACCAACTGTA	ACGTGCCACC	CAAATTTTTT	CAGATTAATA	CATCATTCAT	120
CAGACTTCAT	TCGTGATCTC	GAAGAGTGAC	ATCAGTCTTC	CTTGGAATAT	GAAGAGAATT	180
TCTTTGGTTC	TTCTTTTGCA	TTTCTATTTG	ATTTATTTTA	TTTTATTTTA	TTTTATGTTT	240
TTTGGTACAG	AAAGCTCATT	ACTAGTCCTG	TCCAGCAACG	TGCCTCTCCT	GGCCCTAGAG	300
TTCTTGGAAA	TAGCCCAGGC	CAAAGAGAAG	GCCTTTCTCC	CCATGGTCAG	CCACACGTTC	360
CACATGCGCA	CAGAGGAGTC	TGATGCCTCA	CAGGAGGGCG	ATGACCTACC	CAAGTCCTCA	420
GCAAACACCA	GCCATCCCAA	GCAGGATGAC	AGCCCCAAGT	CCTCAGAAGA	AACCATCCAG	480
CCCAAGGAGG	GTGACATCCC	CAAGGCCCCA	GAAGAAACCA	TCCAATCCAA	GAAGGAGGAC	540
CTCCCCAAGT	CCTCGGAAAA	AGCCATCCAG	CCCAAAGAGA	GTAACATCCC	CAGAGCCCTC	600
GAG						603

- (2) INFORMATION FOR SEQ ID NO:1230:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

GAATTCGGCC	TTCATGGCCT	ACCGGGCAGT	TAGGCCCAAG	CGCCGGGTTC	AGGCCTCCAA	60
AAACCCCCTG	AAAATGCTGG	CGGCAAGAGA	AGATCTCCTT	CAGGAATACA	CTGAGCAGAG	120
ATTAAACGTT	GCCTTCATGG	AGTCAAAGCG	GATGAAAGTA	GAAAAGATGT	CTTCCAACTC	180
CAACTTCTCA	GAAGTCACCC	TGGCGGGTTT	AGCCAGTAAA	GAAAACTTCA	GCAACGTCAG	240
CCTGCGGAGC	GTCAACCTGA	CGGAACAGAA	CTCTAACAAC	AGCGCCGTGC	CCTACAAGAG	300
GCTGATGCTG	TTGCAGATTA	AAGGAAGAAG	ACATGTGCAG	ACCAGGGTGG	TGGAACCTCG	360
AG						362

- (2) INFORMATION FOR SEQ ID NO:1231:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

GAATTCGGCC	TTCATGGCCT	AGTCCCTGTT	CAATTTCTCT	CAGCCTCAAT	ATCTTTTACT	60
TTAAACTAGG	TAGGGTTACC	AGTTCAATGA	TCTGCTCATT	AAATACTTAC	TATACCTTAG	120
GTACTATATG	AGAAGCTAGG	AAAAGAGTGA	TGAAAAAGAC	ACACCTAGAG	AGGGCATTGG	180
TAAATTATTA	CAGCAGCTAC	TGTAAAGGTA	TTTAAGTTCT	GTGACAGGCA	GCATTCTGGG	240
TATCACAGGA	ACATCTTACA	AGAATTTCTA	ACTTCAGGAG	GAGGGTTCAG	AGAATTAGCC	300
AGGCCAGGGG	TGAGAGTGTT	CTTCCCGGAA	GAGGGAACAA	TGAAGACCCA	GGAGGAGATA	360
CAGAGTATCT	CGCTGTATTT	AAAATAACCA	GAAATAGATT	TATATATTTA	GTACAGAGGC	420
TGAGGGGAAG	AGAAGTGAGT	GTGAGAAGAT	CAAAAGGAGA	AGCTCGAG		468

(2) INFORMATION FOR SEQ ID NO:1232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

GAATTCGGCC	TTCATGGCCT	ACAATCATCT	CAAACAGTTC	CGGGTTGCTG	CCCTTTTGGC	60
TTTCCTAGGT	GCTACAGTAG	CAGGCTGTTT	TCCCCTTTTC	CATAGAGGGG	AATATTCTGC	120
ATCACCCCTT	TGTTTGCCAT	TTCCTACAGG	TGAAACGCCA	TCATTAGGAT	TCACTGTAAC	180
GTTAGTGCTA	TTAAACTCAC	TAGCATTTTT	ATTAATGGCC	GTTATCTACA	CTAAGCTATA	240
CTGCAACTTG	GAAAAAGAGG	ACCTCTCAGA	AAACTCACAA	TCTAGCATGA	TTAAGCATGT	300
CGCTTGGCTA	ATCTTCACCA	ATTGCATCTT	TTTCTGCCCT	GTGGCGTTTT	TTTCATTTGC	360
ACCATTGATC	ACTGCAATCT	CTATCAGCCC	CCCACTCGAG			400

- (2) INFORMATION FOR SEQ ID NO:1233:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

GAATTCGGCC	TTCATGGCCT	AGGATATAGA	CCAAACCCAA	ATCCTGTTGG	ACAAGGGATT	60
AGACCACCTA	TGGCTGGATG	CAACAGTTCG	GTAGGCGGCA	TGAGTATGTC	GCCAAACCAA	120
GGCTTACAGA	TGCCGAGCAG	CAGGGCCTAT	GGCTTGGCAG	ACCCTAGCAC	CACAGGGCAG	180
ATGAGTGGAG	CTAGGTATGG	GGGTTCCAGT	AACATAGCTT	CATTGACCCC	TGGGCCAGGC	240
ATGCAATCAC	CATCTTCCTA	CCAGAACAAC	AACTATGGGC	TCAACATGAG	TAGCCCCCCA	300
CATGGGAGTC	CTGGTCTTGC	CCCAAACCAG	CAGAATATCA	TGATTTCTCC	TCGTAATCGT	360
GGGAGTCCAA	AGATAGCCTC	ACATCAGTTT	TCTCCTGTTG	CAGGIGCGCA	CTCTCGAG	418

- (2) INFORMATION FOR SEQ ID NO:1234:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

GAATTCGGCC	TTCATGGCCT	ACGCCTCTTT	AACACATGGG	CCTTTGTGTG	GACACCATCT	60
TTCCCTGAAA	CCTGTCTGCA	TCTTTTCTGT	CCCTTCTAAC	CATCCAGTTT	GTTCTTCCCC	120
				TGGTTCCAGA		180
GCAGACACAG	GGAAGGAATC	TTATCTCGTT	TTTGTTTTTT	TGTTGTTGTT	TTTGTTTTTT	240
TCTTTTTTGT	TGTGGTTGTT	GCTGTTGTTT	TGAAACGGAG	TCTCACTCTG	TTGCCAAGGC	300
	TGGCGCAATC					325

- (2) INFORMATION FOR SEQ ID NO:1235:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

				AGAAAATGTT		60
GGTCTGAGCT	TTATGGAGAA	AGAAGGTTTG	AAGTAGCTTC	TGGGATATGG	AAAAAGAACT	120
TATGAGAGAA	ACAGACTTCT	GGGAATCCTT	CAAGGACTAG	AAGAGAACAT	AGATTATGAA	180
AGAATGAGTC	ATTGATCAGT	GTAGTTGTAG	ATTAGAATAG	TTGGACAGTT	AGGATTTGCT	240
AGGCAGAAGA	ATGGAGGAAG	TCACGGCCTA	GGGAGTTAAC	AGTGTTAGGA	GCAAGAGAGG	300
TTTTAACTAA	TGAGCCATGG	AGTTTAAGCA	GAGACAATAG	AGAATAAAGT	AAAATAGGAA	360
GAAAAATTTA	AAAAGAAAGT	AGAAAAGTCC	TCGAG			395

- (2) INFORMATION FOR SEQ ID NO:1236:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 565 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

GAATTCGGCC	TTCATGGCCT	ACACAATTCC	AAAGAAGGTG	GTGTGCCACT	TCAGTGGGAA	60
GGCCTATGCC	GACGAGGAGC	GGTGGGACCT	TGACAGCTGC	ACCCACTGCT	ACTGCCTGCA	120
GGGCCAGACC	CTCTGCTCGA	CCGTCAGCTG	CCCCCCTCTG	CCCTGTGTTG	AGCCCATCAA	180
				GTCCCAGAAC		240
				GAGGTTCCCC		300
				GGTCACCTCC		360
CAGAGATAAC	AGGCTGCACC	CAAGTGAAGA	TTCTTCACTG	GACTCCATTG	CCTCAGTTGT	420
GGTTCCCATA	ATTATATGCC	TCTCTATTAT	AATAGCATTC	CTATTCATCA	ATCAGAAGAA	480
ACAGTGGATA	CCACTGCTTT	GCTGGTATCG	AACACCAACT	AAGCCTTCTT	CCTTAAATAA	540
TCAGCTAGTA	TCTGTGACGC	TCGAG				565

- (2) INFORMATION FOR SEQ ID NO:1237:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

GAATTCGGCC	TTCATGGCCT	ACACTGAGAA	CGAGATGGCT	ATTTATGAAT	TCATTCATAA	60
CTTTGTGGAA	GTTTTAGATG	AGTATTTCAG	CCGAGTGAGT	GAATTAGATG	TATCCTTTTT	120
CAATACTGTT	TTCCACAGTA	CTTGGCAAAT	GCACTCTGGT	CCTTATCAGG	TAAGTACCAC	180
AAGGCAGGAA	AACTATTCAG	CAGAGTCCAG	AGTGTTCATC	ACCAACAACT	ATGACAAGAC	240
AGCCAGAGGT	GTGTGTGTTC	TGCAGAACTC	CTCCCCAACT	TCGTCACCCA	AGCTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:1238:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

120
180
240
300
303

- (2) INFORMATION FOR SEQ ID NO:1239:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

GAATTCGGCT TCATGGCCT	a amammamama	3C3C3C3333	CTACCCAACC	CCAGGGGAAG	60
GTGCCGTGTG GAGAGCACT	TCGGATTCGG	CAGAATCTAC	CAGAGCACAC	CCAAGGCTGG	120
CTTGGGAGCA AATGGCTCT	GCTTCTTTT	GTTGTTGTGC	CGTTTGTGAT	ACTGCAGTGT	180
CAAAGAGACA GTGAGAAGA					240
CACTCTCCAT TAAAGAAAA	A AAGAAATGCT	TCCCCCAACA	AAGACTGTGC	ATTCAATACC	300
TTARTCGARC TCGAG					315

- (2) INFORMATION FOR SEQ ID NO:1240:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 553 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

GAATTCGGCC TT	CATGGCCT A	AAAATGACCT	TGGTAAGAAT	GGGTTTTTAC	AATAAATGAA	60
TTTTTAATTC CA	AGATGTTT 3	TTTCATTGAA	ATTACTGCCC	CAGTTGCATT	AAAAGTGTGG	120
CTGTGCAAAG CT	TCCTTCTA (CCAGGCTTCA	TGTGCAGGAC	CTTGGTTTTT	GTTGCCTTGG	180
CAATTCCAAA AG	CAGGTGTT (GAAAGAGAAG	AAGACAGGAA	AAAGAAGATG	GGAGAAAAAT	240
TTTCCAAATC AG	AGTTCTCA (GTCCAAGGAC	TTATTCTTGG	GGGTTCAAAA	ATTCTAACAG	300
TATTTTTAAA TI	GCCTCTAT 1	TTCGATGGTT	ACTTGATTAA	ACTGTTCTAA	CATTTCTAAA	360
AATAAAAATT TO	CAATGATA	ACTTTTATAT	CAGACTTTAC	CTCTGTTTCC	CAAATTGGAA	420
TCTTTAGGAA TA	TTTTTTTG /	AGATCACTTT	TTTCCTTTTT	TTCTTTAACA	AAGATTGGGA	480
ACCGCTCTTA GO	AACAGACA	AATGGATTTC	CATATTTCTT	AAAGCGTTGA	AGTAAATCTC	540
TGCCACCCTC GA	√G					553

- (2) INFORMATION FOR SEQ ID NO:1241:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

GAATTCGGCC	TTCATGGCCT	ACTCTTCTCA	AGGCTTTGAA	ATCTCCCCTT	GCACTGAGAT	60
TAGTCGTCAG	ATCTCTCCCC	GTCTCCCTCC	CAACTTATAC	GACCTGATTT	CCTTAGGACG	120
GAACCGCAGG	CACCTGCGCC	GGGCGTCTTA	CTCCCGCTGC	TTGTTCTGTC	CCCTCCCTCG	180
GACCAAACAG	TGCTCATGCT	TCAGGACCTT	GTTTGTCGAA	GATGTTGGTT	TCCCTTTCTC	240
TGTTATTTAT	ATAAAAATAA	TTTATCAAAA	GGATATTTTA	AAAAAGCTAG	TCTGTCTTGA	300
AACTTGTTTA	CCTTAAAATT	ATCAGAATCT	CAGTGTTTGA	AAGTACTGAA	GCACAAACAT	360
ATATCATCTC	TGTACCATTC	TGTACTAAAG	CACTTGAGTC	TAATAAATAA	AGAAATCAGC	420
ACCCCTAGGC	CATGAAG					437

- (2) INFORMATION FOR SEQ ID NO:1242:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 523 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

GAATTCGGCC	TTCATGGCCT	ACAAAAATAT	GTCTTTTGAA	AACCNAGTCA	AGTACCTAGA	60
GATGAAAACC	ACAAATGAGA	AACTGTTACA	GGAATTAGAT	ACACTTCAAC	AACAATTGGA	120
TTCACAGAAC	ATGAAAAAAG	AGAGCCTGGA	AGCAGAAATA	GCTCACTCCC	AGGTGAAACA	180
GGAGGCGGTA	TTGCTGCATG	AAAAACTTTA	TGAGTTGGAG	TCCCATCGAG	ATCAAATGAT	240
TGCAGAAGAC	AAAAGCATAG	GATCTCCAAT	GGAAGAGAGA	GAGAAATTAC	TTAAGCAGAT	300
TAAAGATGAT	AATCAGGAAA	TAGCCAGCAT	GGAAAGACAG	TTAACAGATA	CAAAAGAAAA	360
GATAAATCAG	TTTATTGAAG	AAATTAGACA	ACTTGACATG	GATTTAGAGG	AACACCAAGG	420
TGAAATGAAC	CAGAAATACA	AGGAGCTAAA	GAAAAGGGAG	GAACATATGG	ACACTTTTAT	480
TGAGACTTTT	GAGGAAACAA	AGAATCAGGA	ACCAAAACTC	GAG		523

(2) INFORMATION FOR SEQ ID NO:1243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

GAATTCGGCC	TTCATGGCCT	AACTGATTAC	AGGGAAAGAC	AAAAAGCAAA	AGGTGATTGA	60
AACATAGTTC	TAAATAACAA	GAAGGGAAGT	TTTCTTAAAC	TGATCATCTG	TCTTATTGTC	120
ATGACAAAGG	GTAAAATTTT	ATTTTCAGTC	CTTTAGTGCT	TTTTAATAAT	TCACCATACA	180
TATTTTACTT	ATATCCCATT	AACTGTGGGA	CTTAGCACAG	TTTACATTTT	CAGTCATGTG	240
AATATAATTA	TCTGTATTCC	CTGTTGGACT	GATGGGGGAA	ATTGGATCAT	TATAATATT	300
AAAAGACACC	TCCCCAGGCA	CCCATTGTGT	TCTTAGGAAG	TCAGTGCTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:1244:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

GGCT	TCATGGCCTA	ATTCAGCTTT	ATCGTTCCCT	CTGGCAGTTC	AGTTGTTGGC	60
TAT	TAAGGTTCGA	CAGAAAGCAA	CTGAAATCTC	CCTTAGAAAT	AAAGTTCCTG	120
AGAA	AAAAAAGATC	CATAAAAAGT	CTCATCCTTA	GGACAGCAAC	TTTTATAATG	180
TGAT	CTGAATAGCT	CTCTGGATTG	TGGCCTTGGA	CAACAGTTCA	GACTGCATTA	240
ATGA	ACCTTGAGCT	TTCTGAGTCT	CTTCTTTTTG	CTCTTTTACT	AGCAGACCCT	300
						306
	TTAT AGAA TGAT ATGA	TTAT TAAGGTTCGA AGAA AAAAAAGATC TGAT CTGAATAGCT ATGA ACCTTGAGCT	TTAT TAAGGTTCGA CAGAAAGCAA AGAA AAAAAAGATC CATAAAAAGT IGAT CTGAATAGCT CTCTGGATTG ATGA ACCTTGAGCT TTCTGAGTCT	TTAT TAAGGTTCGA CAGAAAGCAA CTGAAATCTC AGAA AAAAAAGATC CATAAAAAGT CTCATCCTTA IGAT CTGAATAGCT CTCTGGATTG TGGCCTTGGA ATGA ACCTTGAGCT TTCTGAGTCT CTTCTTTTTG	TTAT TAAGGTTCGA CAGAAAGCAA CTGAAATCTC CCTTAGAAAT AGAA AAAAAAGATC CATAAAAAGT CTCATCCTTA GGACAGCAAC IGAT CTGAATAGCT CTCTGGATTG TGGCCTTGGA CAACAGTTCA ATGA ACCTTGAGCT TTCTGAGTCT CTTCTTTTG CTCTTTTACT	GGCT TCATGGCCTA ATTCAGCTTT ATCGTTCCCT CTGGCAGTTC AGITGITGGC ITAT TAAGGTTCGA CAGAAAGCAA CTGAAATCTC CCTTAGAAAT AAAGTTCCTG AGAA AAAAAAGATC CATAAAAAGT CTCATCCTTA GGACAGCAAC TTTTATAATG IGAT CTGAATAGCT CTCTGGATTG TGGCCTTGGA CAACAGTTCA GACTGCATTA ATGA ACCTTGAGCT TTCTGAGTCT CTTCTTTTTG CTCTTTTACT AGCAGACCCT

- (2) INFORMATION FOR SEQ ID NO:1245:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

GAATTCGGCC	TTCATGGCCT	AGGGTTTGGG	GGTTCTGAGA	TGTTACTCTC	ACTGAAGTCT	60
GTGTGGGAGG	CGGATTACTA	AACAAGAAAT	TGCTAATTAA	TCTCCAGATG	GCAAGGAATG	120
GATAAAGCAC	TGTTCCCAAC	AAGGTCCAAA	TGTCTCCGCT	GGAAGAGTGT	ACAATGGATG	180
CAGTTGGTCT	TCCTGCTGGC	AACAGTACCA	CCGAAGCGCT	TGGGGCAAGT	TCCAAATCCA	240
GTAACTTCTT	TTTATAATCT	TCTTTGGTAA	ATTCCCTCCT	GGGAAACATG	GTTGCTAACG	300
AAAAATTACC	GTAAGTGTTG	CCAACAGTCT	GTGCAGCAAA	CTGCCTTGCC	TCTTCTAGAG	360
GAGCATCAGA	AGGGAACTGA	TTTGTAAAGG	AAGAACCATC	AGGAAGACGG	AATTGAATTC	420
TTGCAACAGT	GCTTCTTTCT	CTTGCATAAG	ATTCCCTCTT	GACTTCCATT	TCTGCCTGTT	480
TTGCTAGCAA	GGCAGCAGCT	TTGGCAGCCT	CTACTTCTTC	CTTTGTCTTT	GCAAAACGAG	540
CAGCTCTCTC	TGCACGGTCC	AATGCAATCT	GCTGTTTTAT	ACGTTCTCGA	G	591

- (2) INFORMATION FOR SEQ ID NO:1246:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 593 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

GAATTCGGCC	TTCATGGCCT	ACTTCGGGGA	AGAAACCTTC	ACCAGAGTGG	AGCAGTTCAG	60
ACCATGGAAC	CTCTGATCCA	AGCAGCCCAG	CTCCTGCAAT	TAAAGAAGAA	AACCCAGGAG	120
GACGCAGAGG	CTATCTGCTC	CCTGTGTACC	TCCCTCAGCA	CCCAGCAGAT	TGTCAAAATT	180
TTAAACCTTT	ATACTCCCCT	GAATGAATTT	GAAGAACGGG	TAACAGTGGC	CTTTATACGA	240
ACAATCCAGG	CACAACTACA	AGAGCGGAAT	GACCCTCAGC	AACTGCTATT	AGATGCCAAG	300
CACATGTTTC	CTGTTTTGTT	TCCATTTAAT	CCATCTTCTC	TAACCATGGA	CTCAATCCAC	360
ATCCCAGCGT	GTCTCAATCT	GGAATTCCTC	AATGAAGTCT	GAAGATGCAT	GTTTCCAGCA	420
TTAGTTTGAT	TCCCAATGTG	AGCAAGAAGG	AAGTATATAC	AGTAAAGTAA	ATTCAAGGAT	480
CTGTTAAATC	TGGTAAAAGT	AGATCAAATC	AGAGATTGAC	AGCCTGTGGA	GGGTGCTGAA	540
CTATACAGAA	TTAGACACAA	CTATGTCATT	ATTTTTTGTA	CCAACTACTC	GAG	593

- (2) INFORMATION FOR SEQ ID NO:1247:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 599 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

GAATTCGGCC	AAAGAGGCCT	AAACTCAGAA	TGGTGCTACT	TGAAGACTCT	GGATCTGCTG	60
ACTTCAGAAG	ACATTTTGTC	AACCTGAGTC	CCTTCACCAT	TACTGTGGTC	TTACTTCTCA	120
GTGCCTGTTT	TGTCACCAGT	TCTCTTGGAG	GAACAGACAA	GGAGCTGAGG	CTAGTGGATG	180
GTGAAAACAA	GTGTAGCGGG	AGAGTGGAAG	TGAAAGTCCA	NGAGGAGTGG	GGAACGGTGT	240
GTAATAATGG	CTGGAGCATG	GAAGCGGTCT	CTGTGATTTG	TAACCAGCTG	GGATGTCCAA	300
CTGCTATCAA	AGCCCCTGGA	TGGGCTAATT	CCAGTGCAGG	TTCTGGACGC	ATTTGGATGG	360
ATCATGTTTC	TTGTCGTGGG	AATGAGTCAG	CTCTTTGGGA	TTGCAAACAT	GATGGATGGG	420
GAAAGCATTA	TTGCAATCAC	AATGAAGATG	CTGGCGTGAC	ATGTTCTGAT	GGATCAGATC	480
TGGAGCTAAG	ACTTAGAGGT	GGAGGCAGCC	GCTGTGCTGG	GACAGTTGAG	GTGGACATTC	540
AGAGACTGTT	AGGGAAGGTG	TGTGACAGAG	GCTGGGGACT	GAAAGAAGCT	GAACTCGAG	599

- (2) INFORMATION FOR SEQ ID NO:1248:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

GAATTCGGCC AAAGAGGCCT AACCGAATGG ATTATCTGTG GGAGTAACAT CTCAGAAGAC

60

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TATGAAGCTA	ATTCCTGCCT	CAAGACACAG	AGCTACACAA	AAGGTGGTTA	TTGGAGATCA	120
TGATGGGGTA	GTTATGTGCT	TTGGCATGAA	GAAAGGAGAA	GCAGCAGCAG	TGTTCAAGAC	180
TTTACCCGGG	CCGAAGATTG	CAAGGCTGGA	ACTGGGAGGG	GTTATCAACA	CACCTCAGGA	240
GAAAATTTTT	ATTGCTGCAG	CATCTGAGAT	TAGAGGCTTC	ACAAAAAGAG	GAAAACAGTT	300
CCTCTCCTTT	GAAACAAACC	TCACTGAAAG	CATTAAAGCT	ATGTATGTCT	TTTGTTCTCT	360
TTTGTATTTT	TACATACTTA	TTTATAATAT	TTTGGATAGA	TGTGAGGCAA	CCCTCGAG	418

- (2) INFORMATION FOR SEQ ID NO:1249:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 800 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

GAATTCGGCC	AAAGAGGCCT	AGCAGAGCAC	AGCATCGTCG	GGACCAGACT	CGTCTCAGGC	60
CAGTTGCAGC	CTTCTCAGCC	AAACGCCGAC	CAAGGAAAAC	TCACTACCAT	GAGAATTGCA	120
GTGATTTGCT	TTTGCCTCCT	AGGCATCACC	TGTGCCATAC	CAGTTAAACA	GGCTGATTCT	180
GGAAGTTCTG	AGGAAAAGCA	GCTTTACAAC	AAATACCCAG	ATGCTGTGGC	CACATGGCTA	240
AACCCTGACC	CTTCTCAGAA	GCAGAATCTC	CTAGCCCCAC	AGACCCTTCC	AAGTAAGTCC	300
AACGAAAGCC	ATGACCACAT	GGATGATATG	GATGATGAAG	ATGATGATGA	CCATGTGGAC	360
AGCCAGGACT	CCATTGACTC	GAACGACTCT	GATGATGTAG	ATGACACTGA	TGATCTCACC	420
AGTCTGATGA	GTCTCACCAT	TCTGATGAAT	CTGATGAACT	GGTCACTGAT	TTTCCCACGG	480
ACCTGCCAGC	AACCGAAGTT	TTCACTCCAG	TTGTCCCCAC	AGTAGACACA	TATGATGGCC	540
GAGGTGATAG	TGTGGTTTAT	GGACTGAGGT	CAAAATCTAA	GAAGTTTCGC	AGACCTGACA	600
TCCAGTACCC	TGATGCTACA	GACGAGGACA	TCACCTCACA	CATGGAAAGC	GAGGAGTTGA	660
ATGGTGCATA	CAAGGCCATC	CCCGTTGCCC	AGGACCTGAA	CGCGCCTTCT	GATTGGGACA	720
GCCGTGGGAA	GGACAGTTAT	GAAACGAGTC	AGCTGGATGA	CCAGAGTGCT	GAAACCCACA	780
GCCACAAGCA	GTACCTCGAG					800

- (2) INFORMATION FOR SEQ ID NO:1250:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

CAATTGCCAA GGAAAC	AGGC CTTGGCCTGA	AGGTACTAGG	AGGAATTAAC	CGGAATGAAG	60
GCCCATTGGT ATATAT	TCAG GAAATTATTC	CTGGAGGAGA	CTGTTATAAG	GATGGTCGTT	120
TGAAGCCAGG AGATCA	ACTT GTCTCAGTCA	ACAAGGAATC	TATGATTGGT	GTATCATTTG	180
AAGAAGCAAA AAGCAT	AATT ACCGGAGCCA	AGTTGAGTAC	TAGGTTAGAA	TCTGCTTGGG	240
AGATAGCATT CATAAG	ACAA AAATCCGACA	ACATTCAGCC	AGAAAATCTG	TCATGTACAT	300
CACTTATAGA AGCTTC	AGGA GAATATGGAC	CTCAAGCCTC	CCTCGAG		347

- (2) INFORMATION FOR SEQ ID NO:1251:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

GAATTCGGCC	TTCATGGCCT	ACAGCCCTCT	TACTAGGCCA	GCACGCTTTC	GCTTTTGCAT	60
TTACAATCAC	ATACCCCATC	CCCTCCACTT	GAAAAAGAAT	TTTGTTTTTG	TCGTTATCCA	120
AAAATCTCAT	CTTAAATCAA	CCGTCTCGTC	TCCCTGTAGC	TTCATTACCA	TCTCAGAAGC	180
AGCAAAGGAG	CCAGCAAAAG	CTAAGGTACA	GAAAGTCGCT	TTGGAGGATG	ATGGTGAGTG	240
GTTATACTTA	ATAGAAGCTA	TCATTTATTA	AGCACCTAAT	GTGTGTCTGG	AGGGGCTCGA	300
G						301

- (2) INFORMATION FOR SEQ ID NO:1252:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

GAATTCGGCC	TTCATGGCCT	TGCATGCCCA	CAGTGAGCTG	AGATCGCAGC	ACTGTACTCC	60
ATCCTGGGGG	ACAGAGCTAG	ACTCCATCTC	AAAAACGAAA	GTGCCTGGTC	GTCTTTCCAC	120
ACGACTCCGT	TTCCACTCCC	ATAAAATGCT	ACGTTAGCTG	TTTTGAGGGT	AGATGCCCTT	180
AGACTGCCAA	CTCACAAAGT	TTTATTGGGC	ACCTGTTACC	TGTTCAGCAG	AGATTTGTAA	240
AAAAAGACAC	ATCAGGTGGC	CTTTGCTTGC	AAGAAATCAG	CCTTTGGAAC	CTGTGGAGAA	300
AAGTTAAATA	CTGCGTACTG	TGCAAATGAA	GGGTGGGAGC	TATTGAAGGG	AAGAGATTCA	360
CCCTGAAAAC	CCAAGAATGG	CCAAATCTCG	AG			392

- (2) INFORMATION FOR SEQ ID NO:1253:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 610 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

GATTCGGCCT	TCATGGCCTA	GCTGGTCTCT	GGTTGCAGGA	TCGAATCGCC	CCCAGCAGTA	60
TGTGTATATG	CATCAGATAA	GGTGAGGGAC	AACCTTCCTC	ACCCCCATAC	CTGGCCAGCC	120
TGTAATGGGG	AGGAGGCCTT	TCTGTGGTGT	GGTGGGGCTG	GAGATTGGGC	AGGGACAGAG	180
ACATACCTTC	TCTGGGAATC	TGAGAGAGAT	ACCTTGAATC	TAGGGGAAAG	GGATTAGGTT	240
TTGAAAATGT	TAGCCATTTT	GTAAAGAGAA	GTCCCTCACC	ATTTCCCTTC	CCATTAGTCC	300
TGGGAAATAG	ATTGGGTAGA	GGCTCAGAGC	CTGGCCCCTG	CTGCACTCCC	AGCTTGGAGC	360
TACTGGGTTG	TTGACAATGT	TTTGGGGTTT	CCAGGCCTTA	GCAAGAGAAA	GCCTCCCCAG	420
ATACCAGTCT	AGGGGTAGAT	GAAGGGGGCA	GGAGCCCTGA	AGGAAGGATT	TGGGGCCGGC	480
CATTCATTCA	TTCAGAAACA	CTTATCATCC	CTTATCAGAA	GCCCTGACCT	ATTGAGAGTC	540
AGGCACGTGC	TATTGAGAGT	CAGGCACGTG	CTCATATAAA	GATGAGTTTA	ACATGGATCT	600
CCCTCTCGAG		•				610

- (2) INFORMATION FOR SEQ ID NO:1254:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 328 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

GAATTCGGCC	TTCATGGCCT	AGAGGATTTA	CACATGGCAT	TCAGTGTTCT	GTATAGATCT	60
GCCTACCTTT	GTGAATTCAT	CTGTTAACCC	CTCTTCCTTT	GAGAGAGCAC	CGGCGATGGT	120
GGTTAACTCC	TGTGTTTTCT	CTCTCTCCTA	CTGGTTATTC	TTGAATTAAG	CACAGACTCG	180
TCAGCTCGGT	TGCTTTATCA	TGAATAATGT	GTGTGACCTT	GCAGTTCTTC	CACAGTTCAG	240
CAAACAAGTG	CTAGCTTCAC	TGACCAAAAA	TTAAGGAAGG	AAAACACAGT	TTTTAAAACG	300
ATCCATCTTT	TAACAGCCGA	AACTCGAG				328

- (2) INFORMATION FOR SEQ ID NO:1255:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

GAATTCGGCC	TTCATGGCCT	ACTAAGAGAA	CAATTAGAAT	ATTGGAAGAT	AAAGGGACAA	60
GTACTGAATT	AGTTAAAGAA	AATCAGAAAC	TTAAGCAGCA	TTTGGAAGAG	GAAAAGCAGA	120
AAAAACACAG	CTGTCTTAGT	CAAAGGGAGA	CTCTGTTGAC	AGAAGCAAAG	ATGCTAAAGA	180
GAGAACTGGA	GAGAGAACGA	CTAGTAACTA	CGGCTTTAAG	GGGGGAACTC	CAGCAGTTAA	240
GTGGTAGTCA	GTTACATGGC	AAGTCAGATT	CTCCCAATGT	ATATACTGAA	AAAAAGGAAA	300
TAGCAATCTT	ACGGGAAAGA	CTCACTGAGC	TGGAACGGAA	GCTAACCTTC	GAACAGCAGC	360
GTTCTGATTT	GTGGGAAAGA	TTGTATGTTG	AGGCAAAAGA	TCAAAATGGA	AAACAAGGAA	420
CAGATGGAAA	AAAGAAAGGG	GGCAGAGGAA	GCCACAGGGC	TAAAAATAAG	TCAAAGGAAA	480
CACTCGAG						488

- (2) INFORMATION FOR SEQ ID NO:1256:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

GAATTCGGCC	TTCATGGCCT	AGATCCAGAC	ACGGCACTGC	AGCTTTCAGC	TGACTAGCTG	60
TGTGACTTGG	GCAAGCCCCT	TAATCTCTCT	GATCTCGGGC	TCCCTCCTCT	GTAAAATGGA	120
ATTAAGAATA	ACCTCATTGA	GGAGCTTCCT	GAGGAGGTAA	GGAAAGTGCC	TGGCACAGTG	180
CCAGGCTGCT	AAGAGATCAA	TAAATGTCCC	ATCCCCCAGC	CCCACCCCAG	TTCTTTCCAG	240
GAATTTGAGA	GACTCCTCCC	CCTGTGTTTG	AAAGTGGCAA	AGTCTGGCAC	ACTTGCCTCA	300
TAACACATAA	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:1257:
 - (i) SEQUENCE CHARACTERISTICS:

PCT/US98/06955 WO 98/45436

(A) LENGTH: 346 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) Torobodi. Illiear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:	
GAATTCGGCC TTCATGCCTA AGCTTCCTTC AGCAGCGCAG GCGGTGGTCC CTGAGGCCCG	60
TGGAAGGAGT CAAACTTGCG GGAATTTTGC AGTTTATCTG CAGGGCTGTT GTTTCCAGCA	120
AGACCCAAAG CTAGAAAAGG AGGAGGAAGA AACTGACCCG ATCAGTGCCA GAAGTCATTG	180
TATTCAAAGA AGAATAAGCA AGAAAGAAAA GAAGGAAGGA AGAGAGGTAG ACAGATACAA GATGAAATCC TGTCAAAAAA TGGAAGGAAA ACCAGAAAAT GAGAGTGAAC CAAAGCATGA	240 300
GGAAGAGCCA AAGCCTGAGG AAAAGCCAGA AGAGGAGGAG CTCGAG	346
	2.0
(2) INFORMATION FOR SEQ ID NO:1258:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 346 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:	
(XI) SEQUENCE BESCRIFTION. SEQ ID NO:1256.	
GAATTCGGCC TTCATGGCCT ACGGCACTTC AAAAATATAA ATCAAAGTCC ATGACTCTAA	60
AAATAACATA TGCATTGATA TGCTCGCCCC TTTGACCCTT CTCTCAAGAG AAATTCCCTG	120
CCAAGTAATC CACATACATA AGAAGTGTAA AAAGTCCCTA GATTAAAAGA GCATAAAACT	180
TCATTATGGA AACACAGTAG TCCCGGCTAT TTGGGAGGCT GAGACAGGAG GATCACGAGT CCAGGAGTTT GAGGCTACAG TGAGCTATGA TCGCGCCATT GCACTCCAGC CTGGATGACA	240 300
GAGGAAATAT TAATTTTAGA GTAATCAGAG AAAGCCAGGT CTCGAG	346
(2) INFORMATION FOR SEQ ID NO:1259:	
(2) Internation for page 12 no. 1235.	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 341 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:	
GAATTCGGCC TTCATGGCCT ACCCCATTCA TGCAGGAATA AATCAAGTGA GCAGTTCCAG	60
ACTITICAT AATATITITA CTATGATGCT GTTTTATTAA TATTITCTAA ATTTCAAAAC	120
AAAAAGTGAA TGTTTGAAAT TGCTGGGTCC CGATGTTGGT GGCTGTTGGA GTTTTGGACC	180 240
ACTCGCTAGC AGTGATTTGA AGATTATAAT TAGCTAAAAT CCAAAAACAAA AAACCAACAA CAAAAATTGT ATGGTGCGGA ACATGCACCT TGACAATGGT ACTAACTTGT TATTCTATAG	300
AACACGTTAG AATAGATCTA TTTTTGCCAG AGCTTCTCGA G	341

- (2) INFORMATION FOR SEQ ID NO:1260:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 416 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

GAATTCGGCC	TTCATGGCCT	AAAGATAAGG	TGGCTGTAAA	TGCGTGGATT	TATACCTGAG	60
TTCTCTCATC	TGTTTCACTG	ATCCATGTGT	CTGTTTTTAT	GCCAGTACCA	TGCTGTTTTG	120
ATNACTATAG	CTTTGTAATA	AATTTTGAAG	TCAGGTAGTG	TGATNCCTCC	AGCTTCATTC	180
TTTTTGCTCA	GGATNGCTTT	GGNTATTCAT	AGTCTTGTGG	TTCCATGTAA	ATTTTAGGTT	240
TTTTTTTTT	TTTTTTTTT	TTTTTACTAT	TTCTGTGAAG	AATGTTATTG	GTATTTTGAT	300
AAGGATTGTA	TTGAATCTGT	AAATTGCTTT	GGGTAGTCTT	GTCATTTAAA	AATATTGTTA	360
TAGTTCTTCT	AATCCATGAA	CATAGAATAC	CTTTCCATTT	TTTTGGTGTC	CTCGAG	416

- (2) INFORMATION FOR SEQ ID NO:1261:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 base pairs

 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

GAATTCGGCC AAAGAGGCCT AGGCAGACAT CCATAAACAT TTTCAAAATG CAGGGTATGT TTTTCAGTGT TAAGGCAACT GTTCTG 86

- (2) INFORMATION FOR SEQ ID NO:1262:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

GAATTCGGCC	AAAGAGGCCT	ACTTTTGGTA	ATAACATTTT	AAAGCAGGAA	GTATCTACGG	60
TGTGATCGTG	GTACAGCTCT	TAGTTCAAGT	GTGAAGACAT	TTGGTTGTCT	TGTATATGAC	120
CTAGAAGAAG	GGGCGTCTGC	TGGAAAACAA	TGCTGTTCTT	TTTCTCTTTG	TTTTTTGGGA	180
CGGGGTCTTA	CTCTGTTGCC	CAGGCTGCAG	TGCAGTGCCT	CAATTTTTCA	GTTCAGTGCA	240
GCCTCGACCT	CTGGGGCTTA	AGCGATCCTC	CTGCCTCGGC	CTCCCCAGTG	ACTGAGACCG	300
CAGGCACACA	CCACCACACC	CGGCACCTCG	AG			332

- (2) INFORMATION FOR SEQ ID NO:1263:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

GAATTCGGCC	AAAGAGGCCT	AAGCCAGGGT	AGGGACAGCA	GACTGGCAGG	AATGAGTGAC	60
AGTTCTATGC	AAATGGAGTT	ATTATTATTA	TTGTTATTAT	TAATAAGGGC	AGGTTTGTAC	120
CAGAACTGCC	CAGTATGGCC	TGTGACTTCT	GCGCAGCAAT	TATTTCTCCA	GGGACAGGGC	180
CTGAAGCTAC	CTCACAGTGA	TGCAAAAAAA	TGGGATTCCC	CACTAACCCC	CACACACACC	240
CCCTTCCTAC	CAAACCACAC	ATCTCTCAGT	CCTCTCGAG			279

- (2) INFORMATION FOR SEQ ID NO:1264:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 629 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

GAATTCGGCC AAAGAGGCCT	AGGATCACGG	AGGTGGTGCC	TGTGTGTCCC	ACAGGAAGCA	60
AAAGCTGATG CCCAGTTCCC	AGCATACCTA	AGTAAACTTC	AGGTCCACTC	CCAGCACGTT	120
TCTCGTGATA GTAAAACTAT	GAAGGAACTC	AGTGTACAAG	GAGCTTCTAC	AAAATAGGCA	180
GAAGACAGTA GCCAGATGGG	CCAAGGCCC	CAGCCACCCA	CGCCCCTCCC	TCTCCTTGAA	240
GACCTTCGGT TCCAACCCCA	CCATCAGCAG	GGCTCTGCTC	AGTTCCTCCT	TATGTGTATC	300
ACCACAGGGC TGCTGGCTCG	TGTCACGTTC	ACCACCAGAC	CCCACATCAG	GAGTCCCGCC	360
AGGGGTGTGG GGAGGCAGCG	CTGCCTGGTT	GGCCGTGGAG	CCGTATGGAA	CATGGTGCCT	420
CACAGGCAGT CTGCTTGGCG	TCCTGGATCC	TGGCTGTATC	CCGCTGGAAA	GGATGTGTGT	480
GGGTCTAAGA TATGTATATA	ATAGAAACAT	TTATTCAGAA	GCTTTAGTCA	AGACTTCATT	540
TTTAAGTTCA GAGTAATAAA	CTCATAGTCT	AAATTTCCTA	ATTTTTCTGT	TTAATTTACA	600
TAAATAAAAT GAAATGCAAT	TTCCTCGAG				629

- (2) INFORMATION FOR SEQ ID NO:1265:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

GAATTCGGCC	AAAGAGGCCT	AGAGGTGCCC	ATTTCAATAA	ATTTTAGCAC	ACTGGATGAT	60
AAAGGAGAAA	TGCTTTGGTT	TAAGAGAGGG	AAATCTTTGT	TACCAATACT	ATCGGTGAGT	120
TCACCTAATA	CTTCCTCGTC	ATCAAGTTCA	TTGGAGTACG	CATCTTCTTC	ATCCTCATCT	180
CCCGGTTCAG	TGGGTTCACT	TTTGACAGGG	CACTCCCCGT	TTGGGTGTAA	AACGTTGCTT	240
TCTTTTGGCC	TTTCACAGTT	GTTCTCTTGG	TCTTTGCTCT	CTGACATCTT	GCTAGACTCA	300
GACGATGAGT	GGCTGAGGGA	GACAGAGGTA	ATTGGGGTGT	TCACTACTAA	ACTAGACAGC	360
CCCCCAGAT	TCACTTCAGC	CTTTGGCATT	TGGGTAATCC	CCAGCGGCTG	CTCTGCTGAG	420
CTCGAG						426

- (2) INFORMATION FOR SEQ ID NO:1266:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

GAATTCGGCC	AAAGAGGCCT	ACCGCCCATC	GCGCCGGCGC	GACCCGCAGG	AGCGTAGAGA	60
GCGCGGGACT	AGAGTGCAGA	GCTCCGGGAC	GTGGATCGGA	GCCGGCGCGA	TGGGCGGAGA	120
GCAGGAGGAG	GAGCGGTTCG	ACGGCATGTT	GCTGGCCATG	GCTCAGCAGC	ACGAGGGCGG	180
CGTGCAGGAG	CTTGTGAACA	CCTTCTTCAG	CTTCCTTCGA	CGCAAAACAG	ACTTTTTCAT	240
TGGAGGAGAA	GAAGGGATGG	CAGAGAAGCT	TATCACACAG	ACTTTCAGCC	ACCACAATCA	300
GCTGGCACAG	AAGACCCGGC	GGGAGAAGAG	AGCCCGGCAG	GAGGCCGAGC	GGCGGGAGAA	360
GGCGGAGCGG	GCGGCCAGAC	TGGCCAAGGA	AGCCAAGTCA	GAGACCTCAG	GGCCCCAGAT	420
CAAGGAGCTA	ACTGATGGAG	AAGACTCGAG				450

- (2) INFORMATION FOR SEQ ID NO:1267:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

GAATTCGGCC	AAAGAGGCCT	AGCTACTAAG	GCAGGTGCAG	CATCAATGAT	TCACTACATG	60
GTTCTGATAT	CAGCTCGCTT	GGTACTACTC	ACTTTGTGTG	GATGGGTACT	TTGTTGGACC	120
CTCGTCAATC	TCTTTCGAAG	CCATTCAGTC	CTCAATCTCC	TTTTCCTTGG	CTACCCGTTT	180
GGTGTTTATG	TTCCTCTTTG	CTGTTTTCAT	CAAGATAGTA	GAGCACATCT	TCTTCTCACA	240
GACTACAACT	ATGTGGTTCA	GCACGAGGCA	GTAGAGGAAA	GTGCCTCGAC	TGTGGGAGGC	300
TTGGCCAAAT	CCAAAGACTT	TCTCTCCTTG	TTGCTGGAGT	CGCTAAAAGA	ACAGTTTAAT	360
AATGCCACAC	CCATCCCCAC	CCACAGTTGT	CCCCTATCTC	CAGACCTCAT	TCGCAATGAA	420
GTAGAATGTC	TGAAAGCAGA	TTTCAACCAC	CAACTCGAG			459

- (2) INFORMATION FOR SEQ ID NO:1268:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

GAATTCGGCC	AAAGAGGCCT	AGAGTTTTCA	TAAGCCCGGC	TGGTGTTTAA	AACGTGTTTT	60
GGCTTTGTTC	ATTTTATGGT	GTTGGTGTTG	GTATTGGTGG	TCATGTACTG	GCATGTAAGA	120
TTTCTTTTCT	CTTTCCCTCT	TCTCTCTGCT	TCTACATTCT	GTTCATTGAG	GCTTCCAACT	180
GAATATGAGA	GGAACGGGAG	ATATGAGGGC	TCAAGTCGCA	ATGTATCTGC	TGAGCAAAAA	240
GATGAAAACA	AAGAAGCAAA	GCCTCGATCC	CTACGCTTCA	CCTGGAGCAT	GAAAACCACT	300
AGTTCAATGG	ATCCCGGGGA	CATGATGCGG	GAAATCCGCA	AAGTGTTGGA	CGCCAATAAC	360
TGCGACTATG	AGCAGAGGGA	GCGCTTCTTG	CTCTTCTGCG	TCCACGGAGA	TGGGCACGCT	420
GGTAACCTCG	AG					432

(2) INFORMATION FOR SEQ ID NO:1269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

GAATTCGGCC	AAAGAGGCCT	ACCCTGAACT	ACTCCAGTGT	GCACCTGCAC	AACCTCCATG	60
GTGCCTCTGG	AATTGGGTAG	CATGGTGGCC	CTGCTGATGA	GCACCCCAAG	GGGCCATTGG	120
GGGACCTCTG	AGAATCTCTG	CCAGAGCAGT	TTGGGTGGGA	GTCGATTAAG	GAAAGAAGCA	180
GCAAGATCCA	GGACTTTTAA	TCTTAAAAGA	GAGAGAAATG	CTGGCAGATG	AACATTCTGA	240
GGATAAGGAG	CCTGAGTAAT	TGAGCGATTA	GGGATGGAGA	CATACGATTG	AATTCTAGAC	300
CTGCCTCGAG	TAGCCAATCA	AGCTGTGTCT	GGCTGTGCAC	TATCCAGGCC	TCCACATTCT	360
GTGACAAACT	AACAGGGCCG	GCTCCTGTCA	CTCCTGTTCT	CGCCAGCGGG	TTTTACCCTG	420
AAGGTGACTC	AGGCCTTCTC	TTTGCCCTAG	ATCGTGGGGA	TCATCACACG	GCACAACCTC	480
ACCTATGAAT	TTCTGCAGGC	GTAGCTCGAG				510

- (2) INFORMATION FOR SEQ ID NO:1270:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

GAATTCGGCC	AAAGAGGCCT	ACGCATCCCC	TGCAGCTCTT	GCCCCCAGAC	GTTTGGTACC	60
AACTCGAAAC	TGCGCTTGCA	CCGGTTAAGG	GTACATGACA	AAACACCTAC	CCACTTCTGT	120
CCACTTTGTG	ACTATAGTGG	CTACCTTCGC	CATGACATCA	CTCGTCATGT	CAACAGCTGC	180
CACCAAGGCA	CCCCAGCCTT	TGCCTGCTCC	CAGTGTGAAG	CCCAGTTCAG	CTCAGAGACA	240
GCACTTAAGC	AGCATGCTCT	GCGCCGACAC	CCCGAGCCTG	CACAGCCTGC	CCCTGGCTCT	300
CCTGCAGAGA	CCACTGAGGG	CCCCCTGCAC	TGTTCCCGCT	GTGGGTTGCT	GTGCCCCAGC	360
CCTGCCAGCT	TACGAGGACG	GCCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:1271:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

GAATTCGGCC	AAAGAGGCCT	ACAGAACTGT	GCCATATTCT	TAAACATCAT	ACAATATTGC	60
CTTTCAGGCA	TGAAAAGCAA	AGGGAATTAT	TTGTTCATTT	GATAGCGCTT	TAGTAATGTA	120
AGTGGATACA	CTTAGGGCTA	GCCCTCTGGC	TTGTTACCAT	GGTAAGCTAG	GGGAATATAG	180
TTGAGGGGTC	TGCAGCAGAG	CTTGGAGAGG	ATCTGGGATG	TTAAATTCTC	AAGTACTTGA	240
ACTTAGCAAC	AGGACTTGGT	CCCATCCACA	CCCTGCTCTC	CACCCCAGCT	GGAAATAATT	300
AGTGCTGACT	ATGGAGGCAA	AGAGAAACAT	ACTTGTAAGC	TTTTTTGTTT	GGATTTTCTT	360
TGGGGTTTCC	TTTTTGTCTT	TTCTGAACTG	GAGGGTGAAA	TCTCGAG		407

- (2) INFORMATION FOR SEQ ID NO:1272:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:

GAATTCGGCC	AAAGAGGCCT	ACATAAATCA	AAAATTTCTG	TGAAGATGGG	AAATAAGGCC	60
AAGATTGCAA	AATGTCCTTT	AAGAACAAAA	ACTGGGCACA	TTCTAAAATC	AACACAAGAT	120
ACTTGTATTG	GGAGTGAAAA	ACTTTTGCAA	AAGAAGCCAG	TTGGTTCAGA	AACATCACAG	180
GCAAAAGGTG	AAAAAAATGG	AATGACTTTT	TCATCCACTA	AGGATTTATG	TAAACAATGT	240
ATAGATAAAG	ACTGTCTTCA	TATCCAGAAA	GAGATTTCAC	CTGCAACCCC	TAATATGCAG	300
AAGACTAGAA	ACACCCTCGA	G				321

- (2) INFORMATION FOR SEQ ID NO:1273:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

GAATTCGGCC	AAAGAGGCCT	ACGAGAACTT	CCTTTTCATC	TGAATCTTCG	TCAAACTCTC	60
TCTCAGAGCC	TTCCTCATCT	AACACTTTTT	CAGAGCCGTC	ATCTTCAAAT	TCGGAGTTTT	120
CAGAGTCATT	TTCTTCTAAC	TCTTTGTCAA	GAACATTTTC	ATGAAGCTCC	TTTTCAGAAC	180
CTTCCTCGTC	CAAATCTTTC	TCGAG			•	205

- (2) INFORMATION FOR SEQ ID NO:1274:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

GAATTCGGCC	AAAGAGGCCT	ACTCAATACT	GAGGCTGATT	GGTCGTTTAG	GCCAATTGGG	60
TTTGAAAGAA	GGATTTCCAT	CTGCTGTGAA	AAATATTAGT	TCGGTTATTG	GTATGTTTAT	120
ACAGCATGCT	CACGATGAAG	ATATACCATG	GGGTATACAG	TTAGCAGCCG	TGTATGCTCT	180
TTGTGACTTG	AGTCCCAGCA	ATCCAGCAGA	AATTTCCAAG	ATCCTGGAAG	CTTGGCGGAG	240
AGAGGCCTCC	AAAAGCGTTC	CGTCTGCGAT	TGTCAGCTGC	CTAGAGGAAG	TCAGTGCCCT	300
GAGCACAGAG	GAGCTTGGCT	GACCTGGGAT	GCCACTGAGG	CTTGAGAAGT	GCCTTGACAC	360
ATTTTGAACA	CAAATAGTTT	GATCAGCTTT	CAGAATACAA	AGGGAGGTTT	CAAAACAAAA	420
AGACATAAAA	TAGATAAAAG	CAGACTCGAG				450

(2) INFORMATION FOR SEQ ID NO:1275:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

GAATTCGGCC	AAAGAGGCCT	AAAGCAACAG	GAAAGGATAA	ATTCACAGAG	GGAAGAGATA	60
GAAAGACAAC	GGAAAATGTT	AGCAAAGCGG	AAACCTCCTG	CCATGGGTCA	GGCCCCTCCT	120
GCAACCAATG	AGCAGAAACA	GCGGAAAAGC	AAGACCAATG	GAGCTGAAAA	TGAAACGTTA	180
ACGTTAGCAG	AATACCATGA	ACAAGAAGAA	ATCTTCAAAC	TCAGATTAGG	TCATCTTAAA	240
AAGGAGGCTC	TCGAG					255

- (2) INFORMATION FOR SEQ ID NO:1276:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

GAATTCGGCC	AAAGAGGCCT	AACAAGATTG	ACCGTGAATG	GTTCACTGTT	GAAACTCTGT	60
GATGGGTACT	TGAGAATTTA	TTATTATTT	ATGCCTATAT	TGCAGATATT	TGAAGTTTCC	120
CAATAAAATG	TTTAAAATAG	TGGCAGGGG	CAAGAAGAAA	AGGACCACTC	AATTTAAAGA	180
AAAAATAATT	TTAAAAGACA	CAGAGAATAG	GAAGAGGGAA	AAATTGGTGA	GGCAAGAGAA	240
AGGCAGCAGG	TGGGGCCATA	TCAAGAGTGA	TTCTTCAGCA	GGTGAGGCGT	GATACCACCG	300
CAAAAGTAGA	GGGTTGGCTG	TAAGATAGGG	GGCACAGATG	GCTATAATGC	AAGGGAAGGC	360
GCTCGAG						367

- (2) INFORMATION FOR SEQ ID NO:1277:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 624 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

GAATTCGGCC	AAAGAGGCCT	ACTCAGAAAC	AAAGCCAAAA	TTAAGTTCAT	CATTAAAAAG	60
CCCGAAATGT	TTGAGACGGC	GATTAAGGAG	AGCACCTCCT	CTAAGAGCCC	TCCCAGAAAA	120
ATAAATTCAT	CACCCAATGT	TAATACTACT	GCATCAGGTG	TTGAAGACCT	TAACATCATT	180
CAGGTGACAA	TTCCAGATGA	TGATAATGAA	AGACTCTCGA	AAGTTGAAAA	AGCTAGACAG	240
CTAAGAGAAC	AAGTGAATGA	CCTCTTTAGT	CGGAAATTTG	GTGAAGCTAT	TGGTATGGGT	300
TTTCCTGTGA	AAGTTCCCTA	CAGGAAAATC	ACAATTAACC	CTGGCTGTGT	GGTAGTTGAT	360
GGCATGCCCC	CGGGGGTGTC	CTTCAAAGCC	CCCAGCTACC	TGGAAATCAG	CTCCATGAGA	420
AGGATCTTAG	ACTCTGCCGA	GTTTATCAAA	TTCACGGTCA	TTAGACCATT	TCCAGGACTT	480
GTGATTAATA	ACCAGCTGGT	TGATCAGAGT	GAGTCAGAAG	GCCCCGTGAT	ACAAGAATCA	540
GCTGAACCAA	GCCAGTTGGA	AGTTCCAGCC	ACAGAAGAAA	TAAAAGAGAC	TGATGGAAGC	600
TCTCAGATCA	AGCAGAACCT	CGAG				624

- (2) INFORMATION FOR SEQ ID NO:1278:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

GAATTCGGCC AAAGAGGCCT	ACCCAAATCC	CATTTAGATA	AATTGAGGTT	CATTTTTCAC	60
ATAGACTTGC AATTTTTAGA	CACCACATTT	TTTTTATAGT	AACAGCCTCA	TTTGCCTGTA	120
CAATAACTAA TAATACAGTA	TTTCATAGGT	ACATTGTATG	TGCACAGGAA	ATTTTTCTTT	180
AAATCTTAAA AGCCTTTAAT	AAACGGGATA	TTTTAATATT	TTAATGTTAC	TACATTTAAA	240
AAATAGTGTT TTCCTACAAA	ATTTTCTGTA	TTCAGTAATA	CTCGAG		286

- (2) INFORMATION FOR SEQ ID NO:1279:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 227 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

GAATTCGGCC	AAAGAGGCCT	ACTCATCATT	AGCTGAAAGT	TTGAGAGCTG	CAGCAGAAGC	60
GGCTGTATCA	CAGACTGGAT	TTAGTTATGA	TGAAAATACT	GGACTGTATT	TTGACCACAG	120
CACTGGTTTC	TATTATGATT	CTGAAAATCA	ACTCTATTAT	GATCCTTCCA	CTGGAATTTA	180
TTACTATTGT	GATGTGGAAA	GTGGTCGTTA	TCAGTTTCAT	TCTCGAG		227

- (2) INFORMATION FOR SEQ ID NO:1280:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

GAATTCGGCC	AAAGAGGCCT	ACCCGTGCGC	TCTACAAATA	GTTCCGTGAG	AAAGATGGCC	60
GGGAACTCGA	TCCTGCTGGC	TGCTGTCTCT	ATTCTCTCGG	CCTGTCAGCA	AAGTTATTT1	120
GCTTTGCAAG	TTGGAAAGGC	AAGATTAAAA	TACAAAGTTA	CGCCCCCAGC	AGTCACTGGG	180
TCACCAGAGT	TTGAGAGAGT	ATTTCGGGCA	CAACAAAACT	GTGTGGAGTT	TTATCCTATA	240
TTCATAATTA	CATTGTGGAT	GGCTGGGTGG	TATTTCAACC	AAGTTTTTGC	TACTTGTCTG	300
GGTCTGGTGT	ACATATATGG	CCGTCACCTA	TACTTCTGGG	GATATTCAGA	AGCTGCTAAA	360
AAACGGATCA	CCGGTTTCCG	ACTGAGTCTG	GGGATTTTGG	CCTTGTTGAC	CCTCCTAGGT	420
GCCCTGGGAA	TTGCAAACAG	CTTTCTGGAT	GAATATCTGG	ACCTCAATAT	TGCCAAGAAA	480
CTCGAG						486

(2) INFORMATION FOR SEQ ID NO:1281:

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 430 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281: GAATTCGGCC AAAGAGGCCT AGACAAATTT CCTTTCATTG CTTCCAGCCG TGTTATTTAA 60 AGTAATTAAC CTTAATTTAT AAATTTTTAT ATCAAACTGC CTTTTAACTT TTAGAACTGG 120 CAGGAACAGC CTTATCCCTG GGCTCCTAAT AGTTCTCCAT TTAATCAAAA TTCATCCATC 180 AGGTTCCAGT GTTAAATCAT CTTTTAATTG GGAGTTACAT TCTGGTTAAT AGTTTTATAA 240 TTCGCCTCCT CTAATAGTTT TTACCACAGG GATCTCGACT CCATTTTTCC TGACTCTATT 300 ATTGCTGGCA TGCGATTTCT GCGGGGATGG CTTAACGCGG CCCTGCCTCT CTGGCCTCTG 360 CTGGTCGCCT CTTTTGTTCT TGGTGGTCTC ATTAATTCCT GAGAAGAGTT ATCCTTCCTC 420 CTCACTCGAG 430 (2) INFORMATION FOR SEQ ID NO:1282: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282: GAATTCGGCC AAAGAGGCCT AATCCCCTTC TGCATGTTCC CTTCCTGCAG GTCTGATGGG 60 GCCATCCCAC CCTGCTGGGG AGCACAGCTT GCCCTCCCTC CCCTCCTTCT CTTCTGGCGT TGCCTGCTGG GTGCCATCGG AGCAGTCCTC ATTACTTCCC ACTTTTGCCC AACTTCTGCT 180 GCTGTGACCA GTCGCATACA CGTGGACACC GTGGGGACTG CCCCTCCATA CAGCTCCTCT 240 GTAAGCTTAG GACCAAGGCT GCCTCTCCAG TCTCCCTGGC CCATGCCTGC CCCGGCATCC 300 TCCGCCCAG CTACACTGGC CCCCGATCTC GAG 333 (2) INFORMATION FOR SEQ ID NO:1283: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 269 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283: GAATTCGGCC AAAGAGGCCT AGGACGTTGG TGTTGAGGTT AGCATACGTA TCAAGGACAG 60 TAACTACCAT GGCTCCCGAA GTTTTGCCAA AACCTCGGAT GCGTGGCCTT CTGGCCAGGC 120 GTCTGCGAAA TCATATGGCT GTAGCATTCG TGCTATCCCT GGGGGTTGCA GCTTTGTATA 180 AGTTTCGTGT GGCTGATCAA AGAAAGAAGG CATACGCAGA TTTCTACAGA AACTACGATG 240 TCATGAAAGA TTTTGAGGAT GAGCTCGAG 269
 - (2) INFORMATION FOR SEQ ID NO:1284:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

GAATTCGGCC	AAAGAGGCCT	AGAGCGTCAA	TTATATCAAT	TTGTCCCAGA	TTTGGATGAG	60
CTGTGAGGAT	GTAACACAAG	GCTGGAGGAG	GCAGATGAGT	TTTTATCTCT	TCACAGGGCT	120
GGTCGCGGCC	AGGTGTTTTC	AGAGGTATCG	CTGGGGGCCA	CAGGGTGTCA	ATCAAACTGA	180
AAATCCCCGC	TGTCCTTCCT	CTGGTGACTT	TCTGTAGAAC	CTTCATTCCC	ACCAGGCTGC	240
AAGACTTCCC	TTCCAACTGT	CTTGCCTTCG	ACATGGTGAA	CTCCAAGTGC	ACTTCACCGA	300
ACATTCCACA	GGCATCTTGT	ACCAGAAGGC	AGGCTCGAG			339

- (2) INFORMATION FOR SEQ ID NO:1285:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

AAGTTCTAAA AACATCAGTT CATCTCCAAG CGTTGAGAGT TTGCCTGGAG GAAGAGAATT 12	n
ANDITETIBLE ANGREGATION CONTINUES INCOME.	•
CACTGGCTCT CCACCTTCAT CTGCTACTAA AAAAGATTCC TTTTTTAGCA ACATCTCACG 18	0
TTCTCGCTCA CACAGCAAAA CTATGGGCAG AAAAGAATCT GAAGAAGAAT TAGAAGCCCA 24	0
AATTTCCTTC CTTCAAGGGC AGTTGAATGA CCTGGATGCC ATGTGCAAAT ACTGTGCAAA 30	0
GGTGATGGAC ACTCATCTTG TAAATATTCA AGATGTGATA TTACAAGAAA ATTTGGAAAA 36	0
AGAAGATCAA ATTCTGGTTT CCCTGGCAGG ATTAAAACAG ATCAAAGACA TTCTAAAAAGG 42	0 !
TTCCCTGCGT TTTAACCAGA GCCAGCTAGA GGCCGAAGAG AACGAACAGA TCACCATTGC 48	0
GGACAACTCA CTCGAG 49	6

- (2) INFORMATION FOR SEQ ID NO:1286:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

GAATTCGGCC	TTCATGGCCT	AGCAGAAGCT	AAGAACTGTC	TTAAAATAAA	TTTTAAAAGT	60
AAATAAGTTA	TAATGCATAG	GTTAGCCCAT	TCATTAATGA	TTTTCAGTTT	CAAGTGTAAA	120
TATTTCTTAA	TGATTACTAG	TTGATCAGTG	TAATGAAAAC	ATTGAGTAGA	CAAACTAAAT	180
GCACAGTATA	AATGTGACAT	AAACACTGGT	TTCAATTTGT	CTCAAGAAAA	AAGAAAAAA	240
AAAGGCCCCT	GCAATGGCAA	AGAGTGGCCA	CTATTGGGGT	AATTCAAACA	ACCCACTGTA	300
ATACAGGAAA	GCACTCGAG					319

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:

(1)	(A) LENGTH: 261 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1287:	
	AGTTACTGGC TGGAGAAGAT GGGACAAGTG AACGAAGGAA AAGCATCAAA	60
	AAATTGTTCA AGAAAAAGAG CGGAGAGAGA GAGAGCTGCA TGAAGCATAT	120
	GGTCCCAGGA GGAGGCAGAG GGGATCCTTC AACAGTACAT TGAGAGGTTC	180
	AGGCTGTTCT CGAACGCTTG GAGATGCCAA AAATTCTGGA AAGAAGCCAT CAAAACTCGA G	240 261
(2) INFORMA	ATION FOR SEQ ID NO:1288:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 275 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1288:	
GAATTCGGCC	TTCATGGCCT ACTCTGAAGA TATTTATAGC TCTCTTAGAG GTGTCACTGA	60
	AATTTCAGCT TCCGTAGCCA AGAAGATATG AATGAGCCAT TGAAAAGGGA	120
	GATGATGGCG ATTCAATGTG TGGTGGTCCT GGGATGTCTG ACCCAAGAGC	180
	GCTACTGACT CAAGTCAAAC AGCTCTTGAT AATAAAGCTT CATTGCTCCA	240
TTCAATGCCT	ACTCACTCCT CTCCACGCTC TCGAG	275
(2) INFORM	ATION FOR SEQ ID NO:1289:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 139 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1289:	
GCGATTGAAT	TCTAGACCTG CCTCGAGAAC GCCGGGGTCC ATCATTAGCA GTCCTCACAT	60
GCGCCGGAGA CTCATCTTCC	GCTACATCAA CACGAGAGTG TCCATCTCGC CCACACCAGA CTATGCCCAA CCCCTCGAG	139
(2) INFORM	ATION FOR SEQ ID NO:1290:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 358 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)) MOLECULE TYPE: CDNA	

506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

GAATTCGGCC	AAAGAGGCCT	AATAAGTTTG	ATTAAGCTTG	CAGACATTAA	GCTTTTCTAG	60
CAGCTGGTGT	GTGCAGAGGC	AGATGGCTCT	CTGGTTCCAG	GACTACCTAC	AATATAGAGA	120
		ATTCATCATG				180
					TTGACATTTC	240
					GAGTAGTTTC	300
		GAAGAAATGG				358

- (2) INFORMATION FOR SEQ ID NO:1291:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

GAATTCGGCC TTCATGGCCT	AGAGGATCCT	AATGAAATAC	CTGAAACATA	TATTGGCATT	60
TATCAATGGC TCAAATCTTC					
CAGCAGAGCC CAGGTCGAG					139

- (2) INFORMATION FOR SEQ ID NO:1292:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

GAATTCGGCC	TTCATGGCCT	ACTATCAGGA	AGTGATTCGT	GGAGAGGGGA	TTTTACCTGA	60
				AGAGACTATT		120
				CTTTTTCTAA		180
				CATCACAGTG		240
						300
				ATAGCATGGC		360
				CCTTTACACA		500
TGATAGCACA	AACATGCCAT	TGATGCAAAC	GCAGCAGAAC	TTGCCACATC	AGACTCAGAT	420
TCCCCAACAG	CAGACTCTCG	AG				442

- (2) INFORMATION FOR SEQ ID NO:1293:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

GAATTCGGCC TTCATGGCCT ACATGAATTA TCTGTGAGTT GGTTAAAGGT AATATTGGTT	60
AGCATCAAGA ATAGGAAGCT ATTAGTTTTC AATCAAGAAT AAGCTCAAAT TTGGTCTAAA	120
TCTTAATTTT AAGCTGGGTA ATCATTGATT TACAATTTTT TTCTTGGTGT CACATTTCTT	180
CCAAAACAAT AATCAATGAA GCCTTTCCCA CCCTGTGCCT TTGCTCTCGA G	231
(2) INFORMATION FOR SEQ ID NO:1294:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 355 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) Torobogi. Illiear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:	
CANDOCCO DECARDO DECARDO A CERCOCO A CONTRACTOR A CONTRAC	
GAATTCGGCC TTCATGGCCT ACTCTGCTAA CTTCCTGCCT CTATGTCTTT CCCCACCTAC CTCCTCTCCC CATTCACACT CCTGCGTGAC CTCATCCATT TACCTGCCTT CAATTAGCAT	60 120
CCATACGTTC CTCCTTTCTC AATATAAGTC CCCAGCTGAG ACTCTGTTTC TGAAATCCAG	180
ATTITTATTT CCAATTCTAC TGAACAAACT CAGTCTAAAG CCAAGCCCAT TATCTTCTCC	240
TATAAGCCTG CATCTTTCT TTTCTTTCTT TCTTTTTTTT TTTTTAACAG AGGTTAATGG	300
CATTCAACAT CTACCCAAGC ACCAGGGAGT TAGATTCAGA ACGGATGGAC TCGAG	355
(2) INFORMATION FOR SEQ ID NO:1295:	
(i) appropriate analysis and the second seco	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 429 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:	
, - <u>-</u>	
GAATTCGGCC TTCATGGCCT AGGCTAACTG TTATTTGCAT CTTACAGCTC AGAAAACAAG	60
CATGGTGAGA TAAGGAAACT TTACTAAGGT CACATAACTA GTAAGTGGTG GAGCCAGCGT	120
TGAAACTCAG GAAGTCTGTA CACAACTGGG AGGGAAGGCT AATATTTGAA ATGATAGACT	180
CAACATTCAA TATTTCAGTA TCGATGAGCT CTAAGTTGAT AGAGCTATGT GTAAAAACCC	240
TGCATTTAAT ATTAAGAAAT CATTGGCAGA AGAGTAAGAG AGGGCTTTGG TCAAGTAAGC	300
TGAGTGCATA AGAAAACTCT GGCATTTGAG GTGTCCTTAG CTCCAGATGC TTTGGTAGGG	360
CAGAGTGTAT CCATGGAGGT ACCATGAGCT ACCATGGAGG TAGCTCAGAG AGGAAAGGGA	420
AACCTCGAG	429
(2) INFORMATION FOR SEQ ID NO:1296:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 406 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:	

60 120

CTCGAGCTGT TCTGTAAATA CCTGGTGCTA ACATCCCATG CCGCTCCCTC CTCACGATGC ACCCACCGCC CTGAGGGCCC GTCCTAGGAA TGGATGTGGG GATGGTCGCT TTGTAATGTG

CTGGTTCTCT	TTTTTTTTC	TTTCCCCTCT	ATGGCCCTTA	AGACTTTCAT	TTTGTTCAGA	180
ACCATGCTGG	GCTAGCTAAA	GGGTGGGGAG	AGGGAAGATG	GGCCCCACCA	CGCTCTCAAG	240
AGAACGCACC	TGCAATAAAA	CAGTCTTGTC	GGCCAGCTGC	CCAGGGGACG	GCAGCTACAG	300
CAGCCTCTGC	GTCCTGGTCC	GCCAGCACCT	CCCGCTTCTC	CGTGGTGACT	TGGCGCCGCT	360
		GCCCCTAGGC				406

- (2) INFORMATION FOR SEQ ID NO:1297:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 639 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

GAATTCGGCC	AAAGAGGCCT	ACGCCCGCCA	ACACGCCTGG	GTAATTTTTT	GTATTTTTAG	60
TAGAGACGGG	GTTTCACCGT	GTTAGCCAGG	GTGGTCTTGA	TCTCATGATC	TCGTGATCCA	120
	CCTCCCAAAG					180
TGTTGCTCTT	AAGCAGAAGC	AAAATCAAAA	GGCAGACAGG	ACTCAAAGAA	TGGTTCTAAA	240
CCTAAAAGTA	CTAAGGCCTC	TAGGAACTAT	GATGATGACA	ATTACTGTGC	AATTTATATC	300
ATGCTGAATT	TTAGTAAAAC	CCCTGGCAAA	CCACTCTCAC	TTGGTGACAC	TCCGTCCACA	360
GCACGGGGCC	ACAGCATAGT	GGATCAGTAC	AACTTTCCTG	GACAGCCTTG	CTACCTGTAC	420
ACTCTTATGG	ACTCAATTCC	ACTTCAATGT	ATTCGTTCTA	GAGGTAAATG	GACATGTGAA	480
CACAGATTCA	CAGGCAAAGA	TGTTTATATG	CACCACTGTC	TTGATGTTCA	AGAAAATGGA	540
ACTGGTTACA	TGCATGTGAT	TAGCTATATA	ATGTAACTGT	ATTCAGCCCC	TAAAAAATGT	600
AGGCCTCTTT		ATTCTAGACC				639

- (2) INFORMATION FOR SEQ ID NO:1298:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 606 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

GCGATTGAAT T	CTAGACCTG	CCTCGAGTCC	AACGGCATCG	ACGTGTACCC	CCAGAAGGAA	60
TTTGATGAGG A	ACTCGGAGGA	CCGGCTGGTG	AACGAGAAGT	TCCGGGAGAT	GATCCCATTT	- 120
GCTGTGGTGG G	CAGTGACCA	CGAGTACCAG	GTCAACGGCA	AGAGGATCCT	TGGGAGGAAG	180
ACCAAGTGGG G	STACCATCGA	AGTTGAAAAC	ACCACACACT	GTGAGTTTGC	CTACCTGCGG	240
GACCTTCTCA I						300
GAGGCGTACC C	STGTGAAGCG	CCTCAACGAG	GGCAGCAGCG	CCATGGCCAA	CGGCGTGGAG	360
GAGAAGGAGC C	CAGAAGCCCC	GGAGATGTAG	ACGCCACCCT	GCCCACCCCC	GGGATCCTGC	420
CCCCAAGTCA T	TTTCCGTCCC	CCCCCCAGGC	CCTCCTCCCA	CGGAGTGGCA	AGACTGGCTG	480
AGGCCTAGCT C	CTCTAAAACG	GTGGGGGAGG	GGGGAGCGCC	CTGAGAGAGG	CATTCTACTA	540
ACCCCACCC A	AATCACCCCT	ATTTTTACTC	TTTCTACTTT	CGGAATTGGA	AAGAACGACA	600
CTCGAG						606

- (2) INFORMATION FOR SEQ ID NO:1299:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:

GAATTCGGCC AAAGAGGCCT	AGGAGTGATG	TTCATTTTGG	GATTTGCAGG	GTGCATTGGA	60
GCGCTACGGG AAAACACTTT	CCTTCTCAAG	TTTTTTTCTG	TGTTCCTGGG	AATTATTTTC	120
TTCCTGGAGC TCACTGCCGG	AGTTCTAGCA	TTTGTTTTCA	AAGACTGGAT	CAAAGACCAG	180
CTGTATTTCT TTATAAACAA	CAACATCAGA	GCATATCGGG	ATGACATTGA	TTTGCAAAAC	240
CTCATAGACT TCACCCAGGG	ACTCGAG				267

- (2) INFORMATION FOR SEQ ID NO:1300:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

GAATTCGGCC	AAAGAGGCCT	AGTGTTTTCC	AATCAAGTTA	ATAAATATCT	GTCTTCGTAC	60
CAGGAAAAAT	TCAATATTAT	TTTAAAGGAG	AAAAAATAAG	AATGTATTGG	TAAAATGCTT	120
TCTCTCACTT	CGAAATATCT	TAGTGAACAA	GAACACTGAC	ATAGAATTAA	AATTCTATGA	180
ACAGCCATAA	CCAAAGGAAT	CTCATTTAGT	GAATATTTAT	GTCCAGTAAC	TGCAACCCAC	240
ACTTAGAGCT	ATCCTTTTGC	TTAAAAACAA	AAATTTGGGC	CTTAAGAAGT	GATTAATATC	300
AGGCAAAAAT	AAATTATACT	TTTGTTTATT	TATTCAGGGC	CTTGCTCTGC	TGCCCAGGCT	360
GGACTGCAGT	AGTGCAATCA	TAGCTCACTG	CATCCTTGAA	TTCCTGGGCT	CGAG	414

- (2) INFORMATION FOR SEQ ID NO:1301:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

GAATTCGGCC	AAAGAGGCCT	AGTGAAGTTT	ACTGTGATTC	TATGGAACAA	TTTGGACAAG	60
AAGAGTCTTT	AGACAGCTTT	ACGTCCAACA	ATGGACCATT	TCAGTATTAC	TTGGGTGGTC	120
ATTCCAGTCA	ACCCATGGAA	AATTCTGGAT	TTCGTGAAGA	TATTCAAGTA	CCTCCTGGAA	180
ATGGCAACAT	TGGGAATATG	CAGGTGGTTG	CAGTTGAAGG	AAAAGGTGAA	GTCAAGCATG	240
GAGGAGAAGA	TGGCAGGAAT	AACAGCGGAG	CACCACAACT	CGAG		284

- (2) INFORMATION FOR SEQ ID NO:1302:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

GAATTCGATT	GAATTCTAGA	CCTGCCTCGA	GCCTGTGCGA	GAAAAGTGAA	CGCCAGTCTA	60
ААААААААА	AAAAATCTAA	AAGAAGCCAA	AAATCCACTT	GTAATGAGAT	TCATAGACCC	120
CTTATTTATA	CAACTCACAT	ATTTGAATTT	TTACATATTG	AATTTTCTTT	TAAAGGGGTG	180
GAGGGGTCTC	GAG					193

- (2) INFORMATION FOR SEQ ID NO:1303:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:

GAATTCGGCC	TTCATGGCCT	AGGGATACAG	CAACTATTTT	ATCAATTGTT	TGTATTTCCC	60
TTTAAGGTAA	CATTTTAAAT	GAAATGTATT	ATATTTTAAT	CTATCCTTTT	CCTTTGTTTT	120
TGTTCTTATT	ATCTCTTCTG	ATATATAACC	AAAAAATGAA	AAAATCTGTA	CACTTGGTGT	180
TTGATTTACC	TAAGCACCTA	GTTAATTTAA	TCTTTGTAAC	ACTTTGGATG	GTTAACTTAA	240
CCTTTACTCA	AGTTGGTTTT	TGTTTTGTTG	AAAATGACTT	ACTTGGTGGA	ACCACTACTC	300
TCGAG						305

- (2) INFORMATION FOR SEQ ID NO:1304:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

GCAGCGAGCA	GTATACCAGC	AGCAGCAAGC	GAAAGGAAGA	GTTTGCTGAT	ATGTCAAAAG	60
TTCATTCAGT	GGGAAGCAAT	GGGCTTCTGG	ACTTTGATTC	AGAATATCAG	GAGCTCTGGG	120
ATTGGCTGAT	TGACATGGAG	TCCCTTGTGA	TGGACAGCCA	CGACCTGATG	ATGTCAGAGG	180
AGCAGCAGCA	GCATCTTTAC	AAGCGATACA	GTGTGGAAAT	GTCCATCAGA	CACCTGAAAA	240
AGACGGAGCT	GCTTAGTAAG	GTTGAAGCTT	TGAAGAAAGG	TGGCGTTTTA	CTACCAAATG	300
ATCTCCTTGA	AAAAGTGGAT	TCAATTAATG	AAAAATGGGA	ACTGCTTGGG	GTATTTGCAT	360
TTTTATTACT	GTTTGTAGGT	TATGTGTACA	TTTTTTGCGT	AGTGAAGTCA	CTCGAG	416

- (2) INFORMATION FOR SEQ ID NO:1305:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

GAATTCGGCC TTCATGGCCT ACCAATGTCC TGCACATTGC CAGACTTCCA AACAGGTACA AGTTCCCATC TGTTCTGCAA TAGATGAAAG CAAGTCACAG TTCCCAGGGC TACCAGTGTA ATTTCTCAAG TGGCCAAGTT ACCTGGCTTC ATGGCTTGAC CTGCTGTGTT CTTTTGGAAA	60 120 180
TGGAGAATGC CTGAGGGCTG TCTCTAACAG AAGGGTATGT GGCAGTATAT TACAGAATTT	240
ACAAGAAGCA AGGTGCAAAT GAATTACATT GAATTTCATT GTTAAGAAGA GATGATTTAA AATTTGGTAT TTAACAACAT AAACGACTTT GGGGCCCAAC TCGAG	300 345
(2) INFORMATION FOR SEQ ID NO:1306:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 209 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:	
GATTTCTCTC AGCTTTTATT TGTTTGAAAA ATTTTTTAAT TCACCTTCTT TTTTGAAAGA TTTTTACTGA TTATAGAATT CTAAGTAGTT TATTCTTCTA GGACTGTGAA CATATAATTC TACTGTCTTC TGGCATTTAT AGTTTCTTTA TTTTATTTTT TATTGAAAAA CATTTTTTT GAGACATGGT CTCACTCAGA ATACTCGAG	60 120 180 209
(2) INFORMATION FOR SEQ ID NO:1307:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 251 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:	
GAATTCGGCC TTCATGGCCT AAGCTTTTGC TTTTTTAATA ACTTGTATAG CTAAAAACTT	60
GACGGTGAAA AGCTCTCAGA TCAAAGCTGA TCCTTCTGTC AGTAATGATT CTAAAAATAA GCAAGATTTT AATGGGGAAT ATATTTTATT TCATTCTTAT CTCAAACCTA GGTACTGTGG	120 180
TCGTTTTGAG TTCATTTCGA GGCATTTTCA ATGTGCCTCA GGCCACATCC AACCTCTCCC CAGAACTCGA G	240 251
(2) INFORMATION FOR SEQ ID NO:1308:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 317 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:	
GAATTCGGCC TTCATGGCCT ACCTGACTCT TGAGATACTG ACTGGAAGAT AGACTGTTTT	60
GTTCCACCTG ATTGTATGGG AGAAATTTTT GACCTTAGAA AGTGGAAATG AGGTTGCTAT	120
GGAAACTGGT AATTCTGCTG CCACTCATAA ACTCTTCTGC AGGTGATGGT CTTTTAAGCC GTCCTATTTT TACTCAGGAG CCACATGATG TCATTTTTCC TTTGGATTTA TCAAAATCTG	180 240
AGGTCATCCT GAATTGTGCT GCTAACGGTT ACCCTTCGCC TCATTATAGG TGGAAGCAAA	300

ATO	GGCACAGA ACTCGAG	317
(2) INFORMATION FOR SEQ ID NO:1309:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 412 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:	
TA GC AA AA GC	ATTCGGCC TTCATGGCCT ACACAGTATC ACTAAAAGAT TTTCATTCGG AAGATCACAT GTAAAAAG ACTGAGGAAG TGGTTCTGAA AGATGGAAGA ATTGAAAGAC TAAAGTTAGA TTGAAAAG AAAGATGCTG AAATCCAGAA GCTGAAAAAT GTAATCACTC AATGGGAGGC AGTATAAG GAAGTAAAGG CAAGAAATGC ACAATTATTG AAAATGCTTC AGGAAGGTGA TGAAAGAT AAGGCAGAAA TACTTCTGCA AGTTGATGAA TCACAAAGTA TCAAGAATGA TCACTATT CAGGTGACTT CACTTCATGC TGCATTAGAA CAAGAAAGAT CTAAAGTGAA TATTACAA GCAGAGTTAG CCAAATACCA GGGTGGCAGA AAAGGGCTCG AG	60 120 180 240 300 360 412
(2) INFORMATION FOR SEQ ID NO:1310:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 239 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:	
GA AG CA	CGAGTGTG GTGGTATGTG AATTATATCT CAGTAAAGCC ATCACAGGGC AGAAGAAAAA AGAAAAGAA AAAGAAAACC TTCGAGGAAG TCCAACAAAA AACATGAGGA AGAAAAGGTG BAGCCTGAG GATCCACACA GCAGGTACAG CAACTAACTG ACAGAAATTC TAGAGCCAGA AACAATGAC TAATCAAACT AACCTCAAAA CAAATGATTA GGCCATGAAG GCCGAATTC	60 120 180 239
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 278 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:	
AP GG TP AP	AATTCGGCC TTCATGGCCT ACAAGGAAGC ACAAGGAGAA AATTATGATG AAATGGAGCA AACAGGTAA GAGAGAGGT CAGAGAAGTG AATGTGGGCC TTGATGCTGA AGCCATTGGA GGTTTTCTG TTGAGGAGGA GTATGGGAAT GATATGATCT GACTTATGTT TCAAAAAGTG ACTCTAGCT GCTTTGTGGG AAATATNGGA GGGAGAGAGC AGAATCAAGG AGGCCATTTA AATGCCATT GCAAATATCC AAGAGAGGCG GACTCGAG	60 120 180 240 278
(2	2) INFORMATION FOR SEQ ID NO:1312:	

(A) LENGTH: 247 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:	
GAATTCGGCT TCATGGCCTA ATCACATATG GTAGAGATTT TATACAGAAT TTTAAAATGT GGCATTAAAA AAACTTGTTC CATGGAAAAC TGCTTTCAGA GATTTTTAAT AAGTGTTTCT CTCACATAGG AACCTAAGCT TCTCAGAGCT TTTAATAGGC TTCTAACAGG CTAATAGTCA AGGCCGTGAC CCAAGAAGGG ATATAGTTCA CAGTGTTTTC CACAAATATT TCACCCCAGA GCTCGAG	60 120 180 240 247
(2) INFORMATION FOR SEQ ID NO:1313:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 311 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:	
GAATTCGGCC TTCATGGCCT AGGGTCTTAG CTTTGGCTCT CCTTGCAAAG TTATTTCTAG TTAATTCATT ATGCAGAAGG TATAGGGGTT AGTCCTTGCT ATATTATGCT TGGTTATAAT TTTTCATCTT TCCCTTGCGG TACTATATCT ATTGCGCCAG GTTTCCTCTG TCTCAAAAAA AAAGAAGTTA CTTCCAAGAC AGACTTTTAA GATGTAACCA GCACAAAGCA ATGTCAGGGA GGAGTGATAC ATGACAATAA ATGAGTCAGA TGAGCAAGAA GGCCCCAGAA CCCATGCCCC CAGGACTCGA G	60 120 180 240 300 311
(2) INFORMATION FOR SEQ ID NO:1314:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 261 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:	
GGGGAGCTGC AAACGCCCGC GATACTGTCA GAGATGGAGA AAGGTATGAC AGGAAGAGCA GATCAAGAAG ACGGGAACAG CACGAGGCAC TGGGAGCTGC AAACGCCCGC GATACTGTCA GAGATGGAGA AAGGTATGAC AGGAAGAGCA GATCAAGAAG ACGGGAACAG CACGAGGCAC TGGGAGNTGC AAACGCCCGC GATACTGTCA GAGATGGAGA AAGGTATGAC AGGAAGAGCA GATCAAGAAG ACGAACTCGA G	60 120 180 240 261
(2) INFORMATION FOR SEQ ID NO:1315:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 326 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

514

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

CTCGACTTGC	ACGAGGAGTG	GCAGGATTAT	CTGCAGAGGG	ACCATTGGGA	CAGCTAGTAA	60
GGCCAGGTGC						120
TGCTGAGAAG	CCAATCTTTG	ACGTTAGAAT	CAGAAGGCAA	AAGGCCAGAA	CTGCTGGCAT	180
TTTTATAATT	GAGAATAGCA	GCTTGTAAGT	GTCTGTGATC	CCTTGGGTCT	CTTCTTTTAC	240
TATTGACGCT						300
TACAGTAGGC						326

- (2) INFORMATION FOR SEQ ID NO:1316:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 244 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

GAA	ATTCGGCC	TTCATGGCCT	AACGTCACTC	ACTGTCCTTC	TTAGTATCTA	ATTCTCCTTC	60
AC	TAATAGA	ACAGCAAATT	CTTTGAGTTT	AGGATCCTTA	ATGCAGTGTA	AATATTGCCT	120
						TGGTGGCTCC	180
						CCAGTGTCCT	240
CG		<u> </u>	•				244

- (2) INFORMATION FOR SEQ ID NO:1317:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

GAATTCGGCC	TTCATGGCCT	AGAAAGGTTT	GCCTGGTAAG	ACTGAACTGT	TCATAGTTCT	60
TTAAATAAGC	TACAATATTT	CCTAATTGTG	TACCCTTGAT	TTTACTGTTT	TCTTGCCCTA	120
GAATGCTGTT						149

- (2) INFORMATION FOR SEQ ID NO:1318:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

GAATTCGGCC TTCATGGCCT AGTCAGCAAA GCAAGGGGAG GCAGACCACA GGCCTCATGA CTCTCACTGG AGTGCAATGG GACCCCCATG GGGTGAAAGC AGAGGAGTGA GCTGCTCTGA TGTGAGCACT CACTCTGCTT GCCATATAGT GAGTAGACAG GAGAGACCAG GGCAGAAGTA AGAAGACCCA TCAGAGGCTC CTCAGGAACC CGAGTGGGAG ATGGTGGTGG AACAGGGTTG TAGTAGTGGC AGTAGTGAAA AAATGATCAG GTTTTGGAAA TATTTGGAAG GTCGAACTCG AG	60 120 180 240 300 302
(2) INFORMATION FOR SEQ ID NO:1319:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 219 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:	
GAATTCGGCC TTCATGGCCT AAGAAAAAA GAAAGAAAG AAAAAGAAAG TACAAGTTTA TAAAGTATTA TAGTGAAAAA TTCGCATTCT GGCTGATTTT AAGCCATTTA AAATTATAT AAAACAACCT TCCATAAAAA TTTGACAGGT GCCCAGATGT TGCTTTCTCC ATTTATTTT TGTTTTTTT TAATCACAGT GGTCTTGAGG CAGGTCGAG	60 120 180 219
(2) INFORMATION FOR SEQ ID NO:1320:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 361 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:	
GAATTCGGCC TTCATGGCCT ACTGAGTTAG GTTTTATTAA TGCAGTTTT ACAGATGAGG CTACTGTGAC ACAGAGGGCA TAAACTTGTC AAAGACATGC AGCAAACAGG ACAGACAAAT CTGAAGCCAG GTTGTCTAAG CTCAGAATCC ACACCTATAA CCGCTGTACC CCACTGCTTT TGCCAGCAGG AGCTCACGTA CTTAGGACAG ACAATCAGTA CAGTGCTAGG CTCACTGAAG GTGTTGAACA AATGTCTGTT CACTCTTTTT GTTCTCAAAA GTACCAGGAA AGGCCAGAAG AAAAAACTAC AAGACTTAGA AACTACAATG GATCAGATCA	60 120 180 240 300 360 361
(2) INFORMATION FOR SEQ ID NO:1321:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:	
GAATTCAAAC GAAAGCCAGC TGAGAATACA GGAAACATGT TTCCAGCCAA ACCCAAAACA CTCGAG	60 66

- (2) INFORMATION FOR SEQ ID NO:1322:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

GATTGAATTC	TAGACCTGCA	GCTACAGAAG	TCAAGATTCC	AAAACCAAGA	GGCAGACCCA	60
AAATGGTAAA	ACAGCCCTGT	CCTTCAGAGA	GTGACATCAT	TACTGAAGAG	GACAAAAGTA	120
AGAAAAAGGG	GCAAGAGGAA	AAACAACCTA	AAAAGCAGCC	TAAGAAGGAT	GAAGAGGCC	180
AGAAGGAAGA	AGATAAGCCA	AGAAAAGAGC	CGGATAAAAA	AGAGGGGAAG	AAAGAAGTTG	240
AATCAAAAAG	GAAAAATTTA	GCTAAAACAG	GGGTTACTTC	AACCTCCGAT	TCTGAAGAAG	300
AAGGAGACGA	TCTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:1323:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

GAATTCGGCC TTCATGGCCT ACTGTAAGGA GGAGATGAAA GAATTAGTAG AAAAGGTTTT 60 AAAAACAGTT ATTATAACTA TATTCCATAT GCTGAAGGCG CTCGAG 106

- (2) INFORMATION FOR SEQ ID NO:1324:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

GAATTCGGCC	TTCATGGCCT	ACTCCTTTAT	TTCCTTTGTC	TGTAGAATAA	AGTCTTAGAA	60
TAATATTCCT	GTTAAGGCCC	TGCTTATCCC	AATACCGTAT	CCATACTGAA	CTTTCAGTTC	120
TTTATATGCA	CTCTACTCTC	TGTCTTTCAG	ATTTTTGCAG	GTATTCCTTT	AGAACACTCT	180
TTCTCTTCCA	TCTTATCGCC	TACTCTTTGG	GTTTCTGTTT	AAACATTACA	TTTCTCGGTG	240
GGGGGGCTTA	TCTCGAG					257

- (2) INFORMATION FOR SEQ ID NO:1325:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

CTCGAGACCG CAAGCACTTC CCACCTCATC CTTATTTCCT CTATCCCTTT TCATTGTTTT 60
TTTCTCCTTT TTAAATTC 78

- (2) INFORMATION FOR SEQ ID NO:1326:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

GAATTCGGCC TTCATGGCCT AGAATTGTCC TCTGTGGAAG GGACTTTCTT TTGGCCCTAG 60
GCCCCTTCCT GCCCCTGTCG TCAGCAGAGA GATGGAAAAC TTGATGACTA GCTCCACCCT 120
ACCGCCCCTT TTTGCAGATG AAGACGGTTC CAAGGAGAGT AATGATCTGG CTACCACTGG 180
GTTAAATCAC CCAGAGGTTC CATACAGTAG TGGCGCCACA TCATCCACCA ACAATCCAGA 240
ATTTGTGGAG GATCTCTCC AAGGTCAGTT GCTTCAGAGT GAGTCTTCAA ATGCAGCAGA 300
AGGCACCTCG AG 312

- (2) INFORMATION FOR SEQ ID NO:1327:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:

GCGATTGATT CTAGACCTGC CTCTCCTTCA AGCATTGCAG CAAACAATTG TACTGTGAAT

ACGTCATCAA TTGCAACGTC TTCAATGAAG GGTCTTACGA CTACAGGAAA CTCGTCTCTT 120

AATAGCACAT CTAACACTAA AGTATCAGCA GTGCCTACAA ATATGGCTGC CAAGAAAACA 180

TCTACCCCCA AAATAAATTT TGTTGGTGGT AATAAGCTGC AGTCAACAGG AAATAAAGCA 240

GAAGACACAA AAGGAACCGA ATGTGTTAAA AGTACTCCTG TCACTTCTGC TGTGCAGATT 300

CCTGAAGTAA AGCAAGACAC AGTGTCAGAA CCAGTCACAC CTGCATCTCT TGCTGCTTTA 360

CAGAGTGATG TGCAGCCAGT GGGCCATGAT TATGTGGAAG GGATACTCGA G 411

- (2) INFORMATION FOR SEQ ID NO:1328:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

GAATTCGGCC	TTCATGGCCT	ACTTTTTCCT	TGGTCAGATC	ACAATGCTCC	TATAAATGTT	60
				CCTCAGGGGC		120
				AATTCCTTCC		180
CAGCCTACGT	GCAGAGATAA	GCAAAAGTAG	TTAACCTAAA	AGATATCACC	CTTTGGGGGG	240
	AAAATAGAGT					286

- (2) INFORMATION FOR SEQ ID NO:1329:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

GAATTCGGCC TTCATGGCCT	AGGGGGATTG	AAGATTTTTT	GTAGGTGGAA	GGCCTGAAGT	60
GCGACTAGAG GGCAATAAAT					120
CTGTTTATGG ACTGGGCTGT					180
ACTGGAACTA CTTGGGGATA	CAGTAGGCTT	GGGAGTTGGG	TTGGATTTAG	AAATAAGTTT	240
AGTTGATACT GAAGGCTTAG	CTGACAGAGA	GGGCTTGGGT	GAGGCAGAAG	GCTTAGGCGA	300
GGGCAGGGGT TTAGGAGATG	TGGCAGGTCT	AGAATTCGAG			340

- (2) INFORMATION FOR SEQ ID NO:1330:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

GAATTAAAGA	GGGCGATATC	ATCACACTCA	CTAACCAAAT	TGATGAGAAC	TGGTATGAGG	60
	TGGCCATTCA					120
	GGATGTTATG					180
					AGTGGTCCAC	240
	CCCACCAAGT					297

- (2) INFORMATION FOR SEQ ID NO:1331:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

CTCGAGTCCG	CTGAGCTGAG	AAGCACTGCG	ACTTTTCCGT	GACAGACCAA	CGATAGCTAC	60
CATTTTGGCA	CCAAGGCTAG	AGCGCCGCTT	TTTGCCACTG	GTGCCCAAGG	TGCCCACTGC	120
					TGATGCTGGT	180
GCTTTTTGTC	ATGTTCTTCC	CTGATATGCC	CATTTGTCTG	CTTTGCATTT	TGGATGTAAA	240

	GCCGATGGAT CATTAAAAGT GAGGACAAGA GTAAAAAGGA AAAGACAGAA AGATAAAACA TTTGGAGTAT AATTTAGGCC ATGAAGGCCG AATTC	300 355
(2) INFORMA	TION FOR SEQ ID NO:1332:	
(i) S	SEQUENCE CHARACTERISTICS: (A) LENGTH: 438 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1332:	
ACAGTATAAT GTGAGTATGT TTTTATATAA TCAGTCTTGA CTGTCAAATA	TTCATGTGCG GTGAAGGTCC TGTGATTGTA CAGTTAGCAC ATTTTATATG CTTAAAAAAT AACATAGAAA CAGAAACATT AGAAACGTAA GTCACAGTTT CATTTTTAG GGAAAAATAA AATATAGTAA CGATTTATGA GGCCCCAAAG AAATGAAAAA GCTGTTTGGC AGTTAGGACT GACTGTAGCC TTCTGTCAAA CAACTGTTAA AAGACATTAT CATCACAAAT AGGGCTGCAT TTCACTCTGT CAATCAATAT ATATGACTTT AAGAAAGTGT GACCATTTTC CCAGAGTGAC TGGTGGAATA GGAATTTTTG TTTAACTTTA CTCACCTCAC	60 120 180 240 300 360 420 438
(2) INFORMA	TION FOR SEQ ID NO:1333:	
(i) s	SEQUENCE CHARACTERISTICS: (A) LENGTH: 309 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1333:	
CCTCACTAAT ATCTTAAGGG GAATTACTAC	CCCACCCACT TTCTCAGACA TCCCCACCGG AGGATCCCAT CAGTCACAAT TAGACCATTC AAATTCCCCA AAATAAAAAA AGGGAAAGAG GTATAGACTT TCTTAAGTTC TGGCATTTTT CTATTTAATA ATATATATTG CTATAAAATG CAAAATTTAG AAAATCTTTT AGCAGAAGAT ACAGCCCTAA TCTTACCACT CATTATTGAC ATTTATGATG TACTTCGTTA TAGTATCAAA ACAATTCCAG	60 120 180 240 300 309
(2) INFORMA	ATION FOR SEQ ID NO:1334:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 243 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1334:	
AAATGTAAAA TTCACATTAT	TCTAGACCTG CCTCGAGCTG CCGTGTTTTT CATTTAATT GTGTGACATA TGTACCCTCT AAACCATTTT TTAGTGTCCA GTTTTGTGGT ATTAAGTACA TGTGCAACCG TCCCCACCAT CCATTCACAG AACTCTTTCA ACTTGCAAAA ATGCATTAAG CAATAACTAT CCCTTCCTTC TTTCCTCTTC CCCAGAGCTC	60 120 180 240

PCT/US98/06955

WO 98/45436

243 GAG (2) INFORMATION FOR SEQ ID NO:1335: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 280 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335: 60 GAATTCGGCC TTCATGGCCT AATTCTGGGA AAACTGAGAG AAAAATCTGA GGCCATCCAG AAGGAACTAG AACAGACCAA GCAAAAAACA ATCAGTGCGG TTGGTGAGCA GCTCCTGCCC 120 180 ACAGTCGAGC ACCTCCAGCT GGAGCTGGAT CAGCTAAAGT CAGAGCTGTC CAGCTGGCGA CACGTGAAGA CCGGCTGTGA GACAGTGGAT GCCGTACAAG AAAGAGTGGA CGTGCAAGTC 240 280 AGAGAAATGG TGAAACTCCT GTTTTCCGAA ATAGCTCGAG (2) INFORMATION FOR SEQ ID NO:1336: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 281 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336: GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCCGAAT TCGGCCTTCA TGGCCTAGAC TAATCTTACT GTAGAAATGA TGTGAGATTC TTGTTTGACT ATTTTAGAGC AGATTCGGTA 120 180 TCTAATGGGA TTCCATCTTG ATGTACAGAG CACCTTCTAC ATAATGAATT TTGCATTTCA GATGGATGAA GCCTTTAACA CAGACAGAAT TTTAAGTATT GCATATTTCT GGAAGAAAAG 240 CATTGATCAC ATCCTCCTTA GATATTTAGT AATACCTCGA G 281 (2) INFORMATION FOR SEQ ID NO:1337: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 172 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

GAATTCGGCC TTCATGGCCT	AATATTTAGG	TAAAAAGGTA	AACTAGTACA	CCTACCAGAA	60
AAGATAAATA TTAATTTATT	GCATCTCTGA	CATGAGAAAA	AAAGCCTTTA	TGTTTTACTG	120
TTTTTTTCTA ATTTTTCTTT	TTCTTTTTTT	TTTTCACATG	AATGTTCTCG	AG	172

- (2) INFORMATION FOR SEQ ID NO:1338:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

GAATTCGGCC	TTCATGGCCT	ACTGTATTTC	ATAGTGAAGT	GTTCATAAAC	TAAAGAGTCA	60
TTGATTTGGT	TTCCTGGCTA	ATTAAAATCT	GAATTCCATT	TGAAGTTCCA	TTGAAATCAT	120
GGTTTTACTC	TATAGCAGTG	GATGTTTTTT	CCCAACCTTT	CTGATATTTT	TTTCCTTCCT	180
GAGACAGGGT	CTTGCTCTGT	CACCTGGGAT	GGAGTGTAGT	TGCACCAAAC	TCGAG	235

- (2) INFORMATION FOR SEQ ID NO:1339:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:

GAATTCGGCC	TTCATGGCCT	ACTTGTTTTT	AAAGGCATAT	GTTGTTTTAT	TGTGCTTCAC	60
AGGTACTGTA	TCTTTTTTTA	CAAATCTAAG	TTTTGTGGCA	ACTCTGTGTC	AAGCAAGGCT	120
ATTGGCCCCA	TTTTCCCAAC	AAGCACGC				148

- (2) INFORMATION FOR SEQ ID NO:1340:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

GCCTGTGTGA	AGTTTTGACT	TTAATCTACC	AGATCACTCC	TTCACCCTCC	ATAAAGATGT	60
CTGAACCTGA	CACTTCCTCA	GGATTTTCGG	GAAGTGTGGA	GAATGGAACT	TTTCTTGAGC	120
TGTTTCCCAC	ATCCCTGTCC	ACGTCAGTGG	ACCCATCCTC	AGGCCACCTG	TCAAACGTCT	180
ACATCTATGT	GTCCATATTC	CTCAGCCTTT	TAGCGTTTCT	GCTTCTGCTT	TTAATCATTG	240
CCCCCAGAG	GCTCGAG					257

- (2) INFORMATION FOR SEQ ID NO:1341:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

GAATTCGGCC TTCATGGCCT ACTATAAAGT ACTCTCGCTG GTATTGTCAG TATGTGTGTT AACAACAATA CTTGGTTGTA TATTTGGGTT GAAACCAAGC TGTGCCAAAG AAGTTAAAAG TTGCAAAGGT CGCTGTTTCG AGAGAACATT TGGGAACTGT CGCTGTGATG CTGCCTGTGT TGAGCTTGGA AACTGCTGTT TAGATTACCA GGAGACGTGC ATAGAACCAG AACATATATG GACTTGCACC AAACTCGAG	60 120 180 240 259
(2) INFORMATION FOR SEQ ID NO:1342:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 268 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:	
GAATTCGGCC TTCATGGCCT AGTCCTTGAC TCTGGAGTTT TACAAAGCAG TCACATTTCA AATAAAAGTC TGGGAAAGCA ACACATCATC GCCAACTTTT AATTTTGCTA AATAAGGATA TTAGAAAAAG AATAGAAAAT TGCAGTCCCT TACTGTTTAA AGAAAAACCA AAAGAAGTTA AAAAAAAAAAC AACCTCATTA TGTTGTCTTT GTTTTTGTTT TGTTTTCTTT CCTTGGAAAT CAGTGAAAGT TTGGTCAGCC ACCTCGAG	60 120 180 240 268
(2) INFORMATION FOR SEQ ID NO:1343:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 241 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:	
GAATTCGGCC TTCATGGCCT AGCCATTTAA TATACTAAAA CAGTGTTGTA AATTAACTTT GGTACAAATT GCCAGTCATC TCTAGATCAT TTTAAGCATT TTAAGAATAT TTATTATCAA TCTAAGTACA GAAGAATAAC TGCCAGCAGT GATTATTTGC TTTGGATTAG AGTTTTTAAA AATCCACCTC ACTGAAATGG TTATGTTCAT CACAGTTTGC AAGGTTTGTC TGTTTCTCGA G	60 120 180 240 241
(2) INFORMATION FOR SEQ ID NO:1344:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 313 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:	
GAATTCGGCC TTCATGGCCT ACCCATTCCT TCCTTCCTGC CTGGCCTGGG CCCCTCCTGC ACAGATGGCC TAGGTACCCA GCCTGGAGGC CAAGGCTGGA TTCCCAGAGT CTGCCCTGGT GGAGTGGGAA TAGCAGGTTC TCTGCAACTC AGGGGAGCTG CCCTGCAGGG CTTCCCACAT GTGCTCAGGC CCCTGTGCCA GGTCTGGTGA TGCTTCCTCC TTGCCTTTCA GGATCTCCTA TTGCACAGCA GACAAGATGC ACGACAAGGT GTTTGCATAC ATCGCCCAGA GCCAGCACAA	60 120 180 240 300

313

CCAGAGCCTC GAG

,	(2) INFORMATION FOR SEQ ID NO:1345:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 327 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:	
	GAATTCGGCC TTCATGGCCT AGGCTTCTCT TCTGAATTGA TTGGTAGTGT TGTTATTTTC PTGTTATTCA GTTTAACAAG TACATAATCA ACATCAGTGC TTGGGAAGTC AGGAGTACGA GAGATAAATA AGAAGTATAT GATCTTTTCT CTTATTTTCT CTCAGTATAA GTTGGACCTG PTTTTCCCTT CATCTCTTTT TCTTCAAGAA CATAATATCG GCTGAAGTGG AATGAGTATT CAAATTGTCC AAAAAAATAT ACAAGTGAGG GAATTAATAA AATTTTTTGT AATTATAAAT ATGTATATAT TGGGGGGCAG TCTCGAG	60 120 180 240 300 327
	(2) INFORMATION FOR SEQ ID NO:1346:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 189 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:	
	GAATTCGGCC TCATGGCCTA AATCCTTGGA AATACAATGA GACTCATCAG AAACATTTAC ATATTTTGTA GTATAGTTAT GACAGCAGAG GGTGATGCTC CAGAGCTGCC AGAAGAAAGG GAACTGATGA CCAACTGCTC CAACATGTCT CTAAGAAAGG TTCCCGCAGA CTTGACCCCA ACACTCGAG	60 120 180 189
	(2) INFORMATION FOR SEQ ID NO:1347:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 262 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:	
	GAATTCGGCC TTCATGGCCT AGTGGGCTTC AGGAAAGCAA AATATAAATA TTATGGTTAA AGAATTTATA ATTAAGATTT CACCCATAAT TCTTAATACT GTGTTGACAA TCATGGCTGC ATTGTCTCCA AAAACAAAAG AAGATGGATC CAAAGATACG TCTAAGGAAA TGGAAAATCT TTGGGGTATC AAATCGATTA ATGATTATAA CACTTGGTTT CTTGGTGTTG ACACGGCAAC AGAAATAACG GAAAAGCTCG AG	60 120 180 240 262
	(2) INFORMATION FOR SEQ ID NO:1348:	
	(i) SEQUENCE CHARACTERISTICS:	

- (A) LENGTH: 333 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

GAATTCGGCC	TTCATGGCCT	AGTAATGTTA	AAACAAACGA	ATAAAAATA	GAAGGAAAAA	60
CTTTCTGAGT	TTCAAAAACA	ACAGACTAGT	ACTCTAAAGA	ACTCTTTAAA	ACAATTAACT	120
GTTAGGATTG	CAGTTATGAT	TGGATATTAT	TTAATTCTGT	TTCTGATGTG	GGGTTCCTCC	180
ACTGTGTTCT	GTGTGCTATT	AATATTTACC	ATTGCAGAAG	CTTCATTCAG	TGTTGAAAAT	240
GAATGCTTAG	TGGATCTGTG	CCTCTTATGC	ATATGTTACA	AATTATCTGG	AGTTCCTAAT	300
CAATGCAGAG	TTCCCCTCCC	CTCCGCGCTC	GAG			333

- (2) INFORMATION FOR SEQ ID NO:1349:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 553 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

GAATTCGGCC	TTCATGGCCT	AGGAAGACAG	ATTTCACAGA	GAGTGGGTTT	CATGTTAAAT	60
GTCTGATTTC	CTTGTCGGAT	GCCCCCACAA	GGACACTAGG	TTTTGTGGGC	CAATGTGTTA	120
TGTGTGTATG	TAGGCAAGCA	GGAGGGGGTG	GGTGGGCTTC	TTTTTTTTTC	TATTTTTTC	180
TTTTCTTTTT	TGGTTGTGGA	AGAACCACGT	TAACCCCTCT	AATTTCTTTA	AAAAGACATA	240
AGGTTTGAAA	AGGAGATTTT	AGGAAGAAGC	AAAAGAAAAA	AAATGGGATA	CATATATTGC	300
ATCTGTAATC	CAATCAAGCT	GTCACTGAAG	ACAAACTTGA	TCTCTGTTCT	CACCAGTTGA	360
CACACTCATC	AGGCTATAGG	TCAACTCTAA	GTGTGGTGAC	AGGTGATGGA	CTCTATGCCA	420
ATTCTGATAC	TGAATTTTCT	TTTGCTTATT	GAAGCTTCAT	TTTGTGTGTT	TTAATTATGA	480
AAGTATAGTA	ACACCTACCA	TGCATACCAA	AGCAATATCA	ATATTTTCAA	ATGCATCTTC	540
CCCCATTCTC	GAG					553

- (2) INFORMATION FOR SEQ ID NO:1350:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

GAATTCGGCC	TTCATGGCCT	AGGTTTTTGT	TGTTTGTTTT	TAAAGGAGTT	AGACATAGCC	60
TAACAAACTG	GAAATTGACA	TTTCCATCTA	TTTTTCTCCC	TTTTGAAGCT	AAATATGTCT	120
TTGTTATTTT	GGTTCCTAGT	CCCCATTACT	ACTTATTTTC	TGATAGTTCA	TCCACAGCAA	180
CTTCAGTCAG	TTAGCTCACT	AGTTCTTATG	GCTAGAGATT	CCGCCAGTTT	TCCCCTAAAA	240
CTCGAG						246

(2) INFORMATION FOR SEQ ID NO:1351:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 231 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351: AAAGAAAAA TAAAAAAAAA AAAAAAAAA GGAAGTGTAA TGTCAGACAC ACAAGAAAAG 60 CAAATCAGTG TTGTAAGCTT AAAGTACAAT TTCAAAGGTC ATTACCAACA GCAGGGTTTT 120 TTTTATACTT TAAAAACATT ATGCTACATA TCATTGCCAT TTTCATATTT TGGGGTTTTG 180 CTACTCTTAT ACAATGGAAT CAATGGAAAT GTCATCCAGC CAGATCTCGA G 231 (2) INFORMATION FOR SEQ ID NO:1352: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 260 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352: TGAATTCTAG ACCTGCCTCG AGTTGCTCCC AGGAATAGTC CAAAGGAGCT GCTCTTGCCC 60 CTTTATACAC AAGCGCCAGC AACCAAAACC CTCCCTCCTG GCAATAAGGC CTCACTATAG 120 TTGCCCTCAT GCTTCCTAAG CTCTCTCTTG CTCTAATAAC TCTAATTCTG GGCCAAGCCC 180 AAGAGTGCCA TTCTTTCTTC CTAGCTGGGG ATGGAAAGCT GAGAGGGGCA CAAGGAGGGC 240 AAAAGTATCA CCCTATCGAG 260 (2) INFORMATION FOR SEQ ID NO:1353: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 482 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353: GAATTCGCCT TCATGGCCTA CTTTTCAAGT GAATGATTTG GTGTTTGAAC CTTCTTGATT 60 ACCTTAAGAG GGAAAAATGA AGGAGAGGAG GGAACCATCA TCACATACCT TTACAGTTGT 120 GGAATGTTAG CCCACTATAG TGTTTAACTA AGGAAAATCT AATATAATAC ACTCCCAAGT 180 GATCTGAAAT GATCCGCTAT TCAGAATTCC AGAGAAAGAC ATATCCCTGC CAGAAGGGTG 240 TCCTTCATAA CCAAATTTGG TCTTCAGTCT GGTCGGTGCA TACTCAAACA GGAATCACTT 300 CCCTTAAGGA ACCTAAGGTA TGCAGTTGAG ATCAACTTAT TCCTTTTTGA TTTGTCCCCT 360 TAAAGCATCA ATCAGACGTG AATGCATCTT GTGACTTGGA GTTACTAGTA ATATTGAAAT 420 CTGAAACTTG GGGGATCTTT GAAGACACAT GGGATTAAAA GCTGCATAAT ATACATCTCG 480 482 (2) INFORMATION FOR SEQ ID NO:1354:

526

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

GAATTCGGCC	TTCATGGCCT	AATACCCAAA	ATTGGCATGA	CTACTTATAA	AATAGTGCCT	60
CCCAAATCCT	TGGAAATATC	GAAAGACTGG	CAATCAGAAA	CCATAGAGTA	TAAAGATGAT	120
CAGGACATGC	ATGCTTTAGG	GAAAAAGCAC	ACTCATGAGA	ATGTGAAAGA	AACTGCCATC	180
CAAACAGAAG	ATTCTGCTAT	TTCTGAAAGC	CCAGAAGAGC	CACTGCCAAA	CCTTAAACCG	240
AAGCCTAACC	TGAGAACAGA	GCATCAAGTG	CCCAGTTCTG	TGAGCTCACC	TGATGATGCC	300
ATGGTTAGTC	CTCTGAAACC	TGCTCCCAAA	AATCTCGAG			339

- (2) INFORMATION FOR SEQ ID NO:1355:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 203 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

GAATTCGGCC TTCATGGCCT	ACTTTTAGAT	GCTTTACATG	CATAAATTCA	AATAATACAT	60
TAATAACCTT CCATACATCT	TTCTTTGTGT	ACACGTTACT	ATTTCTGTAA	GATAGATTTC	120
TAAAAGTGGA ATTTCTAGGC	CAAATGATTT	ACACTTTTTT	TGTTTGTTTG	TTTTTTTGTT	180
TTTTTGAGAC GGAGTGTCTC	GAG				203

- (2) INFORMATION FOR SEQ ID NO:1356:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

GAATTCGGCC	TTCATGGCCT	AGGAGAATCA	GGCAGGGAGG	TTGCAGTGAG	CCGAGATGGC	60
AGCAGTACAG	TCTAGCTTCG	GCTCGGCATC	AGAGGGAGAC	CGTGGAAAGA	GAGGGAGAGG	120
GAGACCGTGG	GGAGAAGGAG	AANGAGGGG	AGGGGGAGGG	GGGGAGAGGG	AGAGGGACAA	180
TGATGTCTTG	CTGTAGGTAT	TCTTCCCCAT	TTGAATTTTT	TCCTCAGCAT	TATTTTTTT	240
AACATCATTC	AGTCTCCTCT	TATACTACAC	TTGGATTGAA	TTTAATATCT	CATGAAGAAA	300
AAACATTTCT	ACTTTGAAGC	ATGTGAATTA	GCATGTTTTT	ATAACAGCTT	TATTGAGATA	360
TAATTTACAT	ATATAAATAA	ACCGTTTAAA	GTGTATAAAT	CAGTGGTTTT	TAATGAGATA	420
TAATTTACAT	ATATAAATCA	ACCATTTAAA	GTGTATAAAT	CAGTGGTTTT	TAAAATATTC	480
ACAATGTTGT	ACGACCGTCT	TCTCAGTCAA	CTCGAG			516

- (2) INFORMATION FOR SEQ ID NO:1357:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

GAATTACTAA	TCAAGAAAAA	ACAAAATCAC	AAATCACTAC	CAAAGCAGTT	CATTGTCAAT	60
AATTTTTTTC	CCTTGTATTT	TTGTTTACTT	TTTGCGAACC	CTGAGCATAC	ATCCAAGTTG	120
CCCTAAATAT	ACGCACACCT	GAGGTTGTCT	TTATAGGAGC	TTTATGGTTG	CAAGTTTTGT	180
GTATAATCTT	TAATCATTTT	GAGTTGATTA	TTGTGTATCT	AGTACCATAA	GAGTCCTGTA	240
TTATTCTTTT	GCATATGGAT	ATCTAGTTTT	GGAAATCTTC	CCCGTTGTGT	CATTTTGGTG	300
GTGTTTTGAA	AAATGTGTTC	ATTCCATATA	AATTTTTGTT	TATTATCGAG	CACATTCATT	360
TTGCTCACTG	GTCTGTGTTT	CTCTGTGTAC	GCCAGTAACC	TCGAG		405

- (2) INFORMATION FOR SEQ ID NO:1358:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

CTCGAGTCTG	GCTTTGTTTC	AAAATGATTA	AGATTAAATG	ATGAAATAAT	ATTTTATAGC	60
CACTGCATTG	GATACTTGGA	TTGTTTTTCA	AGCATCTTCT	TATGACTAAA	TCTTCTGTTT	120
CATTCTGTTT	TAAATCTAAA	AAGTAAAATG	ATGGTCACTT	GGAATCTGCT	CTATATTTTA	180
ATTATAGTCT	CTTCTGTTTA	TAAACAATAA	CTTACACATA	TTTTTCATAG	TTTTAAGTAA	240
AGATTAAATA	ATGCCATCTT	AGAAAGGATC	TGTTTAACCT	ATATTATAAA	AGTTAGATAC	300
ACAATTTTAG	GCCATGAAGG	CCGAATTC				328

- (2) INFORMATION FOR SEQ ID NO:1359:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

CTCGATGGCC	TAAGGCAGTC	TCCTGGAAGC	ATGACATTGA	TGCCCTGGGC	TCACCTCTTT	60
GTTTTGTTTT	CCTTCCACTT	TAGCGGGAAC	CACATCTTCA	AGGGCCGTGC	TGCCGGCATA	120
GCAGTGAATG	AGAACGGCAA	AGGCCTCATC	ACAGGTACGG	ATGGGAACTG	CCTGGCACCT	180
GGCAGCCAGG	CCAAGGTCCC	CTGGCGTCAC	CCCCCAGCTT	CAGGACCTCT	AGGCCATGAA	240
GGCCGAATTC						250

- (2) INFORMATION FOR SEQ ID NO:1360:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

GAATTCGGCC	TTCATGGCCT	ACGATTCTAT	TTCCTTATCT	GCTTGCAGAG	CTATTTAAGA	60
ATCAATGTCT	TATTTTTCCT	GAGTCCTTTA	TAACCCTATT	CATATTTTCA	ATTGCTGATG	120
CCTCTTTGAG	CTACGAGTTC	TACTTTGTGC	ATAACGTTGA	GGAATTTCTA	CGTTTACTGT	180
TTCTCCTTAC	TTCACTCATC	CTCGAG				206

- (2) INFORMATION FOR SEQ ID NO:1361:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

GAATTCGGCC	TTCATGGCCT	AAGAAATCAA	CGTTGAACCC	TAATGCTAAG	GAGTTCAATC	60
CTACAAAGCC	TCTGCTGTCT	GTGGTGAGCT	GGGACAGGAG	AATGTGGACT	TTGGTTTCTG	120
TGGGGAGACT	TGGGCAGTGC	TTATAGATGA	ATAGGGGGAG	GAACACTTCA	CTTCCAGGAC	180
CACTTGCCTG	GCAGGCAGTG	TGAGGAGATG	TCATAAAAAT	GTAAGGATGG	CACCTTTGGG	240
GCTGGCTTGG	GGAAAATGGA	CTCAGGTCTC	TAGGTTTGGG	TGATCAGGGA	TCCCAGTGAG	300
TCTGATGAGG	GGTTAACAGG	CTTTTCTTTG	GTTCTTGGCA	TTTGGCTGAG	GGAGTATTGG	360
AGTGGGGATA	GCTCGAG					377

- (2) INFORMATION FOR SEQ ID NO:1362:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

GAATTCGGCC	TTCATGGCCT	AGTTAAAGGC	AAGTATGTCA	TATTACTGAG	GCTACAAGTT	60
AGTCAGCAGA	TGAGTGCCAG	TCCAGCCTTT	TCTGGTATGT	TATTGTTAGA	AATATTGAGT	120
TCTAATGTTA	CATCTGAGGA	AGTATGTAAT	TTGAGAATTG	TAACTTCTAA	GGGATTCACT	180
GCATCATAGC	TATGCCTGTA	TGGAGTCTAA	CATATGACCA	ATACCAACCC	ATAATCCAGC	240
ATTGAATTCT	AGACCTGCCT	CGAG				264

- (2) INFORMATION FOR SEQ ID NO:1363:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

GAATTCGGCC TTCATGGCCT ACCCCTCCC TAGTTCCAGT CCAGGTAAAC AAAAATTGAT TCTATTTTTT CAAAACACCA GCCCTTCAG ATGGCCTGGT TAATCTTCAT TAACATGTTA TCTTCATTAA CATGTTTATC TTCATTAACA TATTTCTCAG TGATAAGAAG GGCCCAGGGT TCAACATCCC ACTTTGCATC CATGCAGACA AGGGCTGTGG GAAGCTGTAA AACTGAAGAG GCGGTGAATC CAGGAGGGAT TCCCCAGATA TCCGTGAGTT GGTGTTTGAC TTTCTTGAAC ACGTCTTTCC TTTACTTTAC ACTTCCACTC GAG	60 120 180 240 300 333
(2) INFORMATION FOR SEQ ID NO:1364:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 358 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:	
CTCGAGGGGT CATGTTGTTG GGGAGAAAGA GACCACATCA CACACAGAGA GAACAAGTCT GTATTAGTTG CTTTTGCTAC ATAACAAACC ACTCCAAAAT TTAGTGGTTT AGAACAATCA CCTATTTAGT TAATGATTCT CTGGGTTGCA ACTTGGTCTG GGATCAGCTG GGCAGTTCTT TTGCTGGTCT CAGCTGGGTT CAGCTGCCTA TCAGCTAGGG AGCTCTGTTT CAGAGGTTGG TTGGCTATGG GTGGCAGGGA TCAAGGATGA CGGAGCCATG TGTCTCTTTT CCCTTTATTA CCCAGCAGGT TAGCCCAGAT CTTTTCCTTT TCTTTCCTAG GCCATGAAGG CCGAATTC	60 120 180 240 300 358
(2) INFORMATION FOR SEQ ID NO:1365:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:	
GAATTCGGCC TTCATGGCCT ACTTGTTCAG GGTATGGGGC TAGGATGAGA GAGAATNCCA CAGAGTATGA AGGAAGAGTG ATAGATCCAG ATGAGATACA GCTCAGAGTG CCACGCCCCC AGAAAGAGGA ATCAGGCAAG TACTGTCCCA AGGCAGCTGG AGGGTGAGGG CTGAGTGCCC TGGCTTCCTC ACTTGGGAG ACCATGGGTC TCTGTAGAAA TTCCAATATA AAGGCAGGGA AATTTGACTG CATGGAGTCT TCAGGTAGAA ATGTTTCTCT TGCCTAAATT CA	60 120 180 240 292
(2) INFORMATION FOR SEQ ID NO:1366:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 335 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:	
GAATTGAGCA AGATACCTGG GTCATGATCT CTGAACAGGG TGAGAAACTT TATAAAATGA TGTGCAGACA AGGAAATCTG ATCAAAGACA GAAAAAGAAA ACTGACTACG TTCCCTAAAT GCTTTCTTGG AAGCGAATTT GTGTCATGGC TGTTGGAAAT TGGAGAGATT CACAGGCCTG	60 120 180

AGGAAGGCGT GCACTTGGGA CAAGCATTAT TAGAAAATGG AATCATTCAC CATGTTACTG ATAAACATCA ATTCAAACCA GAACAGATGT TATATAGATT TCGCTATGAT GATGGAACAT TTTATCCAAG AAATGAGATG CAGGACGTTC TCGAG	240 300 335
(2) INFORMATION FOR SEQ ID NO:1367:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 383 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:	
GAATTCGGCC TTCATGGCCT ACTTTCTCTG TTTGCCTTGA CCTTTCTTTT TCATGTTAAA GCCTTTCCTC AAATGTCTGA TTACCCTTGG CTGCCCGTCA TTTAAGAAAG CGCCACTAGT CAGCTCATCG GAAGCTGTGA GGGAGAGGGC TGCATTTGGT CCTGCCAGGT GGAGGAACAC TCAGGCATCA GTACTAGGAG GTCTTTCCTC TCAGCCCATT GGATTTCCCT AGAGTCCTAC ACGGCTGGGA TGAGGCACCT GGGTGCTGAG TAGAGGAAGG GAGTCATGG TCAGTCACCC TGTATGCAGA TTTTCACACA ACCCCCTCTC TCCAGGACAC GCCTCGCCCC CCACCCTAAG TAATGCAGAA CCCCAAATCTC GAG	60 120 180 240 300 360 383
(2) INFORMATION FOR SEQ ID NO:1368:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 347 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:	
GAATTCTTAT GTGACTGCGA TGGATCTCTT TGTTTCTGTT TGTTTCATTT TTGTTTTTGC AGCCTTGATG GAATATGGAA CCTTGCATTA TTTTACCAGC AACCAAAAAG GAAAGACTGC TACTAAAGAC AGAAAGCTAA AAAATAAAGC CTCGATGACT CCTGGTCTCC ATCCTGGATC CACTCTGATT CCAATGAATA ATATTTCTGT GCCGCAAGAA GATGATTATG GGTATCAGTG TTTGGAGGGC AAAGATTGTG CCAGCTTCTT CTGTTGCTTT GAAGACTGCA GAACAGGATC TTGGAGGGAA GGAAGGATAC ACATACGCAT TGCCAAACTG ACTCGAG	120 180 240
(2) INFORMATION FOR SEQ ID-NO:1369:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 243 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:	
GAATTCGGCC TTCATGGCCT ACCATTTTCT ATGAGCAGAG GAGAGTCACA GGGCATCATG	60

120

180

TGTTAGGAGA AAGAGGCTGG ACTTTATCTT GTCAGTAATG CTGGATGATA CAATAAGGGT

AGGGCCTCAA AAAGTAAATG TAAAAATGAT ATTTGGCACA CATTTGGGTG AATAGAGGCT

GGAGAAAGGG AACCAAGTCA CTATGTATTG GAATAATTCA AGTATAGGCC TGGGATACTC

GAG	243
(2) INFORMATION FOR SEQ ID NO:1370:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 256 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:	
GAATTCGGCC TTCATGGCCT AGAGGATTAC TTATTTCTCA GCATTCATCT GGTAACTTAA GCAGCATGAA GCAAGAGTTG CACTTTAAAA AATGACAAGA AAATAGCTAT TCATTTAGTC GACAGAGTAA GGCCCATCTC ATTTCCAGGA TCACTAGTTT CTGCTTATGA CGGGGTGAGC ATCCGCCAGC GCGGTGATTG GGAGGCGCCC CTGTGTCTTT AGGCTGAGGC AGTGCCCATA GCTGCAGTGC CTCGAG	60 120 180 240 256
(2) INFORMATION FOR SEQ ID NO:1371:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 332 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:	
GAATTCGGCC TTCATGGCCT AGTGTAGCAA GCTTCCCCTT TGGGAGGGAT GTGAGAACAG AAGACTGAGG ATTGTCTCTA ACTCTAGGAT TCTTTGATGA TTGATTGGAT TGGGGTTTTG TGTTGTGTCT AATATTACGG ATGCTAAAAT GCCTGTACTT CCAAGGTGAT AGCCACCAAT AACCATACAC GTACTAGTCA TCCTAGAAGT GTTTTTATTT CTTCTGTTGG TTATCTTCCC TACCCCTAGG GTTGGTGTCT GTTTCCTGCT ACTTCAGGTT GGTTTCCCAC TGGGAGGCTT CTGCTGACAG AAAGCCCCAT GCTTTGCTCG AG	60 120 180 240 300 332
(2) INFORMATION FOR SEQ ID NO:1372:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 275 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:	
CTCGAGGGCA ACTGCAGAAG AAAAGATCAG TGAATCTGAT GACATAGCAG AAGAAACTAT CTAAAGCGAA GAAGACAGGA AAAAAAGCCC CAATGTGAAA TGAACAGATC ACCAGTGAGC TGTGGAACAA CCTATATGGG TTATAGGAGA CCCTAAATGA GAGAACAAGG GACTAAAAGA AGGATTTAAA GAAATAATAG TACAATTTTC TCCAAGTTTC ATGAAAACCG ATTGAATTCT AGACCTGCCT CGAGGCAGGT CTAGAATCA ATCGC	60 120 180 240 275
(2) INFORMATION FOR SEQ ID NO:1373:	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

GAATTCGGCC TTCATGGCCT	ACAAGACCAT	CCTGGCCAAC	ATGGTGAAAC	CCTGTCTCTA	60
СТАЛАЛАЛТА САЛАЛАЛТТ	AGCCAGGCAT	GGCAGCGTGT	GCCTGTAGTC	CCAGCTACTC	120
AGAAGGCTGA GGCAGGAGAC	TTGCTTGAAC	CCAGGAGGCA	GAGGCTGCAG	TGAGCCGAGA	180
TCGCGCCATT GCACTCCAGC	CCGGGCGACT	GAAGAGACTC	CATCTCAAAA	АААААААА	240
AAAAAGATGA GCCTTTTCTG	GGAAAGTGGA	AAAGACAGAG	AAGCCTCCTG	ACAGCCAAGG	300
AGACCAGCAG CCAGTAGAGC	AGGTGTTGTA	ACAAGGCCGA	GGCCCTCGAG		350

- (2) INFORMATION FOR SEQ ID NO:1374:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

GGAAAAATCA AGGAGACATA	TTACCACCAA	AAGAACAATA	ATTTCCTAGA	AGCTGCAAAT	60
AAATAGAGAC TATACACTGC	CTTACAGATA	ATTTAAAGTA	ATTGTTTTAA	GGAATCTCAG	120
TGAACTTCAA GAAAATACAG	AGAATCAGTT	CTATGAAATC	AGGGAAACAA	TAAATCAACA	180
AAACGATAAA TTTAACAGGT	TGAAATCACT	AAAAGAACCA	AACAAATTTT	GGGGCTAAAG	240
AATACAATGA ATGAAATGAA	AAATACTCTC	GAG			273

- (2) INFORMATION FOR SEQ ID NO:1375:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

TGTGGACTAA	AAAAGATGCT	GGGAAAAAAG	TTGTTCCATG	TAGACATGAC	TGGCATCAGA	60
CTGGAGGTGA	AGTTACCATT	TCAGTATATG	CTAAAAACTC	ACTTCCAGAA	CTTAGCCGAG	120
TAGAAGCAAA	TAGCACATTG	TTAAATGTGC	ATATTGTATT	TGAAGGAGAG	AAGGAATTTG	180
ATCAAAATGT	GAAATTATGG	GGTGTGATTG	ATGTAAAGCG	AAGTTATGTA	ACTATGACTG	240
CAACAAAGAT	TGAAATCACT	ATGAGAAAAG	CTGAACCGAT	GCAGTGGGCA	AGCCTTGAAC	300
TGCCTGCAGC	TAAAAAGCAG	GAAAAACTCG	AG			332

- (2) INFORMATION FOR SEQ ID NO:1376:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

GAATTCGGCC	TTCATGGCCT	AGGCTTCAGC	AGCTTCCTAC	GATCAGCCGA	AGAAAGCAGA	60
AGCTCTGGAG	GCTGCCATCG	AGAACCTCAA	TGAAGCCAAG	AACTATTTTG	CAAAGGTTGA	120
CTGCAAAGAG	CGCATCAGGG	ACGTCGTTTA	CTTCCAGGCC	AGACTCTACC	ATACCCTGGG	180
GAAGACCCAG	GAGAGGAACC	GGTGTGCGAT	GCTCTTCCGG	CAGCTGCATC	AGGAGCTGCC	240
CTCTCATGGG	GTACCCTTGA	TAAACCATCT	CTAGAGAGGA	CATCCCTGCT	GGGCTGCTGT	300
GCAGAGTATA	AGATTTTGGA	CTTGTTCATG	TCCCCTCTCA	CCCCTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:1377:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

GAATTCGGCC	TTCATGGCCT	AAATATGTTG	AAATAGGTTA	GAAAAGGAGG	TGAATATTAT	60
GGGCTGTTGT	CATTTGTAAA	TTCTGCAGTA	ACTTCAGCGT	TGAGGGTTTT	TTTTGTTTTT	120
GTTTTTGTTT	TGAGTTTTGC	TTACTGAAAT	CAAAGAGTTG	TTACTCTGTC	TGTGGGTGTT	180
TAAGAGACAG	GATCTCACTC	TGCTGCCCAG	GCTGGAGTGC	AGTGCAGCCA	CGAATGCCTG	240
GGCTCCAGGC	CCTCCTGAGT	AGCTAGGACT	TACAGGCATG	CACCACCACA	CCGATTTTTT	300
TATTTTTTA	TTTTTTTTT	TTTTAGTTTT	TAGAGGTGGT	GGGGGGGTCT	CACTGTGTCT	360
GCTTCTGGGC	TCAAATGATC	CTCCTGCCTC	AACCTCCCAA	AGTTCTAGAA	TTACAGAGGT	420
GAGTCACCAC	ACTCGAG					437

- (2) INFORMATION FOR SEQ ID NO:1378:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

GAATTAAAGC	ACTGCCTCTA	TTCAGGCTGC	CGAGGCACTG	CTTTAATTTT	TTGAAAGATT	60
CACCGCGTCT	TCTTGGATTT	CAAGAAAAAT	CCCGTTAAGA	ATTGAGGGGC	TCTCTTCTTC	120
CCCTCCTGAC	GTGAGTGTAA	CTCACTTCCT	GGTATGTCTC	CTTTCCTTTT	GGCCTACATC	180
CTTTGTCTGT	TAGGTGCTTC	CACATCCTTA	TGTCTTAAAT	GGCCAAAATA	CGTCACCCCC	240
ACTGCCAAAA	CAAACAGATC	ACTCGAG				267

- (2) INFORMATION FOR SEQ ID NO:1379:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

GAATTCGGCC	TTCATGGCCT	AGAGGTGACT	AGAAGCGAAG	ATGGAGGTGG	CGCAGCACCT	60
CATCCCAACT	CATGCCACCT	GGGGAAGCAG	CTTCAGGCCT	TTCTGTTGTA	ACCTCAGCAG	120
AAACTTTGGG	GTTTATCCTT	TATCTTGCAC	ATGCCCCAGG	GAGGTAAAGG	GACTTGCCTA	180
GGTTCATGTA	CAAACTTTCT	GCTTCCAGAG	CAGGACTTTA	TTGGGACACC	ATAAGGTTGA	240
GGCTGGGAGG	TACCCAAGAA	TTCCTGGGGA	TGGTATGTCA	TTGACTGTGG	GTAGAGGGGC	300
TCGAG						305

- (2) INFORMATION FOR SEQ ID NO:1380:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

GAATTCGGCC	TTCATGGCCT	AGGCTTGGTT	GCCTCTGAAA	GGAGGGAAAG	TCTCTTGGTA	60
AATTATCTCT	TTTGTGCTGT	TTGCTGTTTC	TCTGCTACCG	TCTTTGCAGT	TCTCCTCTCA	120
CTGGTTGCAG	GCTTTCATAG	TAAGGTTTGG	CGAGAAATGT	TCCAAACATC	ACATTTTGGA	180
TTCTAGGCTG	TCACCCCAGG	CTCGAG				206

- (2) INFORMATION FOR SEQ ID NO:1381:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:

GAATTCGGCC TTCATGGC	T ACTCCTCGAT	GCTGATTCAT	ATCCTACTGC	CCATGGTTTT	60
CTGCGTCTTG CTCATCATC	G TCATGTGCTA	CTTGAAAAGT	CAGTGGATCA	AGGAGACCTG	120
TTATCCTGAC ATCCCTGAC	C CTTACAAGAG	CAGCATCCTG	TCATTAATAA	AATTCAAGGA	180
GAACCCTCAC CTAATAATA	A TGAATGTCAG	TGACTGTATC	CCAGATGCTA	TTGAAGTTGT	240
AAGCAAGCCA GAAGGGACA	A AGATACAGTT	CCTAGGCACT	AGGAAGTCAC	TCACAGAAAC	300
CGAGTTGACT AAGCCTAA	T ACCTTTATCT	CCTTCCAACA	GAAAAGAATC	ACTCTGGCCC	360
TGGCCCCTGC ATCTGTTT	G AGAACTTGAC	CTATAACCAG	GCAGCTTCTG	ACTCTGGCTC	420
TTGTGGCCAT GTTCCAGT	AT CCCCAAAAGC	CCCAAGTATG	CTGGGACTAA	TGACCTCACC	480
TGAAAATGTA CTCGAG					496

- (2) INFORMATION FOR SEQ ID NO:1382:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

GAAACTAGAC	AAGAAATCTC	AAGCCATGGA	GGAGCTAAAA	GCAGAGCGAG	AAAAACGAAA	60
GAACAGAACA	GCTGAGCTCC	TTGCCAAAAA	ACAGCCATTA	AAAACCAGTG	AGGTCTACTC	120
TGATGATGAA	GAGGAGGAAG	AGGATGACAA	ATCCAGTGAA	AAGTCAGACC	GCTCATCACG	180
AACATCATCG	TCTGATGAAG	AAGAGGAGAA	AGAAGAGATC	CCTCCCAAAT	CCCAACCAGT	240
			ATCTCTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:1383:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

GAATTCTAGA						60
					TCTTCTTTGT	120
					GGTCTTTGGG	180
			ACATACTGCT	ATCCCTTTCC	ATTTCTTTTT	240
GTTCCATCAC	TCTCCTCTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:1384:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

GAATTCGGCC	TTCATGGCCT	ACAGATTATC	TTACACTGAA	CTGATCAAGT	ACTTTGAAAA	60
TGACTTCGAA	ATTTATCTTG	GTGTCCTTCA	TACTTGCTGC	ACTGAGTCTT	TCAACCACCT	120
TTTCTCTCCA	ACCAGACCAG	CAAAAGGTTC	TACTAGTTTC	TTTTGATGGA	TTCCGTTGGG	180
ATTACTTATA						240
TGAAGCAAGT	TACTAATGTT	TTTATTACAA	AAACCTACCC	TAACCATTAT	ACTTTGGTAA	300
			TTGCAAATGA			360
			TTTATGATTC			420
		CAGATGGCAG				458

- (2) INFORMATION FOR SEQ ID NO:1385:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

1 1	CEOURNOR	DESCRIPTION:	CEO	Tn	NO. 1205
(X1)	SECUENCE	DESCRIPTION:	SEO	110	NO: 1385

GAATTCGGCC	TTCATGGCCT	AAGTTTTCAT	AATCTTTCTA	AGCAAATAAA	TTGAGCATGC	60
AGGTTTTTTT	TGCTTTCAGT	AAGTATGTTA	AAGATATTTA	TTGTACTTTG	GTTTTCTTTT	120
${\tt CTTTTTTTTT}$	TTTTTTTTT	TTTGAGACTG	AGTCTCTGTC	ACCCAGGGTG	GAGGGCAGTG	180
GCCCAACCTC	AGCTCACTGC	AACCTCCGCC	TCCCATGTTC	CAGTGATTCT	CCTGCCTCAG	240
TCTCCCGAGT	AGCTGGGATT	ACAGGTGTGA	GCCACCACGC	CCAG		284

- (2) INFORMATION FOR SEQ ID NO:1386:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

GAATTCGGCC	TTCATGGCCT	AGTAGTTGTT	CCATGCTGTT	GTTTTTTGTT	TTATCTTTCA	60
TTGCCTTTCC	CTCTGCAGTC	AACATTATGA	CCTGGGGACT	CCAGCATCCT	TCAAGCAAGC	120
CATTTCCGAA	GAAGGTGAAA	AGAAGCCAGG	ATGATTGGCA	CCTCCTCCTC	CTCCTCCTCT	180
TCTTCCTCTT	CCCTTGCCCA	GCCCCCTCCT	GTGCGTGTGT	TTCAGACAAC	ACAGGAGCCA	240
GCACAGGAGT	GGAAAATCCT	GTAGCGCAAC	TCGAG			275

- (2) INFORMATION FOR SEQ ID NO:1387:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

GAATTCGGCT	TCATGGCCTA	ATTGAATTCT	AGACCTGCCT	CGAGCCTCCA	AAAAGAGTAA	60
ATAAATAAAA	ATAAAATTGC	CTTTAAACAG	AAACACACAT	AAAACAAAGT	TATATATTGA	120
ACCTAACCCT	GTATTTCCTC	TGGGAACAGT	GGTTCAGTAT	TCAATAATTC	AGGATTTGCA	180
GCAGCATAGA	ACTTAATGTA	ATGAGAGTCA	AGTATATATT	TCCCAGAACC	CTAAAACTAC	240
TGCATATGTG	AACATATCTT	ATTCATTGAT	TATGTGGGCA	TATAGTGAAA	CTCGAG	296

- (2) INFORMATION FOR SEQ ID NO:1388:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 548 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:

GAATTCGGCC	TTCATGGCCT	ACAACTTGTT	CTAGCTTGTG	ATCCCTCAAA	GTTGGGTCAT	60
ACGTTAGTGC	TAGATACTAG	AAATTTTCAC	TTTTCCACTG	ATCAGAGAGA	CAGACATTAA	120

AAACAAAAAT	AGAAGAAAGG	AAAGCTTTCA	CCCTGCAGCT	TCTTAGCAGG	GAACAATTGT	180
CTTGCCAAAA	CTTTTTTCCC	TTTTCTCTCC	CATTTTCTTT	TACCCAATCC	CTTCTTACTC	240
CTTGCCAGTG	TGACCATGCG	CATTGGTTTA	AAAAGATATT	CTTTCCTAAT	CAGGGCAAGA	300
CAGGCAAGAA	TTTTAAAAAA	GGAAGGGAGG	GAGGGAAGAA	GGGAAGGAAA	ATAAATCCTT	360
TATTTTTTA	AACCTATTTG	AAACCTCTTA	AGAAAATTCC	ACAATAATCA	GGATTTCTGT	420
AAATATTGTC	AATATATATG	AACATATTTG	AAAAACTACA	GTTACAGTAT	ATTTACATTT	480
TTGGAAACTT	TTCTTCAGGG	CCAAGTAACA	TGTTGTATCT	TCCTTTTTGC	TTGTGGGGGC	540
TACTCGAG						548

- (2) INFORMATION FOR SEQ ID NO:1389:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

GAATTCGGCC	TTCATGGCCT	AATATGTTCT	TCACAGGGAT	GAGTCCTAAA	TATTTATCTT	60
CAGCCATGAC	ATTTTTCTTG	AATTCCAGAT	TTGCATATCC	AACTGCCAAC	TTGATATCTC	120
ACTTGGAAGA	ACATCATCAC	AAACCTAACT	CATCTGAAGT	TGGCTTCACA	TTCTCCTCCC	180
CTATCACTAA	CTGCCTTTCC	CACAGTATTC	CCCATTTCGG	TACATGGTAC	CACCATTTAT	240
CCAGTTGTTC	AGACCTAAAC	CCTTCTAATT	ATTCTTTTTC	CTATCGTTAT	CCCACATACC	300
TCGAG						305

- (2) INFORMATION FOR SEQ ID NO:1390:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

GAATTCGGCC	TTCATGGCCT	ACTGGGTTAT	TATTCTATTC	CGTTGATCTA	GCTAGTTTTA	60
AATTTTCTAC	CTTTTCTACC	TGTTTTTGTT	TAATAGTTTA	CTGTTTTTAT	CTGAACAAAA	120
TTCCTCTTTC	AATAGTTGAT	CCTGCTGAAT	GTCTTCCCGT	AGCATTGGGC	TTCCTCAGGT	180
AACCTGGCAT	TTTGGTTTGA	ATAGAAGGGT	TTTTATTGTC	CTTTTTTTCT	TTTTTTTTTT	240
TGAGATATTT	ATCTTTTCTT	TATTTATTTA	TTCGAGTCGG	AGTCTACTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:1391:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

GAATTCGGCC TTCATGGCCT AGGCGATCGT ATTAATTCTC AAGAAATTTC CAACAAATAC

60

PCT/US98/06955 WO 98/45436

CACCTGGTTA ATGTTTTCAT TAAGGGCACA CATTCTTGCT ATTGAGCCAA TGTTGTTGGT GATGGTGATC AAAGTCGCTC TGGCCAGGTC CTCTTTACTG ACAGCCTCTC GCTTCTCCTT GCTCATCATG TTTCCAAAGC TTGAAGCCAC ACTCGAG	120 180 217
(2) INFORMATION FOR SEQ ID NO:1392:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 438 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:	
CGGGAGGCTG AGGCAGGAGA ATCACTTGAA CCCGGGGGGT GGAGATTGCA GTGAGCCGAG ATCAAGACAT TGCATTCCAG CCTGGGCAAG AAGAGGGAAG TTCTGTCTCT AAGAAAAAAA AAAAAAAAA AAAGCTACAC TTTGATCTTT GATTCAGTAG ATATCAGTAA GTATTTGCTG CATTTCATGA GAGCCAACCA TGAGTAAGAC AGAAGTACTT CCTGTCCTCC TGGGCTTTCC TGAGTAGCAG GAGAGATGGA CTAGGAAGAT GAGTGACTGC AGTAGCCTGT GCTGTTCTGC GGTGATGGGA GAGCCCACTG AGAGTCCGGA CAGGCAGGCT GATATTGTGA GAAGGCTTCT GGAAAGAAGA AACATTTAAG CTGAGAGTGA GAGTTGCGTA AGAATTTCCC AGGGAGGGA AAGAGGGAAA CACTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:1393:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 272 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:	
GAATTCGGCC TTCATGGCCT AAAACTTCCT AGGAGAAGGC AAGAGAAAGC CACCAGACCA GAGCCGAGGA CTAAACTTTA AGGTCGAAGA CGGCAGAGGG GCAGGTTCTC CCCTGCACAC CCCAAGGCCT CTCCTGCACC CGCGAGGCCT TCCTTGAGCG CCCAGGCCCC CGAAATGCCT GCCCTCCTTC TGACAAAAGG AGGGGGTAGG ATGTGAAGGG GTAGTGCAAC CAACAATGTT TTTGTAAACA CAACAACAAG GAAATACTCG AG	60 120 180 240 272
(2) INFORMATION FOR SEQ ID NO:1394:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 311 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:	
GTGAAATTGT CAAATAAAAA TATGAAAACT CAGCTGACAA GAGTAAATGT CCTTAAAGAC AAAACAATTG AAGAGCTCAG GCAATCTTTA GCAAATGTTG AAAGGATGAA AGGAAGGCA AATGTTGAAA CGATGAAAGA GAAGGCAGTT GTGAAAACAG AAAACTTGAA AACTACATTA GACTCTGCAG AGCAAAAGGC AAGATCAGAC AAAGAGAAGA CCCAGCAGAT GTTAGATGCT	60 120 180 240

GTCACTTCTG AGCCCCCAAC AGCAAAGAGC GCACCTGAAG AAGTATCAGG ACAAGAACAA

GAAGTACTCG A	311
(2) INFORMATION FOR SEQ ID NO:1395:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 367 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:	
GAATTCGGCC TTCATGGCCT ACTGTGTGCT TAGTTTTAAA GACAACTTTG AAGTAAACAA TGAAATAAAA GATGTCACTA AAACCTCTGA GGCTCCTGAG CACATTTTGC TGATACAGTC TGTGGGGCTT GAGGAGACCG CATGTATTGT TCTTTCTTTT GTTTTTCTTC TGAGTTCTCA ACTGCGGAGA GCACCTGAAC CCCCTTTCCT TTTTGACCGC AGGCTGCACT TTGGGCCCCA GCCAGCCCTT TTTCTTTTTC TTTTTCTTTT GTGGTTCTTC CCTGGAGCGA CTCTGGGGAG TCCTGGATAT CCCGCCTGCC CCTTCCCCTC AGCCCCATGC TTGTTCCAAC AGTCTCCACA GCTCGAG	60 120 180 240 300 360 367
(2) INFORMATION FOR SEQ ID NO:1396:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:	
GAATTCGGCC TTCATGGCCT ACTTGGAAAC GAAAGAGGGC CCAACCTACA ACTAAGAAGG GACAAACCTT GAACTAAGTA AGACCTTACA CACCCAGAAA GAACACTGGG CCCTCCTTCT TCAGGGACAA TGCAGTAGCC ACTTGGCTTG TGGAATTTAC TGAAGGCTAT TTCCTGTAAC TTGCTAGTTA ACTTAGTTTT GTATTTCAGG CAGAGGTGCG CTCTGTAATG TTGGGCCTTT GACTTCACAG TACTGGAGAG CTGTTCACAC AGATGTTTAG ACCTTTCTCT CTCAACAACT CTTATCTCTC GAG	60 120 180 240 300 333
(2) INFORMATION FOR SEQ ID NO:1397:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 356 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:	
GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCGAGAT ACAGCAGCTG CTGCAGAACG TCAAGTCTGA GTTGGAGATG GCCCAGGAAG ACCTGTCCAT GACCCAGAAG GATAAATTTA TGCTCCAGGC AAAAGTGTCG GAGCTGAAGA ACAACATGAA GACCCTGCTC CAGCAGAACC AGCAGCTCAA GCTGGACCTA CGCCGCGCG CGGCCAAGAC GAGAAAGGAG CCGAAAGGCG AGGCCAGGCTC TTCCAACCCT GCCACGCCCA TCAAGATCCC GGACTGCCCA GTTCCCGCCT	60 120 180 240 300

CGCTGCTGGA GGAGCTGCTG AGACCACCGC CCGCCGTGAG CAAGAGCCCC CTCGAG 356 (2) INFORMATION FOR SEQ ID NO:1398: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 447 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398: GAATTCGGCC TTCATGGCCT AATTCTATGA GGTATTATTA TCACTATTTT ACAGATGAGT 60 AAACTAAGGC TCACAGAGAT TAACTGGCAG AACTGAAATT CTCCATATCT TTTTGATTCC 120 AGATTTATTC TCTTAATCAT GATATGATTT TGTCTCATAT AATCCAATAC AATAAATAAG 180 GAGGTCAGGC AGTAGGAGGT GAAGTTGGAG AGACTGGGAG ACCTATCAGG AGGGGTCATT TATGCCTGGC TAGGAGTTTG GACTTTATGC TGAGGCTATG GGAGCACTAT TAAAGTGATT 300 CTAGCACTGC AAAGTTATGA TTAGGTTTAT CAGCCAAAGG AAAAAAAAAG ATCTTGGTGG 360 TCACAGTGCA GGTAGATACG ACATAATCGA GAAATGTGAA GAATGCAGAA TCAAGAGTTT 420 GGTGCTGGAC AGAGAGAGGA ACTCGAG 447 (2) INFORMATION FOR SEO ID NO:1399: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 428 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399: GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACTCTTT TAAATTTTCT GCATTTGCCT GAAAAGCACC CCTGTAAGAA TAGATTTCTC ATGGCTCTAA AAATTATTCC CAAGAATACC 120 TTACTTGGTT CAAAAGCAGA CTGTTTCTCT TCATTTCATC TCAAATCAGA CTTCTGGGCA 180 AGATGTTCTT TAGAGTAAGC AAACCTACAA CCTAAAAATC TCTTCAAGAG GCATCTCTGG 240 TCTTGTGACA AGACCTCTTC AAAAACCCAC AGTAAAACTC CCCTCCCTCC AGTTGGCCAC 300

(2) INFORMATION FOR SEQ ID NO:1400:

TGCTCGAG

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs

CAGTCTGCCA CCAAACATGA ACAAATTCTG CTGCTAATCG GTTTCCCTTG TGATCTGGTT

CCTGAGGTCT TCGGATCTGT GCAATGAATT ATTTATTGTT TTATTAAACC GACAGTGGTG

360

420

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

GAATTCGGCC	TTCATGGCCT	ACTAGACCTG	CCTCAGGGTG	TTCTGTGGTT	TCAGGTGGAA	60
GGTGGAGGGC	CTCGGAGACC	AACTGTGAGT	TAGGCGGGGT	TTAGAATCTG	ATGGGAAGAG	120
GGCAGAGACA	ACAGGTTCGA	AAGAGTCAGG	GCTCCTGGGA	CCTGGGAAGT	AAAGAGTAAA	180

TCACTGCATC CTTGCCCCAT TCAGCCCGGC CTCGAG

CCTGGGGCAG TGGGTCAGGC CAGTAGTTAC ACTCTTAGGT CACTGTAGTC TGTGTAACCT

240

(2) INFORMATION FOR SEQ ID NO:1401:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 316 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:	
GAATTCGGCC TTCATGGCCT AGCCACCGTG CCTGACCTAC TTATTCTTTT TCCTGTTCAG CATCTAGTGT ATGATACGAT TTGCTTATTT GTTTATGTTT CATCATCTGT TCCCCACCCT CAGCCCTGGC CCCCTTGCTG GAACGCAAGC TCCAGGCAAA GCTATTTCAC CGTTGCTGTT TTCCAAGGGC CTCGAACAGT GCCCGGCACA TAGCAAATCC TCAGTGAACA TTAGAGGAAT AAGTGATTCA AGAATAGAGC TGTTAGAAGG TGTTCTGGAG GAAGACGCAT CCGGCTTCAT CCCTGGCACC ATCGAG	60 120 180 240 300 316
(2) INFORMATION FOR SEQ ID NO:1402:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 342 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:	
GAATTCGGCC TTCATGGCCT AAATTCTCCA GCAAAATGAG GATGAAAACC AGGAAAGAAG AAGAAATGAG ATCCATAAAA CAGTGGACCT TACTTAGGAT GTCTCATTCT AGAGTGACAG CCAAAAGGGT ATCTCACCCT AGAGTGACAG CTATCCAGCA GACTAATTTC AGATGAGAGC ATACTGTCTC GGGCTTCTG GGAAGAATGT GCATTCAGTG CCATAGATAG TATCACTGAA GAGCTGGGAT GCTTGAGAAG ATTATTTAGT CAAGAAAAAA GAAAGACAAA TCAACAATAT GTCAAAAAAAT TCAGGTCCAA TTATAGAGCA AAAGGGCTCG AG	60 120 180 240 300 342
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:	
GAATTCGGCC TTCATGGCCT AAGGCTAAAA AGAAGGAAA AGAAAAGGAA AAAAAGGAGG AGGAGAAAAT GGAAGTGGAT GAGGCAGAGA AAAAGGAGGA AAAAAGAAG AAAAAAAA	60 120 180 240 300 333

- (2) INFORMATION FOR SEQ ID NO:1404:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

GGGCCCTGGG	CCCCAGCCCC	CAGCCCATCC	GTGGCCCAGG	CACTGGGGGG	CTGAGGTCCT	60
CTGAGAAGGG	ACACAGGGCC	GGGGGGCTCT	CTCAGCCCAT	CAGCAGGAGA	GGACTGACTC	120
CAGAAAAATC	AGCGTTTGTA	CCCACTCAGG	CTGCCAAGAC	CTGTGTCCGT	CCTTCCAAGC	180
TCAACCTTCA	GAGTTCATGA	GGCCCCTTGC	CCAGAATGTC	CACAGAGTTC	ATGAGGCCCC	240
TTGCCCGGAA	TGTCCACATT	TGAAACCTCC	CAACACCGAG	CCCCATTTCA	AGTATAACCA	300
GGAGGGAAAA	TGGTGCTTGA	AATAAGCATG	CCACAAAGGA	AAACCTGCTT	TCTCGAAATG	360
GGCCCTGGCC	GCCCAGGCCC	TGACCTCCCC	GGCCAGGATG	GAACGTTCCA	GAAACCCTCG	420
AG						422

- (2) INFORMATION FOR SEQ ID NO:1405:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

GAATTCGGCC	TTCATGGCCT	ACTGGGGTCC	AAACTGGATA	TCTTGGTGGA	GAACATGGGG	60
AGGCTCAGCT	TTGGGTCTAA	CAGCAGTGAC	TTCAAGGGCC	TGTTGAAGCC	ACCAATTCTG	120
GGGCAAACAA	TCCTTACCCA	GTGGATGATG	TTCCCTCTGA	AAATTGATAA	CCTTGTGAAG	180
TGGTGGTTTC	CCCTCCAGTT	GCCAAAATGG	CCATATCCTC	AAGCTCCTTC	TGGCCCCACA	240
TTCTACTCCA	AAACATTTCC	AATTTTAGGC	TCAGTTGGGG	ACACATTTCT	ATATCTACCT	300
GATGGACACT	CGAG					314

- (2) INFORMATION FOR SEQ ID NO:1406:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

GAATTCGGCC	TTCATGGCCT	AATTGAATTC	TAGACCTGCC	TCGACTGCCC	CAAACCTGAC	60
CCATCCTCAG	ACCCCCACCC	CCGTCACCGC	TCCTCCCAAT	GATTCCTCCC	TCTGTCAGTC	120
CTGCTCTACT	TTCCAAATCC	TCGCCTGCTC	CAAACCTGAC	CCATCCTCAG	ACCCCCACCC	180
CCGTCACCGC	TCCTCCCAAT	GATTCTTCCT	TCTTTGATCC	TGCCAACTTT	TCCCCAACAG	240
CACCGTAATC	CTCCCCCAAA	TCATCACAAT	CCTCCACCAT	ACAATCCCGC	GTTCTCGAG	299

(2) INFORMATION FOR SEQ ID NO:1407:

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 199 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:	
GAATTCTAGA CCTGCCTCTC GCTGGAAATC AGCGTTGTAA GATGGACGCC CTGCTCAGCA GAGCTCATCT TTCTAGAAAG GCACCTGGCC TTGGAAGGCG AGTGAGGAAC TGTCATAAGG ACTTTTTCTT CCCATGTTGC TTTTCAGGAA AGCTTTCAGG ATGTGGAAAT GATGGTTCAG CTATTGGATG AGGCTCGAG	60 120 180 199
(2) INFORMATION FOR SEQ ID NO:1408:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 220 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:	
GAATTCGGCC TTCATGGCCT AGTGATCCAG AAGAATTACC ATTAACTTTA TTTCAGAATT TAGACTTCCA AATCAGGTTA ATCCTCCAAT TAAAAGAAAG ATTCAGAGTG AATTTTTAA AAGGCAAGGC AGTTATATGT TGCTTACAAG AAACTAAACA TAAAGGCACA GATAAGTTGG AAGTAAGAGG GAAAAAGACA TGCGAATACT AAGTATAGAG	60 120 180 220
(2) INFORMATION FOR SEQ ID NO:1409:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 235 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:	
GAATTCGGCC TTCATGGCCT AGATAAGCCC TTCAGAAACA CATGCACTGT TAATTCTGTT TTAAATATAA TAAAAACCAT TTCACTTTGA CATTACCTAT TAAGTTTTAC TGAAAGTCAA AAGGCCTACT TACTGTGACT TCCAAAAAAAG TATTTTGATA ATATTTTGAA AGAAATAAAT	60 120 180 235
(2) INFORMATION FOR SEQ ID NO:1410:	
(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 577 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

GAATTCGGCC	TTCATGGCCT	ACCCACGTAA	CGGCTTGGCT	GGGCACCCCC	GCTTGGCTTG	60
GTGGTCCTGG	TTTGGATTGG	CTTTACCCTG	GCATTCCTTT	GCTGGGCTTG	ACCTTTTCTT	120
GCTGGGCTTG	GCATTCCCCT	GGCTGGGCTG	GGTGTTTCCC	CGGTGGGGCG	TGCACTTTCC	180
CTGGGTGGTG	GAGGGGGCGT	GGGCTCTCCC	CGGGTGGTGG	GGGGACGTGG	GATCTCCCCA	240
GTTGGTGGTG	GGGGAGGGGT	CGTGGGCTCT	CCCAGGGTGG	GGTTTTGGCT	GGGATTGACC	300
TTTCTCCCCT	AACAGATTGG	AAACTCGTAA	TTTCCCGCTT	TTTGGTGAAA	CTCGTTGACA	360
GACACCATCT	GCTCGCTACT	ACCAGGCTGT	TGAAAGCAGA	TGGTGGCTGA	GGTTTCTCCA	420
AAGCTGGCTG	CCTCCCCTAT	GAAGAAGCCC	TTTGGCTTCA	GGGGCAAGAT	GGGCAAGTGG	480
TGCTGCTGCT	GCTTCCCCTG	CTGCAGGGGA	AGCGGCAAGA	ACAACATGGG	TGCTTGGAGA	540
GACCACGACG	ACAGCGCCTT	CACGGAGCCC	ACTCGAG			577

(2) INFORMATION FOR SEQ ID NO:1411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

GAATTCGGCC	TTCATGGCCT	AGGGATGCCT	CTCAGTGACC	CTTATATGTC	AGGTATGAGG	60
CGGATGGGGC	ATCTCTCTAG	TCCTTTCTAG	GGTTTTTACT	CTTCTAGTCC	CTTCAAGGGC	120
TGAGTGCTCT	GACTTTATGT	CTTCCCACGT	AGGCGTTGAC	CCTGCACTAT	CAGATCCTGT	180
GTTGGCCCGG	CGCCTTCGGG	AAAACCGGAG	TTTGGCCATG	AGTCGGCTGG	ATGAGGTCAT	240
CTCCAAATAT	GCAATGTTGC	AAGACAACCC	TCGAG			275

- (2) INFORMATION FOR SEQ ID NO:1412:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 532 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

GAATTCGGCC	TTCATGGCCT	AGTTTTATTT	TGCACTTGGA	AATATGTCAG	AAATCACTTG	60
AAGGCAAATA	AGATCTGGCC	CTCTGCAGAG	TTAAGTGGCT	AACATGCCCT	AGATCTCCAG	120
GCTTAGAGGC	TGCCCCTTTG	GTACCCATGA	TTCTCCAGGC	CTTTCCAGGG	CAACATTGTC	180
CAGCATCTCT	CTCTCTCCTC	CCGCCGTCTT	CCTTTGGAAG	TTTGACTCTC	ATGTGTGGTG	240
CCCGATCCCT	AGGCCACCTG	TGCCGGCCAG	CCCCTGAACA	GATAAATCCT	ACTAAAGGTT	300
AATCCCAAGC	ACAAGCTTTG	GGCTGGTCCT	TCTGGGTTGA	TTGGCTTTCT	CTCTCTCTCT	360
CCTTTTTTGA	GATGGAGTCT	CCTTCTGTCG	CCCAGGCTGG	AGTGCAGTGG	CACAATCTCG	420
ACAATCTTGG	CTCACTGCAA	CCTCTGCCTC	CCGGGTTCAA	GCAATTCTCC	TGCCTCAGCC	480
TCCTGAGTAG	CTGGGATTAC	AGGTGCCCGC	CACTGCTTCT	GGCATACTCG	AG	532

- (2) INFORMATION FOR SEQ ID NO:1413:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

GAATTCGGCC	TTCATGGCCT	AGGCATCCAG	GACAAAAGTT	TGGAAAACAA	AATAATGGAA	60
CTAAATAGTA	CTAACCAAAG	TATAGGGTGC	TTTATGATTT	ACAGAACTCT	CTTACAGGCA	120
GTATGTTGTT	CAGGCGCCAC	TAGAACCCAC	GTAATGGCAG	AGGCTTCCTG	TTCCATGTTT	180
AAAAACCTTT	CCAAGGCTTT	TCATTATTTT	CTTATCTGTG	GTACCCCTAG	CTTCCTGTGC	240
TCTAGACACA	CTGGCCTACC	TTCAACTTCC	TTGACCAGTG	TAGCTTACAG	TGTAAGCTTA	300
CCCCCCGCCC	CCACCCTCGA	G				321

- (2) INFORMATION FOR SEQ ID NO:1414:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

GAATTCGGCC	TTCATGGCCT	ACATGAACGG	AAGAGTGGAT	TATTTGGTCA	CTGAGGAAGA	60
GATCAATCTT	ACCAGAGGGC	CCTCAGGGCT	GGGCTTCAAC	ATCGTCGGTG	GGACAGATCA	120
GCAGTATGTC	TCCAACGACA	GTGGCATCTA	CGTCAGCCGC	ATCAAAGAAA	ATGGGGCTGC	180
GGCCCTGGAT	GGGCGGCTCC	AGGAGGGTGA	TAAGATCCTT	TCGGTAAATG	GCCAAGACCT	240
AAAGAACCTG	CTGCACCAGG	ATGCTGTAGA	CCTCTTTCGT	AATGCAGGCT	ATGCTGTGTC	300
TCTGAGAGTG	CAGCACAGGT	TACAGGTGCA	GAATGGACCT	ATAGGACATC	GAGGTGAAGG	360
GGACCCAAGT	GGTATTCCCA	TATTTATGGT	GCTGGTGCCA	GTGTTTGCCC	TCACCATGGT	420
AGCAGCCTGG	GCTTTCATGA	GACACCGGCA	ACTCGAG			457

- (2) INFORMATION FOR SEQ ID NO:1415:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

GAATTCGGCC	TTCATGGCCT	AAAAATATCT	AGTCACTGTT	CTGTTTTACC	CATTCTTTTA	60
AACTTTGTTT	TTCAGTTTCA	GTCAGGCTTC	CAAGAAAACT	GATAACATTT	TGATTGGTTG	120
GTTTCTCTTA	TATCTTTTTC	ATTTCACAGT	ACATTGTGAT	TTAATGATTT	ATCTCTTAAA	180
TCTTTTTCAG	TTCATAGGTT	CCTCCTGTCT	CTTTCTTTTT	CCTTGCACTT	CATTTGTTGC	240
AGAACCTTTG	TCCTGTGGTT	TCGCACAGTC	TGGAGGAATT	GGGGAAAGTG	GCTGTCTAAA	300
CTGGTTCCCT	CCTTCCCATT	ACTGCTGCAA	TCAAGATGTT	AGGGGGCCTA	CAAGCAATAG	360
AAGCATCCTC	GAG					373

- (2) INFORMATION FOR SEQ ID NO:1416:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:

GAATTGGCCT	TCATGGCCTA	GTCATTTGCT	TTTATATCAG	ATATCTAATT	AATCAAACTT	60
TCTGGTTAAG	TGCCTCCAAT	TATTAACAAT	CCTGCTCAGA	GTTAAGATTA	GCATCCAAGG	120
ATTTTCCTCC	ATATTTCTTT	TCAGAGGCAA	TGGAATTTAC	TAGTTTTTTA	GCTCTTCAAC	180
TTTGGCTGAT	GGTTTTAGTG	GTGGTTATGC	TATCTTCAGT	AGTTTGGGGA	TCGCTCGAG	239

- (2) INFORMATION FOR SEQ ID NO:1417:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

GAATTCGGCC	TTCATGGCCT	AAGAAAGGTT	AAGTTACTTG	CCTGAGGTAA	CTTAGCATTG	60
ATAGAATTAG	GATTTGAACC	TGGGTAGTAT	GACTCTTAGG	TCCCCATGAG	CTGGCACACA	120
GGTTGCCAAT	CCATCAGTTA	ACCTTCCCAT	CACTGGGTCA	GAGAGCCAAG	GAGCAGAAGG	180
GGGATAGAAC	TTCCCCAGTA	CCAAACTAAG	GGGCTGAGCT	GGGATCGCAA	CCACAGGTTC	240
TGTTCCAAAG	CTGGGGCTCT	TTCGACAAGG	CCATGCCCGC	CTTGTCTCTT	ATGCATGCTC	300
CACTCGAG						308

- (2) INFORMATION FOR SEQ ID NO:1418:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

GAATTCGGCC TTCATGGCC	T AAACAAACAA	AAAAAAATGT	TTTATATGCA	AAAGTTTTTT	60
GTATCATGCT TGTATAAAT	C CAGCTTTTTT	TGTATCATGC	TTGTATTTTT	TTTTTCTAGC	120
TGTTATTGCT TTTCTGATA	A TAGTACTGAA	TTTGGTGTTA	TGGCTGGTCT	CGAG	174

- (2) INFORMATION FOR SEQ ID NO:1419:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

PCT/US98/06955

WO 98/45436

GAATTCGGCC	TTCATGGCCT	TATATTTAAA	TATTGTTAAA	CACTGGGCTG	GAATTATTGT	60
TTTGGGAAAA	GGCCCATGAG	AGTTTTTGCT	CTGTGGGTTT	TTAAAGGTAA	GAATAAATTT	120
CGTGTTTGAG	ATGTTTTTGA	TGTGCCTGTA	ACCAGAATAG	AAGTGTCTTA	GATTATAACT	180
TTCTCTCAGA	TTGAGTAATT	CTGTTGTAAT	AAGTCAGCAT	ATGTTGCCAT	CGAG	234

- (2) INFORMATION FOR SEQ ID NO:1420:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

GAAAATATTT	TTACTTTTAT	AATTGATAGT	ATTTCTTAAC	TCTCAATTAA	AAAAAGTTTT	60
TAAGCATTTC	TGTGATATAG	ATACTATCAT	TTCATATTAC	ACAATGCTTC	TGATGATTTT	120
GCTGTTGTTG	TTAGGGACTA	CTCGAGGCAG	GTCTAGA			157

- (2) INFORMATION FOR SEQ ID NO:1421:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

GAATTCGGCC	TTCATGGCCT	ACCAGGATGA	GAGGGGAAAA	AGAAAGCCTC	CAGTGACTTC	60
AGTTGCTTTG	CCAGTTGTCT	TGGGATTGTT	TTACACCATC	CTTTACTTCC	CTTGCTCAGA	120
CCTCTCTGTT	TCACCATTGC	TCAGGCATTC	AGGAAAGTAT	CTGCTCACTC	CCACTTGGTG	180
AGTCCTCGGC	CTTGAGGTTG	CTGACTCTCA	GGCGTTAGGC	AGCTGGATGA	CTTCCCGCTT	240
CATGCAGCAA	AGGCCAGGGG	CTTGCGCGCC	TCTGCAGAGT	TGTTGCTAGG	GAGACTTGTG	300
TCATCATCCA	CAACCTTGTT	TCTCACTTCC	TGGTTGGGCT	CATCTCTGAA	GAACAGGTCT	360
CCCAGCTTCG	CTCCTTATCA	CTGCATTGTG	AAGAGGAGGA	AAAGTGAATC	ACGGAGAGAG	420
AAAGGAAAGG	ATAGAATCAC	AGGCTGCATC	TGCACCTGAA	AAGTGACCCG	CGGAAACTCT	480
ATGGCGGATC	TCGAG					495

- (2) INFORMATION FOR SEQ ID NO:1422:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 449 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

GAATTCGGCC	TTCATGGCCT	AGACAAAAGT	AGAATTAGTA	AACTACTACA	TTGAGTACAC	60
TTTGTGTTAA	AATTCATAGG	GAAGACTTCT	TAAAAACAAG	TGAAATTGTT	AAACCCCCCC	120
CTAAGCATTA	CAGATGGCTT	ATAGCTGTCC	ACGGGGTTGG	TAGAGGTGGG	AAAGGGAAGG	180
GTTCTAGGCC	AGAATGTTCC	TATTTAGAAG	ACACTCAAAT	TACAGTCTGT	GTTATGTATG	240

TATACCATTT	ATTCAATGCT	ACTGTGTATA	TAATGGAAAA	CTTAAGTCCA	GTTTGAAACA	300
TCTAGTCTTT	CTAGGTGTTT	AAAAGTGTAC	AACAGCCTGT	CGCAGTGGCG	CATGCCTGTG	360
GTCCCAGCAC	TTTGGGAGGC	CGAGGCAGGC	GGATCACGAG	GTCGGGAGAT	CGGGACCATC	420
TTGGCCAGCA	TGGTGAAACC	CCTCTCGAG				449

- (2) INFORMATION FOR SEQ ID NO:1423:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

GGGAGTTTAT	TATTCATTAA	CGAAATTAGC	CCTTTTATCT	GCCATATAAT	TTGCAACAAT	60
				AAAGTTATGG		120
ATGTGGGATT	TTATGTAGCA	CAGTTGTCTC	TTTTTTTTT	TTTTGAGACG	GAGCCTAGCT	180
CTGTCACCCA	GGCTGGAGNG	CAGTGGCATG	ATCTCGGCTC	ACNGCAACCT	GTGCCTCCCA	240
GGTTCAAGCA	ATTCTTCAGT	CTCAGCCTCC	CAAGTAGCTG	GGACTACAGG	CGCCCACCCC	300
CTCGAG						306

- (2) INFORMATION FOR SEQ ID NO:1424:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

GAATTCGGCC	TTCATGGCCT	AGAACTTTGT	ACACCATGGA	ATGTTCTACT	TATTATTTTG	60
TGCTACAATA	TGTGCTGTTT	CTTTTGTTTG	AATTGCAGAT	TGTCTACTAT	GAAGCAGGGA	120
TTATTCTATG	CTGTGTCCTG	GGGCTGCTGT	TTATTATTCT	GATGCCTCTG	GTGGGGTATT	180
TCTTTTGTAT	GTGTCGTTGC	TGTAACAAAT	GTGGTGGAGA	AATGCACCAG	CGACAGAAGG	240
AAAATGGGCC	CTTCCTGAGG	AAATGCTTTG	CAATCTCCCT	GTTGGTGATT	TGTATAATAA	300
TAAGCATTGG	CATCTTCTAT	GGTTTTGTGG	CAAATCACCA	GGTAAGAACC	CGGATCCTCG	360
AG						362

- (2) INFORMATION FOR SEQ ID NO:1425:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 194 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:

GAATTCGGCC TTCATGGCCT	AGTATATCTG	AAAAGTACAC	TGTGTTTTGA	TAAATTATAA	60
TTTCATTCTG AATGAGGTTT	CTTTTTTTGA	TTTTCTTTAA	AAAAAAAAA	CAACCTGCTT	120
TGATTTGCTT TACATTCCTT	GCCCTCCATT	TTTCTTATTA	TATTGTAAAC	ATTAGAAAAA	180

194

TGAACACCCT CGAG

(:	2) INFORMATION FOR SEQ ID NO:1426:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 393 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:	
C' A' T' A A	AAATTCGGCC TTCATGGCCT AGCCATGTAT TTTCTAATAT CCCTTGGACT TCATCTTTGA CTCATGTTTT ATTTTGAAGT ATTGGGATTG TTTTTCAGTT ATCTTTCTGT TATTATTTCT ATTTAATTCT GTTATGGTCA TACAACATAA TTTAAATTCT TCTAAATTTG TTGAGGATTG CTTTTGTTGC CCAGAATATG ATGAATCTCT CATTGAATGT TGTATGTGCA GTTGAAAAGA ATGTTTAATC TGCTGTTGGT GGGTAAAGTG TCATGAATAT AATTAGGAGA AATTAATGAT AGTGTTAAGG TTTTCTATAT CCTTGCTTTT TTGGTGTACT TATTTTATTG ATTATTGAGA AGGAAGGGTT GAATTATCTA GGTGCAACTC GAG	60 120 180 240 300 360 393
((2) INFORMATION FOR SEQ ID NO:1427:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 119 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:	
	GCGATTGAAT TCTAGACCTG CCTCGAGCCA CCCCGTTAAT GTGTGTGTTG ACAGTGAAGT	60 119
((2) INFORMATION FOR SEQ ID NO:1428:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 327 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:	
; C ?	GAAAAAGCAG TAAAAATAGA AATCCATCTT CACCAAGCCT TTAAAGCAAT ATAAATTTAT ACTGAGGTTC CTGCATACTA TAACACACAG AAGGAATTCC TAAAAATGTT CTTTATCCAG CTGTCTACCC AAAGTTCTAT CATCCTGGCA AACTGCTCTC TCCAAAATTC ATCATCTTGG ACTCTCTCT AAACTCCAAC CCTTCTCTCT TATACCCTGT TCTCCAACAT TCGAATTTGT TTAGTTTGTC TTCTTCCTAA TATAGCTATT TCTGTTTACC ATTTTGAGCT CTGGAACTCT AACCACTACT TACCACCAAA ACTCGAG	60 120 180 240 300 327
	(2) INFORMATION FOR SEQ ID NO:1429:	
	(i) SEQUENCE CHARACTERISTICS:	

(A)	LENGTH: 325 base pairs
(B)	TYPE: nucleic acid
(C)	STRANDEDNESS: double
(D)	TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

GAATTCGGCC	TTCATGGCCT	AATCACATAT	ACACAATTTA	CCCATTTCAA	GTGTACACGT	60
			AACTATCACC			120
TTCATCAACC	CCAAAAGAAA	CACCATACCC	TTTAGGTATC	GCCTCCCCTA	TACTCCACCT	180
					TCCTTATTCT	240
GAACTTTTGA	ATGGAATTAC	AGTATCTGGT	CTTTTGTGCC	TGTTTTTTT	TGACTAATGT	300
TTCAAGGTTC	ATCCAGGCCC	TCGAG				325

- (2) INFORMATION FOR SEQ ID NO:1430:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 226 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

GAATTCGGCC TTCATGGCCT	ACCTAAACCT	GGCAGAGTAC	ATCATGCCTC	CGAGAAGAAA	60
CGTCATTCCA CTCCTTTGCC					120
CAGTCCCCGC TCAACAGTCC					180
CAGCAGGAAT TTGCCGGACG					226

- (2) INFORMATION FOR SEQ ID NO:1431:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

GAATTCGGTT	CATGGCCTAG	GATTAACAAC	TTGGAAAAGG	CCTATGATAC	TCCTGGTAAA	60
					TTATCCTAGG	120
		TGTCCAGCGT				180
					ACAAAGAAAA	240
TGCCTTGAAA	CTCGAG					256

- (2) INFORMATION FOR SEQ ID NO:1432:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:	
GAATTCGGCC TTCATGGCCT AGGTTGCGGT GAGTCGAGGT CTGCACTCCA GTCTAGGTGA CAGAGCCAGA CCTGGTCTTT AAAAAAAAAA AAAAAAAAAA	60 120 180 240
(2) INFORMATION FOR SEQ ID NO:1433:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 229 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:	
TCATTCTGAA CAAAAGGGAT TAGAGAAGAA AAATCTCTTG ATATAAGGCT TGAAAGCAAG GGCAGGCAAT CTTGGTTGTG AATATTTTCT GATTTTTCCA GAAATCAAGC AGAAGATTGA GCTGCTGATG TCAGTTAACT CTGAGAAGTC GTCCTCTTCA GAAAGGCCGG AGCCTCAACA GAAAGCTCCT TTAGTTCCTC CTCCTCCACC GCCACCACCA CTCCTCGAG (2) INFORMATION FOR SEQ ID NO:1434:	60 120 180 229
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 268 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:	
GAAATTGAAA CTCAAATCAG TTAGCTTCAA ACAAAAACGA AAGTTAGACC AAGGGAACGT ATTAGATATG GAAGTAAAGA AAAAGAAACA TGATAAACAA GAACAGAAAG GAAGTGTGGG AGCTACATTC AAATTAGGTG ACTCTTTGTC AAACCCAAAC GAAAGAGCCA TTGTTAAAGA AAAGATGGTA TCAAATACTA AGTCTGTAGA CACGAAAGCG AGTTCATCTA AATTTAGTAG AATTCTAACT CCTAAGGAGC ATCTCGAG	60 120 180 240 268
(2) INFORMATION FOR SEQ ID NO:1435:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 247 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:	

60

120

GAATTCGGCC TTCATGGCCT ACAAGACTGT CTCAAAAAGA AAAGAAACAC AAATATTTGA

ACTCCAAATA TTCTTTGTGT GTAGAAAAAT CTAATGGATA ATTAAAACTA GAGCAGAGAG

AAAAGCCTAG GA	AGTTGAGAG	ATTTTTAGAT	ACGTGACTGA	AAAGATTGGA	AAAGGCTATC	180
AGTTTTAATG CT	TGTGTCTG	TCTTTGTGTG	GGCCATGGTA	TTTTGGAAGA	GCACCATGGA	240
GCTCGAG						247

- (2) INFORMATION FOR SEQ ID NO:1436:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

GAATTCGGCC TTCATGGCCT ACCTATTTGT GCATCAAGTG GTTATCTAAA TAGTTTGAAA	60
GGATTGATAT ACTACATTAT ACGTCAAAAA TAAATAAATA AAATTAAGAA GACAGGGATT	120
CCAAGATTGT AGCTGACCAA GCTGTCTTGT TTTGCGTACA TCAACACTAT GCTGCTTCCA	180
ATATTCCTAG CCATTCCACA GGTAATGATT TTTCAACAAT CAAGAGAAAG TCATTCTTGT	240
ACTGTAACAT CTCTCGAG	258

- (2) INFORMATION FOR SEQ ID NO:1437:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 415 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

GAATTCGGCC TTC	CATGGCCT AAATCACT	TG GATTGGTTCT	CTACTTAAAA	CACAAGCTAG	60
CTACCCAGTC TTO	GTATTTTG TATTTTA	AG AATTGTTAAA	AAACTAATTT	TGTTTTGTAT	120
TTGTGTAAAG CA	TAGTCATA ATTCTAAA	TC AAACACACTG	CATCGAGTTT	ATCACTGAAA	180
TTCAGCATCT GCT	TTTTGTCC TCACTTTG	TT ATCTTCTGCT	CTCATCGATT	ACAGGCGTGA	240
GCCACCGCGC CCC	GGCGGTAT GTTCCTTA	CC CTTAAGGACA	AGAAATACCG	TTTGAAAACA	300
	ATTAACAA ACTTAGAA				360
	TTTTGGAA ATATGTTG				415

- (2) INFORMATION FOR SEQ ID NO:1438:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

GCGATTGAAT TCTAGACCTG	CCTCGAAGTG	CCAGCAGCAG	AGGAGATGAC	AGTGACATAT	60
ACAACAGAGG CTGGGGTGGG	CACTCCAGGA	GCCCTGGAGC	GGAAGACCTC	AGGGCTAGGA	120
CAGGAGCAAG AGGAAGGGTC	AGAGGGCCAG	GAGGCAGCCA	CTGGGAGTGG	CGATGGGAGG	180
CAGGAGACAG GAGCAGCTGA	AAAATTCCGA	TTAGGATTAT	CACGGGAGGG	AGAGAGGGAA	240
TTGAGTCCGG AGAGTCTACA					267

- (2) INFORMATION FOR SEQ ID NO:1439:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

GCGATTGAAT	TCTAGACCTG	CCTCGAGTCA	TATCCCTGAG	CAGTAGAGTA	AATTAAATCC	60
TTTCTGAGAG	TCTTAGATGT	TTTTCTATGT	CTCTTCTTTC	TTATTCTCTC	TCTGTTTCTT	120
TCTCTCACTC	ACACACACAC	ACACACACAC	ACACACACCC	CTAAAATTTG	TTCTGAATGG	180
CCCACTAGGG	CTGAATCATT	TAGTGACTTC	ATTGATTACT	ATCCTGAGTT	CTTCTTCCTG	240
CTTCCAGACT	AGTGAAAATA	TTCCAGAAAG	CTTTAATATT	GGAGAAAAGG	CAACGCTCGA	300
G						301

- (2) INFORMATION FOR SEQ ID NO:1440:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

GAATTCGGCT TCATGGCCTA GCATTTGGAA GTAATTTTTT AAAACAACAT TCATATTAAT	60
TTAAGGAGCA TAACAGATTC CAGTGAATGT TATGATTCGC TATTGTAACA TTATTCTAGT	120
AAATATGTTG GAGAAGAACA GTTCTAGTGA ATTAACTATG GTTTTGGAAG GCAGCTATGC	180
TCACCATCAT ACCACCAACA CAACCATGGT TTTATTTTAT	240
GACAGAGTCT C	251

- (2) INFORMATION FOR SEQ ID NO:1441:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:

GGAATTGGAA	AGCGTTTCCT	TGCCAACACC	AGAAATCCAG	TCAGATTTCT	TACATAGCAA	60
AGTCGAAGCT	CCTCCTTCAG	AGGTGGCGGA	TACGTTAGTA	ATAATGACTG	CTTCCAAGGG	120
	CCAGAACCCA	-				180
-	AAGACACCAG					240
				AAAAGCAGAA	TGGCAGAACC	
AATGAAAGGC	TACATGAGAC	CCACCAAGCT	CGAG			274

- (2) INFORMATION FOR SEQ ID NO:1442:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

GAATTCGGCC TTC	ATGGCCT ACCTTTCTCC	ATGTTTAACT	GGGCTGCTCC	CCATTCTCTG	60
	rcagccg ccagagccca				120
	TGAGGGT CCTTTCCTCA				180
	TAAGGCC TCATTCACCT				240
	CCACTGT CCCCTTAACT				274

- (2) INFORMATION FOR SEQ ID NO:1443:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

CTCCATCTCA AAAAAAAAAA AAAAAAAAAN NANTCNGAAA CAGAAAAAAA AAAAAGAATA 120 CACTGCATTG CCATTATCTA GTCACCCTGT GTAATATAGC AGCAGAACTC ATGCTTCCTG 180 TCTTAACTGT AACTTTGTAT CTGCTGACCA ACCTCTCTCC ATCCCCTCCT CCCACCTACC 240	GAATTCGGCC	TTCATGGCCT	AATTGCGCCA	TTGCACTCTA	GCCTGGGCGA	CGGAGCAAAA	60
CACTGCATTG CCATTATCTA GTCACCCTGT GTAATATAGC AGCAGAACTC ATGCTTCCTG 180 TCTTAACTGT AACTTTGTAT CTGCTGACCA ACCTCTCTCC ATCCCCTCCT CCCACCTACC 240							120
TCTTAACTGT AACTTTGTAT CTGCTGACCA ACCTCTCTCC ATCCCCTCCT CCCACCTACC 240							180
257							240
CTCCCCAGTC CCTCGAG	CTCCCCAGTC						257

- (2) INFORMATION FOR SEQ ID NO:1444:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

GAATTCGGCC	TTCATGGCCT	AGGAAGCATT	AAATTGGGCC	ATAGGAAGGA	CAAGTCACAT	60
		GGTTTGGGAA				120
		ACCTAGACCA				180
		GGTTGTAGCA				240
TATGCAAACC						258
11110000						

- (2) INFORMATION FOR SEQ ID NO:1445:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 638 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

GGATGGCTAC	GGCAGGGGGT	GGCTCTGGGG	CTGACCCGGG	AAGTCGGGGT	CTCCTTCGCC	60
TTCTGTCTTT	CTGCGTCCTA	CTAGCAGGTT	TGTGCAGGGG	AAACTCAGTG	GAGAGGAAGA	120
TATATATCCC	CTTAAATAAA	ACAGCTCCCT	GTGTTCGCCT	GCTCAACGCC	ACTCATCAGA	180
TTGGCTGCCA	GTCTTCAATT	AGTGGAGACA	CAGGGGTTAT	CCACGTAGTA	GAGAAAGAGG	240
AGGACCTACA	GTGGGTATTG	ACTGATGGCC	CCAACCCCCC	TTACATGGTT	CTGCTGGAGA	300
GCAAGCATTT	TACCAGGGAT	TTAATGGAGA	AGCTGAAAGG	GAGAACCAGC	CGAATTGCTG	360
GTCTTGCAGT	GTCCTTGACC	AAGCCCAGTC	CTGCCTCAGG	CTTCTCTCCT	AGTGTACAGT	420
GCCCAAATGA	TGGGTTTGGT	GTTTACTCCA	ATTCCNATGG	GCCAGAGTTT	GCTCACTGCA	480
GAGAAATACA	GTGGAATTCG	CTGGGCAATG	GTTTGGCTTA	TGAAGACTTT	AGTTTCCCCA	540
TCTTTCTTCT	TGAAGATGAA	AATGAAACCA	AAGTCATCAA	GCAGTGCTAT	CAAGATCACA	600
ACCTGAGTCA	GAATNGGTCA	GCACCAACCC	GACTCGAG			638

- (2) INFORMATION FOR SEQ ID NO:1446:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

GCGAGCTCGT	GTTTTAAAGG	ACCAAATAGA	AGTTTACCAG	GAGAGAAGTG	ACAGAAGTGC	60
TGTCTAGATA	GAGGAAGGC	ACACACAGAT	GCAAGCATGT	GCAGAAATGA	GCAAACCACT	120
GAGACGCTGC	CTTGAGCTCT	GTGTCACACT	GCTATGTTGC	AGCCTGGGAG	GCTGTTCCCA	180
GTTGAGCCCT	TCGGAACCAG	CCATGAGATG	GCACGGGTAC	GCGGAAGGGA	GCAGTCTCCA	240
TGGCTGGGTG	GTGATGGGGG	CTTCTCGAG				269

- (2) INFORMATION FOR SEQ ID NO:1447:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

GGTCTCTCGC	CGCCGGAGGA	AGATGAGGCT	GAAGATTGGA	TTCATCTTAC	GCAGTTTGCT	60
GGTGGTGGGA	AGCTTCCTGG	GGCTAGTGGT	CCTCTGGTCT	TCCCTGACCC	CGCGGCCGGA	120
CGACCCAAGC	CCGCTGAGCA	GGATGAGGGA	AGACAGAGAT	GTCAATGACC	CCATGCCCAA	180
CCGAGGCGGC	AATGGACTAG	CTCCTGGGGA	GGACAGATTC	AAACCTGTGG	TACCATGGCC	240
TCATGTTGAA	GGAGTAGAAG	TGGACTTAGA	GTCTATTAGA	AGAATAAACA	AGGCCAAAAA	300
TGAACAAGAG	CACCATGCTG	GAGGAGATTC	CCAGAAAGAT	ATCATACTTC	TCGAG	355

- (2) INFORMATION FOR SEQ ID NO:1448:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

GAATTCGGCC TTCATGGCCT	ATCCTCTGCC	AAGACCAAAA	GGAAAGAAGA	AAAAGGGCCA	60
AAAGCCAAAA TGAAACTGAT					120
GTTCAAGCCA TGCCTGCAAA					180
TGTCACAACC TTCCGGAAGG	AGTAGCTGAC	CTGACACAGA	TTGATGTCAA	TGTCCAGGAT	240
CATTTCTGGG ATGGGAAGGG	ATGTGAGATG	ATCTGTTACT	GCAACTTCAG	CGAATTGCTC	300
TGCTGCCCAA AAGACGTTTT	CTTTGGACCA	AAGATCTCTT	TCGTGATTCC	TTGCAACAAT	360
CTCGAG					366

- (2) INFORMATION FOR SEQ ID NO:1449:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

GATTTCTTAC	CCAAAGCTCT	GGAATTGTAC	ATTTATTTTT	TAAAACTCAA	AGAGGGAAAG	60
AGCCTTGTAT	CATATGTGAA	CATTGTATCA	TAGGTAATGT	TGTACAGACC	CTTTTATACA	120
GTGATCTGTC	TTGTTCCTGC	AGCAAAAATC	CTCTATGGAC	ATAGGAGGTG	CTGTGTCCCA	180
TGCCCTCTTG	CCCTGACAGT	GTCCCATGGG	CCCCCTTCTG	CTCCCTGCCC	CCTCCCTGCT	240
ACTGCTGATG	CACTCCCCCC	CCTCGAG				267

- (2) INFORMATION FOR SEQ ID NO:1450:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:

GCGATTGAAT	TCTAGACCTG	CCTCGAGAJC	TGGGGGGAGA	TTGGGCTCCC	TTTCCTCATG	60
ACATCCTGCC	CTATCAGGAC	TCTGGAGATA	GTGGGAGCGA	CTACCTTTTC	CCAGAAGCTA	120
GTGAAGAATC	AGCAGGCATC	CCGGGAAAGT	CAGAACTTCC	CTACGAAGAG	CTGTGGCTGG	180
			CTCGCTCTCT			240
			GTGCGACTTC			300
			CTGCCCTACC			360
			TCCTGAACGC			420
GCGCACTCGA						431

- (2) INFORMATION FOR SEQ ID NO:1451:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

GCCTGCCCCC	ACCTTACAGG	TCTGGGATGT	ACCTTTCCAT	CTGTTGCTGC	TTTCTTCTAT	60
GGGCCCCTGC	CCTCACTCTC	AAGAACCTCA	ACTACTCCGT	GCCGGAGGAG	CAAGGGGCCG	120
GCACGGTGAT	CGGGAACATC	GGCAGGGATG	CTCGACTGCA	GCCTGGGCTT	CCGCCTGCAG	180
AGCGCGGCGG	CGGAGGGCGC	AGCAAGTCGG	GTAGCTACCG	GGTGCTGGAG	AACTCCGCAC	240
CGCACCTGCT	GGACGTGGAC	GCAGACAGCG	GGCTCCTCTA	CACCAAGCAG	CGCATCGACC	300
GCGAGTCCCT	GTGCCGCCAC	AATNCCAAGT	GCCAGCTGTC	CCTCGAG		347

- (2) INFORMATION FOR SEQ ID NO:1452:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

GGGGCAGAAG	TTGAATATAC	CGGCAATTTT	GCGAGCACCC	AAGGAGAGAA	AACCAAGTAA	60
AAAAGAAGGA	GGCACACAAA	AGACATCTAC	TCTTCCTGCA	GTACTTTATA	GTTGTGGGAT	120
TTGTAAGAAG	AACCATGATC	AGCATCTTCT	TTTATTGTGT	GATACCTGTA	AACTACATTA	180
CCATCTTGGA	TGTCTGGATC	CTCCTCTTAC	AAGGATGCCA	AGAAAGACCA	AAAACAGTTA	240
TTGGCAGTGC	TCGGAATGTG	ACCAGGCAGG	GAGCAGTGAC	ATGGAAGCAG	ATATGGCCAT	300
GGAAACCCTA	CCAGATGGAA	CCAAAACAAC	TCGAG			335

- (2) INFORMATION FOR SEQ ID NO:1453:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

GCGATTGAAT	TCTAGACCTG	CCTCGAGATC	CCCATGACTC	CTACATCCTC	TTTTGTGTCT	60
CCGCCACCAC	CCACTGCCTC	ACCTCATTCC	AACCGGACCA	CACCGCCTGA	AGCGGCCCAG	120
AATGGCCAGT	CCCCCATGGC	AGCCCTGATC	TTAGTAGCAG	ACAATGCAGG	GGGCAGTCAT	180
GCCTCAAAAG	ATGCCAACCA	GGTTCACTCC	ACTACCAGGA	GGAATAGCAA	CAGTCCGCCC	240
TCTCCGTCCT	CTATGAACCA	AAGAAGGCTG	GGCCCCAGAG	AGGTGGGGGG	CCAGGGAGCA	300
GGCAACACAG	GAGGACTGGA	GCCAGTGCAC	CCTGCCAGCC	TCCCGGACTC	CTCTCTGGCA	360
ACCAGTGCCC	CGCTGTGCTG	CACCCTCTGC	CACGAGCGGC	TGGAGGACAC	CCATTTTGTG	420
CAGTGCCCGT	CCGTCCCTTC	GCACAAGTTC	TGCTTCCCTT	GCTCCAGACA	AAGCATCAAA	480
CAGCAGGGAG	CTAGTGGAGA	GGTCTATTGT	CCCAGTGGGG	AAAAATGCCC	TCTTGTGGGC	540
TCCAATGTCC	CCTGGGCCTT	TATGCAAGGG	GAAATTGCAA	CCATCCTTGC	TGGAGATGTG	600
AAAGTGGAAA	AAGGAGAGCG	ACTCGAG				627

- (2) INFORMATION FOR SEQ ID NO:1454:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 394 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

GAACTTTGAC	ACCTACACTT	AAATTCTGAG	TCATTAAACA	GGCCTACATT	TATCAACTGT	60
GGAAATATCA	GCCAGTTTTT	GCAAACCTCT	TCTTAGGACA	CTÄAGTTGTT	TGCAGAAATC	120
ACTAGCATTG	ACTGACTCAG	CAACAATGTG	GTTATATTCT	TTGATTAACT	TAGTCCTTTT	180
TCTTGGTCAA	GAGTCAGTAG	ACAGGACTGA	AGCTTATGCC	CCTTGCCCCC	CCACCACCAC	240
TCCATTACTA	CCACCTTGGT	TTAGCCATCC	TTTCTTGATC	TGTTCTCCCC	ACTTCTACTG	300
TGCTACTCTA	CAGACTTGCC	CTGAATGTAA	GAGCAACAAT	TACCTTGTAA	AGTCCAAGTT	360
GGGGCAGGTC	ACTCCCAAAC	TCCACAACCT	CGAG			394

- (2) INFORMATION FOR SEQ ID NO:1455:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

CAGATGTTCA	GATATATCTT	GAATTTTCTA	CGAACATCCA	AACTCCTCAT	TCCTGATGAT	60
TTCAAGGACT	ACACTTTGTT	ATATGAAGAG	GCAAAATATT	TTCAGCTTCA	GCCCATGTTG	120
TTGGAGATGG	AAAGATGGAA	GCAGGACAGA	GAAACTGGTC	GATTTTCAAG	GCCCTGTGAG	180
TGCCTCGTCG	TGCGTGTGGC	CCCAGACCTC	GGAGAAAGGA	TCACGCTAAG	CGGTGACAAA	240
TCCTTGATAG	AAGAAGTATT	TCCAGAGATC	GGCGACGTGA	TGTGTAACTC	TGTCAATGCA	300
GGCTGGAATC	ACGACTCGAC	GCACGTCATC	AGGTTTCCAC	TAAATGGCTA	CTGTCACCTC	360
AACTCAGTCC	AGGTCCTCGA	G				381

- (2) INFORMATION FOR SEQ ID NO:1456:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

GGTGACGCCT	GCTTCACATC	TCTAATGAAC	ACCCTCATGA	CGTCGCTACC	AGCACTAGTG	60
CAGCAACAGG	GAAGGCTGCT	TCTGGCTGCT	AATGTGGCCA	CCCTGGGGCT	CCTCATGGCC	120
CGGCTCCTTA	GCACCTCTCC	AGCTCTTCAG	GGAACACCAG	CATCCCGAGG	GTTCTTCGCA	180
GCTGCCATCC	TCTTCCTATC	ACAGTCCCAC	GTGGCGCGG	CCACCCCGGG	CTCAGACCAG	240
GCAGTGCTAG	CCCTGTCCCC	TGAGTATGAG	GGCATCTGGG	CCGACCTGCA	GGAGCTCTGG	300
TTCCTCGAG						309

- (2) INFORMATION FOR SEQ ID NO:1457:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:

GCACTATTAA	ACAGATACAA	CACAGAATAG	TATGTATAGA	GCATGGTATG	TAGCAGGGGC	60
CTATTCCTGT	CTGAGTGGAC	AAGGAGGCTT	CCTAGAGGAA	GCAACATTTA	AAGCTGAGGG	120
CTGAAGGATG	AATAGGATTT	AACCAAGTAA	AAGTAAGAAA	GGAAGTGGGG	AGCTGGAAAG	180
GGCATTCCAG	GAAGAAGAAA	CTGCATGTGC	AAAGGCCAGG	AGGTCAGAGC	GCACAGTGGA	240
TATGACGATG	TGGCTAGCTG	AGCATGTCTG	TGCAGTGTCA	ACTTTGTTGT	GAACACAGAG	300
GGAGGCTACT	${\tt GGGAAATTTT}$	AAGCAAGAGA	GTTGGAGTAT	GATCACATTT	GCATGTTAGA	360
AAGACACACT	CGAG					374

- (2) INFORMATION FOR SEQ ID NO:1458:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:

GAATTCGGCC	TTCATGGCCT	ACATATTTAT	TATGTCAACC	TGTACTTCCC	TTTCCCTCTT	60
CCTCTCCCTC	TTTTCTCTCC	CTCTCCCTCT	CTCTCTCTTC	CTTCCTCCCC	TTCCAGGTAC	120
CCTAGATGAA	CCATGGGAGG	TCCTGGCTAC	ACAGCCATTC	TGTCTGAGAG	AGTCTGAGGA	180
CTCTGAGACC	CAGCCTTTTG	ACACGCACCT	TGAGGCCTAT	GGACCTTGCC	TGTCTCCACC	240
TAGGGCAATA	CCAGGAGACC	AACATCCAGA	GAGCCCAGTT	CACACAGAGC	CAATGGGGAT	300
TCCGGGCAGG	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:1459:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:

GGAACCACCA	ATTCCGGACA	CACTGGGATT	ACAGTTCCAG	GAAGGATGTT	ACCTTTGACG	60
ATGACAGTGT	TAATCCTGCT	GCTGCTCCCC	ACGGGTCAGG	CTGCCCCAAA	GGATGGAGTC	120
ACAAGGCCAG	ACTCTGAAGT	GCAGCATCAG	CTCCTGCCCA	ACCCCTTCCA	GCCAGGCCAG	180
GAGCAGCTCG	GACTTCTGCA	GAGCTACCTA	AAGGGACTAG	GAAGGACAGA	AGTGCAACTG	240
GAGCATCTGA	GCCGGGAGCA	GGTTCTCCTC	TACCTCTTTG	CCCTCCATGA	CTATGACCAG	300
AGTGGACAGC	TGGATGGCCT	GGAGCTGCTG	TCCATGTTGA	CAGCTGCTCT	GGCCCCTGGA	360
GCTGCCAACT	CTCCTACCAC	CAACCCGGTG	ATCTTGATAG	TGGACAAAGT	GCTCGAG	417

- (2) INFORMATION FOR SEQ ID NO:1460:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:

GAA	TTCGGCC	TTCATGGCCT	ACTGAGAAAA	AAAATCAAAT	CTAATTTTAA	AATGAAGGTA	60
TTT	AAAACCA	TGGCACAAGG	GAGCCTTATT	TATGGAGCTG	GTGGGAAGCC	AGGATGTTTC	120
CAA	TCCGCTG	CTCTTACAGG	AGCCTGTGCC	TCGCCAGTTC	TGTGCTGCAG	TGGGCAGCCA	180
ACT	GAAGTGC	ATGAGTCAAA	TGCACGAAGC	AGCAGACTCG	AG		222

- (2) INFORMATION FOR SEQ ID NO:1461:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

GCTGCCTCCA	TACTGTTTTA	GGCAGCACCG	TTTATGTGAC	AGAGTCCGTG	TTTCTCAAAT	60
GCATGGTGTT	CCTCAGGTGG	AGAGTGGGCA	GAAGTTTTTG	CAACACTTTT	TTTTTAAGTT	120
ATTGGGTGCA	AAATCCCAAA	CCAGGATATG	TGTATGTCTG	TGTGTTTATG	TTTTTTTTTT	180
GACCCTCCCC	TCTTTCAACC	TACCCCCTTT	TATATCTAAT	GTAGAAAAAG	CGAAATTGAA	240
TCTGGAAAAA	CTCGAG					256

- (2) INFORMATION FOR SEQ ID NO:1462:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

GGGGGTGGAA	GGCGTAGTGC	TTGAAATGCA	GGGATCTGGC	AGTCAGCAGA	AGGATCTGAG	60
ACCCAGTGTC	GAGGTTAAAA	AAAAAACAAA	AAACCAAAAA	CCAATGCAGG	AATCCAGTGG	120
GTGGAGTGAG	GGGATCTGGG	ATCCAGTGAT	GGGGGCCCCA	GGATCCAGGC	ATTGTGGTTG	180
TCAGGATCCA	GTGGTGAGGT	TTGTTGACAT	CCAGAATCCA	GCAGCTGAGC	TTGGAGATCC	240
AGGGCTCGAG						250

- (2) INFORMATION FOR SEQ ID NO:1463:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

TTTTTTTAT AGATTTTAAA CTTCTTATCT	TTCATGGCCT AAGTTTATAA AAATTTCAGC CAGAAAAACC CAGGTAAGGA TTTTTTTTTA TTTTTATTTT TAGACCAGGT GAGAATCCTT TGTTCCACTG ATTTAGTACA TTCAAAATTG ATATTTCTAC CATTTTCTCA GCCTGCTTGT TTGCAGCACT GCTTATTGCC ATCACTGCTT ATCTGTTCAC TCAACTTGAA TGTCCTTGAC CTCATCCCCA CATCTCGAG	60 120 180 240 279
(2) INFORMA	ATION FOR SEQ ID NO:1464:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 266 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1464:	
ACATAATTCC AATCTCCTGG TAGTCACAAA	TTCATGGCCT AGGCCATTTG GTTCTAAACT GCTTGACTAG TTTTAAGCTC TTAAGCTTTC ATATTTTCTT AAATGCAAGG AAATGAATAT AAAAGCACTA TTCACTGGTA CAAAAATTAC AATGGTCAGT TCCCTTAGGT CATCAAAAAC AATAGTTCTT GTATTCAACC TGAATGTGCC ACAGGAAAAA AAAAATATTT CCAGCTCAGC CTCGAG	60 120 180 240 266
(2) INFORMA	ATION FOR SEQ ID NO:1465:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 259 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1465:	
GTTTCTAGGA TAACAAAGTG	TTCATGGCCT AAACATTTTC TGAAAAACGT GATAGAAAGA AGGAGGAGCT GGGAAATAAA TAATTTGGCA GGAGACTTTT TGAACTAGAT ATCTATTGAA ACAATGTTCC CCATCCTCTC ATTTCCATTC CCAATTTTAC TTCTCGTCCC ATTCTTACTT ATGATCGGCG CTATGTCAGT GCCTCTAGC TGGTCTTCCC ACCCTCGAG	60 120 180 240 259
(2) INFORMA	ATION FOR SEQ ID NO:1466:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 332 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1466:	
TCCGCAAGGC CCTACCATTT	CAAGCAGATC ATGGGTGGCT TCAAGGAGAC GAAGGAGGCT GAAGATGGCT CCAGAAGCCT TGGGCCAAGA AGATGAAGGA GCTGGAGGCA GCCAAGAAGG GGCTTGCAAA GAGGAAAAGC TGGCCATGAC ACGGGAGATG AACAGCAAGA GGTCACACCT GAGCAGCAAA AGAAGCTGCA GGACAAAGTG GACAAGTGCA	60 120 180 240

AGCAGGATGT GCAGAAGACA CAGGAGAAGT ATGAGAAAGT GCTGGAAGAT GTGGGCAAGA	300
CCACACCCCA GTACATGGAG AACAAACTCG AG	332
(2) INFORMATION FOR SEQ ID NO:1467:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 301 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:	
GCTCGAGATG TGCTGTCTTC CATGCAAAGT GGAATTTGAC AATCACTGTG CCGTGCCTTG	60
GGACATCCTG AAAGCCAGCA TGAACACATC CTCTAATCCT GGGACACCGC TTCCGCTCCC	120
CCTCCGAATT CAGAATGACC TCCACCGACA GCAGTACTCC TATATTGATG CCGTCTGTTA	180
CGAGAAACAG CTCCATTGGT TTGCAAAGTT TTTCCCCTAT CTGGTGCTCT TGCACACGCT CATCTTTGCA GCCTGCAGCA ACTTTTGGCT TCACTACCCC AGTACCAGTT CCAGGCTCGA	240 300
G	301
(2) INFORMATION FOR SEQ ID NO:1468:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 436 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
//···	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT	60
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG	120
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA	120 180
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG	120
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA	120 180 240
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTTGCAGCCG AGTCAGATGTT CCAAATGTTC ATTGCCTTTC TCCTGTGCAT ATTCCTCATC TGTGCTGCCC	120 180 240 300 360 420
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG AGTCAGATGT CCAAATGTTC ATTGCCTTCT TCCTGTGCAT ATTCCTCATC TGTGCTGCCC TCGCTGCCCA GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCGA	120 180 240 300 360
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG AGTCAGATGT CCAAATGTTC ATTGCCTTCT TCCTGTGCAT ATTCCTCATC TGTGCTGCCC TCGCTGCCCA GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCGA GTACAATGGG ACAACTTACC AACATGGAGA GCTGTTCGTA GCTGAAGGGC TCTTTCAGAA TCGGCCAACCA CTCGAG	120 180 240 300 360 420
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG AGTCAGATGT CCAAATGTTC ATTGCCTTCT TCCTGTGCAT ATTCCTCATC TGTGCTGCCC TCGCTGCCCA GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCGA GTACAATGGG ACAACTTACC AACATGGAGA GCTGTTCGTA GCTGAAGGGC TCTTTCAGAA	120 180 240 300 360 420
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG AGTCAGATGT CCAAATGTTC ATTGCCTTTC TCCTGTGCAT ATTCCTCATC TGTGCTGCCC TCGCTGCCCA GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCGA GTACAATGGG ACAACTTACC AACATGGAGA GCTGTTCGTA GCTGAAGGGC TCTTTCAGAA TCGGCAACCA CTCGAG (2) INFORMATION FOR SEQ ID NO:1469:	120 180 240 300 360 420
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG AGTCAGATGT CCAAATGTTC ATTGCCTTTC TCCTGTGCAT ATTCCTCATC TGTGCTGCCC TCGCTGCCCA GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCGA GTACAATGGG ACAACTTACC AACATGGAGA GCTGTTCGTA GCTGAAGGGC TCTTTCAGAA TCGGCAACCA CTCGAG (2) INFORMATION FOR SEQ ID NO:1469: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs	120 180 240 300 360 420
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG AGTCAGATGT CCAAATGTTC ATTGCCTTTC TCCTGTGCAT ATTCCTCATC TGTGCTGCCC TCGCTGCCCA GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCGA GTACAATGGG ACAACTTACC AACATGGAGA GCTGTTCGTA GCTGAAGGGC TCTTTCAGAA TCGGCAACCA CTCGAG (2) INFORMATION FOR SEQ ID NO:1469: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs (B) TYPE: nucleic acid	120 180 240 300 360 420
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG AGTCAGATGT CCAAATGTTC ATTGCCTTTC TCCTGTGCAT ATTCCTCATC TGTGCTGCCC TCGCTGCCCA GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCGA GTACAATGGG ACAACTTACC AACATGGAGA GCTGTTCGTA GCTGAAGGGC TCTTTCAGAA TCGGCAACCA CTCGAG (2) INFORMATION FOR SEQ ID NO:1469: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs	120 180 240 300 360 420
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGG TGAGAGATG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG AGTCAGATGT CCAAATGTTC ATTGCCTTTC TCCTGTGCAT ATTCCTCATC TGTGCTGCCC TCGCTGCCCA GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCGA GTACAATGGG ACAACTTACC AACATGGAGA GCTGTTCGTA GCTGAAGGGC TCTTTCAGAA TCGGCAACCA CTCGAG (2) INFORMATION FOR SEQ ID NO:1469: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	120 180 240 300 360 420
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG AGTCAGATGT CCAAATGTTC ATTGCCTTTC TCCTGTGCAT ATTCCTCATC TGTGCTGCCC TCGCTGCCCA GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCGA GTACAATGGG ACAACTTACC AACATGGAGA GCTGTTCGTA GCTGAAGGGC TCTTTCAGAA TCGGCAACCA CTCGAG (2) INFORMATION FOR SEQ ID NO:1469: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	120 180 240 300 360 420
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGG TGAGAGATG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG AGTCAGATGT CCAAATGTTC ATTGCCTTTC TCCTGTGCAT ATTCCTCATC TGTGCTGCCC TCGCTGCCCA GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCGA GTACAATGGG ACAACTTACC AACATGGAGA GCTGTTCGTA GCTGAAGGGC TCTTTCAGAA TCGGCAACCA CTCGAG (2) INFORMATION FOR SEQ ID NO:1469: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	120 180 240 300 360 420
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG AGTCAGATGT CCAAATGTTC ATTGCCTTTC TCCTGTGCAT ATTCCTCATC TGTGCTGCCC TCGCTGCCCA GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCGA GTACAATGGG ACAACTTACC AACATGGAGA GCTGTTCGTA GCTGAAGGGC TCTTTCAGAA TCGGCAACCA CTCGAG (2) INFORMATION FOR SEQ ID NO:1469: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	120 180 240 300 360 420
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG AGTCAGATGT CCAAATGTTC ATTGCCTTTC TCCTGTGCAT ATTCCTCATC TGTGCTGCCC TCGCTGCCCA GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCAG GTACAATGGG ACAACTTACC AACATGGAGA GCTGTTCGTA GCTGAAGGGC TCTTTCAGAA TCGGCAACCA CTCGAG (2) INFORMATION FOR SEQ ID NO:1469: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:	120 180 240 300 360 420 436
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCCTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG AGTCAGATGT CCAAATGTTC ATTGCCTTTC TCCTGTGCAT ATTCCTATC TGTGCTGCCC TCGCTGCCCA GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCGA GTACAATGGG ACAACTTACC AACATGGAGA GCTGTTCGTA GCTGAAGGGC TCTTTCAGAA TCGGCAACCA CTCGAG (2) INFORMATION FOR SEQ ID NO:1469: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:	120 180 240 300 360 420
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT GTTCTTTCTT TTGCTAGAAG GAGGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG CATGTTTCAA GACAAGAAGT ACAGAGTGGG TGAGAGATGG CATCCTTACC TGGAACCTTA TGGGTTGGTT TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG AGTCAGATGT CCAAATGTTC ATTGCCTTTC TCCTGTGCAT ATTCCTCATC TGTGCTGCCC TCGCTGCCCA GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCAG GTACAATGGG ACAACTTACC AACATGGAGA GCTGTTCGTA GCTGAAGGGC TCTTTCAGAA TCGGCAACCA CTCGAG (2) INFORMATION FOR SEQ ID NO:1469: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:	120 180 240 300 360 420 436

GGACAGGAAA CAGTGGTTCA GAGAGATGAA GCACCCTGCC CACCACATGC ACTCGAG 297 (2) INFORMATION FOR SEQ ID NO:1470: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 325 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470: GAATTCGGCC TTCATGGCCT AGGACCTATT CTATCAGCAG CATTTGACAC CACTGATTAC 60 TCATTCTGCT CTGGTGTACT TTCTTCAATT GCTTCCAAGA CACCATAAAT TCTTCTGCCT 120 TGCTGGCTGC CTTTGCTGGT TCCTCCTCTT CTCCCTGACC TCTTAATGTT GGAGAACCAC 180 AGGGCTTAGT CCTTGGTCCT CTTCTCTCTT TTCTTTACAC TGTGGTCCTC AGTGAGGGAG 240 ATAGGTAGAT CCACTGTCCC GATCTTAACC CAAAGAAAGA CTTGCTGTCC AGCTACGGGG 300 GCTGTGGTCA GAAGGCAGCC TCGAG 325 (2) INFORMATION FOR SEQ ID NO:1471: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 421 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471: GAATTCGGCC TTCATGGCCT ACAAAAGGAT GGGAAATGCC TGCATTCCCC TGAAAAGAAT 60 TGCTTATTTC CTATGTCTCT TATCTGCGCT TTTGCTGACT GAGGGGAAGA AACCAGCGAA GCCAAAATGC CCTGCCGTGT GTACTTGTAC CAAAGATAAT GCTTTATGTG AGAATGCCAG 180 ATCCATTCCA CGCACCGTTC CTCCTGATGT TATCTCATTA TCCTTTGTGA GATCTGGTTT 240 TACTGAAATC TCAGAAGGGA GTTTTTTATT CACGCCATCG CTGCAGCTCT TGTTATTCAC 300 ATCGAACTCC TTTGATGTGA TCAGTGATGA TGCTTTTATT GGTCTTCCAC ATCTAGAGTA 360 TTTATTCATA GAAAACAACA ACATCAAGTC AATTTCAAGA CATACTTTCC GGGTACTCGA 420 421 (2) INFORMATION FOR SEQ ID NO:1472: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 233 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472: GAATTCGGCC TTCATGGCCT AGTACTCCAT CTCATCCATC TCATGGTAGT TCAGAAATGC 60 CTATATTCCT TCTTAAATTC ACCAGGATTT TTGTTTTTTC TTTCACCCCC TTTTTGCCTT 120 TCTTATTTTC ATCCTTCCAT TTCACTCATT TCCACTCATG TTTAGCAGTT TCTATCCTTT 180 TCTTTCCTGG CGTTTTAGCG TCACACATAG AAACCTATCA CCATCAGCCC TCG 233

- (2) INFORMATION FOR SEQ ID NO:1473:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

GCGATTGAAT	TCTAGTTGCC	TACCTACCAA	ACTACCTACT	GAACTTTTTA	ATTTGAAGAT	60
ATTCTTCCTG	GACTACTTGT	TTATAGTTTA	TTAAATGAAC	TGCTCTATTT	CTAAAAACTT	120
TATTTTTAAA	GTCCTTTCCC	GTTTAGAATG	CGGCATACTC	TTGCTTGTGG	GGTATATATC	180
TCTGATCGTG	ATAACTACCT	ACCGAAAACC	TTTCATGGCT	CCTTGCCAAC	TACAAAATTG	240
CGATATCCTC	GAG					253

- (2) INFORMATION FOR SEQ ID NO:1474:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 424 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

GAATTCGGNC	TTCATGGCCT	ACCGCAAGTT	CCTCCTGACC	TTCAGGGAGC	CTGACTTAGA	60
GAAGAAGTAC	TCCAAGCAGG	TAGACGACCG	ATTTGGTGCC	TATGTGGCGT	GTGCCTCGCT	120
CGTCTTCCTC	TTCATCTGCT	TTGTCCAGAT	CACCATCGTG	CCCCACTCCA	TATTCATGCT	180
CAGCTTCTAC	CTGACCTGTT	CCCTGCTGCT	GACCTTGGTG	GTGTTTGTGT	CTGTGATCTA	240
CTCCTGCGTA	AAGCTCTTCC	CCTCCCCACT	GCAGACCCTC	TCCAGGAAGA	TCGTGCGGTC	300
CAAGATGAAC	AGCACCCTGG	TTGGGGTGTT	CACCATCACC	CTGGTGTTCC	TGGCGGCTTT	360
TGTCAACATG	TTCACGTGCA	ACTCCAGGGA	CCTGCTGGGC	TGCTTGGCAC	AGGAGCGTCT	420
CGAG						424

- (2) INFORMATION FOR SEQ ID NO:1475:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

GAATTCGGCC	TTCATGGCCT	ACTCTGTGTT	GGTAAGTAAA	AGCCCTCCAG	CATAGGTATA	60
CACTTAGTTG	TTCCTTCCAG	TGGTTATCAT	ACTTCTTTTC	TTGCCATAGT	TACATGCTAA	120
CAACGTCCCA	AAGCTATAGT	TGCTCTTGCA	TTTTGTTCTT	AATTCTTGTA	AGATAAACTA	180
ATAATACAGG	GAGTAAATGT	GCACTGTTTA	TTAATTAAAA	TCCCCGGGAC	ACGGGATAAA	240
CTGAAGGAAA	TCGTGCTTTT	TGAAAAGTAG	GTGTAGCTTG	CCATGCTGCA	TTGTCTTATA	300
CCCACAAAAC	TCGAG					315

(2) INFORMATION FOR SEQ ID NO:1476:

(i) SEQUENCE CHARACTERISTICS:

	CHARACIERISTICS:	
	(A) LENGTH: 321 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(b) for oboot: linear	
(ii) MC	DLECULE TYPE: cDNA	
(xi) SE	EQUENCE DESCRIPTION: SEQ ID NO:1476:	
	CATGGCCT AGCCATCATG TTTATTAGAA GGTTGGATTT TGGTGTGTGC	60
TCTAGACAGA TAG	CAGAATAA ATACCTGCGC CTTGAGAACA GGAAGTCCAC GATTCATACA	120
AAGTGCTCAC TAG	CAGGAAGT TGCTGTGTCA AAATCCAGGC AAGGACCCAA CTCCGGGCAG	180
CCCCTCCTCC CTC	GCTGACCT CAACAAGGGC TGTGCTATTG TTTTTTATTT TATTATTTTA	240
TTTCTCTTTA TT	ATTATTAA TATTATTATT ATTTGCTTTT GCTGTGGTCA CTATCATTGG	300
CAAAGTTCCT TT	TCCCTCGA G	321
(2) INFORMATION	ON FOR SEQ ID NO:1477:	
(1) 550	QUENCE CHARACTERISTICS:	
(1) 350	-	
	(A) LENGTH: 215 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii) MO	OLECULE TYPE: cDNA	
(12)		
(xi) SI	EQUENCE DESCRIPTION: SEQ ID NO:1477:	
GAATTCGGCC TT	CATGGCCT AAGCAAAGCT AAGTGTAAAA CTAAAAAGCA GTTIGTTGCA	60
ACTGGTCATA AA	AGTGATTA AATCTAAAGC TGGCATTAAT AAGGAAGCAA GGTAATAAAA	120
CAAAAATATA AA	CAGCTTTG AGAAAGTACA CCTAATAACA AAATCTTGTA ACACAACAAA	180
TGAAAATCAC AA	AAAATATA AGGAGACTCC TCGAG	215
(2) INFORMATI	ON FOR SEQ ID NO:1478:	
(i) SE(QUENCE CHARACTERISTICS:	
	(A) LENGTH: 291 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii) M	OLECULE TYPE: cDNA	
(xi) S	EQUENCE DESCRIPTION: SEQ ID NO:1478:	
GAATTCGGCC TI	CATGGCCT AATCGGTCTC CTTTGGAGAG ATCACTAGAA CAGAAAAACA	60
ACCCAGATTA TA	AACTGGAAT GTTCGGAAAA CATAAAGGAC AGCTCGTAAA GGAGAGAGTA	120
AGAGTCACCA AA	ACACGTGGA TATTTTTGGT CTGATCCTAC AGTAGCCGGT TATCTAGACC	180
AGTAAGTGGA GI	TTTTGGACA TGCTGCTGCT GTCAACTCAC TGGCTGAAGG AGCACTTCAA	240
	CCTTTCACT GGGTCCAGCT CTGATTCGGA TCACTCTCGA G	291
(2) INFORMATI	ION FOR SEQ ID NO:1479:	
(4) 00	CONTENIOR ON A DA CHED YOUR OR	
(1) SE	QUENCE CHARACTERISTICS:	
	(A) LENGTH: 514 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

GAATTCGGCC	TTCATGGCCT	AGAGAAAGAA	ATGGCTCGAA	CAGAAAACAG	TGGTCTTGAA	60
AGGCAACGCA	ACAGTAGGTT	ACAAATAGCA	TTAGCTTTTT	CTTTAAAGAA	ATTCATTGTA	120
ACCAGTGAAG	GATAAGATTT	TAAATTAGAA	AAATGGAAAT	CCTATGAATA	AAAAACTAGT	180
AAGCTTGAGA	GCAGAATCAC	TGTGGAAAAA	AAACAGATTG	AAAAATAACT	TGCAGGTATC	240
ATAGACAGGA	AATTGCCACT	AGAGAAAACA	GGAAACTTGT	GATAGATAAA	AATGAAGTAT	300
TTTCATTTGG	AACAAGAGAC	CAACTGAAGA	GAGATCAAGT	${\tt GAAGGGGGTT}$	TATTTTAATG	360
AAACACAAAG	ATTCTTGTGG	AAATCAAAGT	GCCGGAGCCA	GAAACAGGGC	TCAACCTTCA	420
AGATTAGAGC	TGTATTCAAG	TTGTTCAAGT	TGGCTCTCGG	TCCCAAAGCA	ACAGCAATGT	480
CACTAAGGTT	ACAAGTAAAA	GGTAAGCCCT	CGAG			514

- (2) INFORMATION FOR SEQ ID NO:1480:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 194 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

GAATTCTAGA	CCTGCCCCTC	CACTGCTCCC	CATACCCTGG	CACGATGCGT	TCCTGGTCAC	60
TGATCACCAT	CATTTTGGGA	AGAGAATCCC	AATCCCTGGC	ACCTGGGTTT	GCCTCATCCA	120
ACCATCCTTC	CCTTTCTCAG	CTGCACCCCC	TCTGCAGATC	TGAAGACACA	CCTCACTCTT	180
CCAGGGCCCT	CGAG					194

- (2) INFORMATION FOR SEQ ID NO:1481:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:

C	GACGCGCCCG	GCCTCCTCTT	TCATTTCAGT	ATACGTAATA	AGAAGTCAGA	AATTACCTTT	60
7	AACCAAGCCT	GGAAATCTCC	TTATCTAGAT	CATTATATTC	TTTAGGTACA	TTTTTTACTT	120
7	TCTACATTAC	CACTCACAAC	AATATTGCTA	AATTTTTTCC	TCTAAATAAG	AAGGATTCCC	180
7	TTTTTCTAAT	AACACTTTCT	TTATTTTTCT	TTAACCTTTC	ACTGAAAGCC	CCCTCAAAAG	240
(CTACCTGGCT	TATGCTAACA	GTATGTTTGA	TGTCCTTTCA	ATACTACTCT	GTTTCCATCT	300
(GTCTAGCATC	CACCTGCCTC	CCAATCTCAA	AGTCTCCATC	ATATTTTGTC	AGTTTTTAGT	360
•	TTTTTTGTTA	TGGTGCAACC	TCGAG				385

- (2) INFORMATION FOR SEQ ID NO:1482:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:

GAATTCGGCC	TTCATGGCCT	AGGTTCTGGG	ATAGCTGATT	GTTGGCCACC	CCCGCCCTGG	60
AATGGAAACC	CTGTTAGGCC	AGGGCCAGAG	CAGGTGGCCA	TGAAGCAAGA	CGGCAAAGGC	120
ATTGGAGGAT	GTCCCACCTC	CACACATACG	CCCAGGCATT	TCTTGGCTGG	GGAATGGTGT	180
TACAGGATCC	ACAAGCACAG	AGATGGGAAA	ACAGTGTGTC	TGGGGAACAC	CAAGAGTTGG	240
GGTTGCCTGG	AGGACAGATA	GACTCAGGGG	GGACATCCAG	AGGTAACACT	AGGTCCGCAG	300
GTGGGTTCAG	AGGCCCCAGC	TCTATCCCCT	TATTCCCAGC	CGGATTAAAG	AATAATCTGA	360
GTATGGTTCC	CTCGAG					376

- (2) INFORMATION FOR SEQ ID NO:1483:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:

GAATTCGGCC	TTCATGGCCT	ATGGATCCAT	CATGGGACAA	TTACTAGTTA	TTTACTTTCC	60
TCCGCTTCAG	AAGGTTTTTC	AGACTGAGAG	CCTAAGCATA	CTGGATCTGT	TGTTTCTTTT	120
GGGTCTCACC	TCATCAGTGT	GCATAGTGGC	AGGCCTGGTC	AGTAATCTTC	TCTACTGTTA	180
TAGTACAGCA	GCTTTTAGGT	CCACTGATTG	CATTCTTAAT	TTGAGTATTT	AATATTTATT	240
TTATTAACCT	AAGGTTTTCA	TTTGTCACTA	TAGCATGGTC	TCATAATTTT	CAAAAAATCA	300
GAAAACAGTA	GATGTTGGCG	TGGATGCAGT	GAACAGGGTT	ACTCGAG		347

- (2) INFORMATION FOR SEQ ID NO:1484:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 709 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

GAATTCGGCC	TTCATGGCCT	ACGAGAATAT	TGTGGAGAAC	TGGTCAGTAG	AAGAACAAGC	60
AATGGAAATG	GATTTGAGTG	TCCTTCAACA	GGTAGAAGAT	CTAGAAAGGA	GAGTTGCATC	120
AGCAAGTTTG	CAAGTGAAGG	GTTGGATGTG	TCCAGAGCCT	GCATCAGAAA	GGGAGGACTT	180
GGTATATTTT	GAACATAAAT	CATTTACTAA	ATTGTGCAAG	GAGCATGATG	GAGAATTTAC	240
TGGCGAAGAC	GAAAGCAGTG	CACATGCACT	AGAACGGAAG	AGTGACAACC	CCCTAGATAT	300
AGCTGTAACC	AGGCTGGCTG	ATTTGGAGCG	GAACATTGAA	AGAAGGTATC	TGAAGAGCCC	360
CTTAAGTACC	ACCATTCAGA	TCAAACTGGA	TAATGTGGGC	ACAGTTACTG	TCCCTGCTCC	420
TGCACCATCC	GTTAGTGGTG	ATGGTGACGG	AATTGAAGAG	GATATTGCTC	CAGGGCTCAG	480
GGTATGGAGA	AGGGCATTAT	CAGAAGCTCG	CAGTGCTGCA	CAGGTAGCTC	TGTGCATTCA	540
GCAATTACAG	AAATCAATAG	CATGGGAAAA	ATCAATTATG	AAAGTTTACT	GCCAAATCTG	600
TCGAAAGGGA	GATAATGAAG	AACTGCTTCT	TCTTTGTGAT	GGCTGTGACA	AAGGCTGTCA	660
TACCTACTGC	CATAGACCCA	AGATTACAAC	AATCCCAGAT	GCTCTCGAG		709

- (2) INFORMATION FOR SEQ ID NO:1485:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

GAATTCGGCC TTCATGGCCT	ACTGTTTCAG	AACTTCCGTA	CCTTTTTCTT	GTATGTAGCA	60
CGTATAAATG CAGCTGTCAT	GCAGTTCTTT	TCTTTTGCTA	GAAAATTAGT	CAGGAGGTAA	120
GATGAATCTT CCAAAGTTAT	GTTAAATTTT	GTTTAACTTG	ACAAATTAAA	CTTTGTTCTT	180
ATTAAACAAA TACGTAAACA	AATACTGGAA	AAGCAAAGCT	TATATTTGGG	AGTAAAATGT	240
ATCTTAAAAT GCATGTTCAA					272

- (2) INFORMATION FOR SEQ ID NO:1486:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

GAATTCGGCC	TTCATGGCCT	ACCGAGGACG	AGGGGAAGAT	GTCACGCAAG	ATAGAAGGCT	60
		GGCTATGAAG				120
		CAAAAAGCAT				180
CTCTGTGGTC	TGCAGGTGCC	ACCTCCTTGG	ACTGTATACC	AGAATGCCCA	TATCACAAGC	240
CTCTGGGTTT	CGAGTCAGGG	GAGGTCACAC	CGGACCAGAT	CACCTGCTCT	AACCCGGAGC	300
		TCGTGGACTG				350

- (2) INFORMATION FOR SEQ ID NO:1487:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

GAATTCGGCC TTCAT	GGCCT AGTACCTGAA	GGCCTTCAAG	GTGGCCTACA	GCCTTAATGG	60
ACACGAATTC GATTT	CATCC ATGATGTTAA	TAAAAAACAC	AAGGAGTTTG	TGGGTAACTG	120
GAACAAAAAC GCGGT	GCATG TCAACCTGTT	TGAGACCCCT	GTGGAGGCTC	AGTACGTGAG	180
ATTGTACCCC ACGAG	CTGCC ACACGGCCTG	CACTCTGCGC	TTTGAGCTAC	TGGGCTGTGA	240
GCTGAACGGA TGCGC	CAATC CCCTGGGCGT	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:1488:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 595 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

GAATTCGGCC	TTCATGGCCT	AGTGGAGATT	ACTTGGCACC	ACTCTCCTTT	CACAGAGCAG	60
AGTCTGAATA	GTCTTCAGAG	ATAGGCCTGT	GGGCCAGATT	GCCATCCCCT	ATGGACCAGA	120
AGCCAAGGAT	CTCTCTAGTG	ATGGTCAGAG	GGCCCAAATG	GCAGGGATAC	CCAGTGATGT	180
CAGGAGGAAT	AGTACAGACA	GAAGGTGCTA	AGCAGACAAT	TCAACTGCCA	TGTTTTGCCA	240
CCCCCTGTGA	GCAGGGATTA	GGTGTTCAGG	CCAGTATCTT	GGGCATGGGG	GAGCCTTTGG	300
CCAGAAGAGG	TATAAAGCTC	AGAAGTTTTT	CAGTCTGATA	ACTATTGATA	TAATTTCCAT	360
AGTGTGAGGG	AGCGGTATGC	TCTACCCTTG	TGTATTTAAG	GCAGGACAGA	GAAATTGAGG	420
ATGCCCCTGG	GGCTAGATCG	ATGATATGAC	CAGAAATCAA	AAAGGGAATG	CATTATTTAT	480
TGCTGTGTAA	CACTGTTAAG	AGAGGAGGTA	GTTAAGGGAT	GGATAGGCAC	ATAGAGAGGG	540
AAGGTCTCAG	GAGAAGGGAT	AGAAAGGAAC	TATGTTCACA	AGAACAACAC	TCGAG	595

- (2) INFORMATION FOR SEQ ID NO:1489:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

GAATTCGGCC	TTCATGGCCT	ACAATTTAAT	AGTATAACAA	ATCCCCTAGA	ATAGTAGAGG	60
AGAGAGGAAT	CTTCCCCTGA	TATGTTTTTG	TAATACTTCT	TCCTCCTCTT	CAGTCAATAG	120
GGAAATGTTT	GTTGAAAGAC	TACTTTGCAG	ACATTTAGAA	AGATACAGAG	TAAGTGTAAG	180
ATGTCCCTCC	TTGTCCTTGA	GGAGTCTCTA	GTCAGGCACA	GGTAGGACTA	AATGAAAAAC	240
AACTACAGAA	CTAAGTAGAA	GAGTGTACAA	TAATATGGGG	AATGTGGAAC	ACTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:1490:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

GAATTCGGCC	TTCATGGCCT	ACTTACTTTT	CCAAAGAATT	TTTTCCACCT	GGAATAAGAA	60
GAGAGGACTA	GTTGAAACAT	TTGAGCTGGA	GAGGCTTATG	GGCAATATGA	AGTGGGCCAA	120
ATTCTTGCAA	TACACCCTAT	TCAATTGAAA	GTACAGTGTC	TAAGGATAAG	AATACTTCTT	180
TAAAGACCAA	CAATTGTTTT	AATGCAATCT	TAATTAGTAA	ATGGTTTACA	TTTTTTCTAT	240
TGTTATTGGT	TTTAAAATTT	GCTACCGCTC	GAG			273

- (2) INFORMATION FOR SEQ ID NO:1491:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

GAATTCGGCC	TTCATGGCCT	ATTGAATTCT	AGACCTGCCT	CAGGGTAAGG	GAGATTTAAT	60
CTTTTTCTTT	ACTATTTTCT	AGTTTCTATG	AGCATGGATT	ACTTGTGCAA	ATCAAAACAA	120
AACAAACGGA	TGGCTCATCC	GGCAAACATC	CATGGGCAGG	GTTGGTGTCG	GGTGCTGGAC	180
GCAGAGATGA	ATGGAGGGCT	CTGGCCTCAG	CGGCTCACAG	TCTGGTGAGC	ATAGACAGTG	240
CTTTCGATGT	GAGAGCAGAC	CTGAGTGTCG	CCTGGGACTC	CAGGCACAGT	TCTCCCTGCA	300
GCTCACAGCA	CTTACCCTTA	CTGCACCATT	AACTTCTACT	CTAGCTCACT	GCCTCTTAAC	360
TCTGAGCGCC	TTGAAGGCAC	AAAATGAGTC	CCATCTGGGT	CTTTAGCAGC	TGGCAGAAAA	420
CCTAGCTCAA	ACTCATGCTC	TAAAAACCCC	TGCTGAGGGA	GTGGGCGAAT	GCAGGCAGCC	480
CTGGCAGTGG	GATCAAGTTC	AGGGAGTGGC	ACTGGAGGCA	TCACCCCAAG	GCTGAGAAGA	540
CCTTGAACTG	CTGTTCAGGG	TTTTGCTGTC	TCTCCCAAGG	CATGACTCGG	CCCAGGAGGA	600
GATGGGGCAG	ATGCTGCAGA	AGGAGGGTTC	ATGCCCCTCC	ACTGCTGCCC	ATGACTCGAG	660

- (2) INFORMATION FOR SEQ ID NO:1492:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

GCTGTGCTAT	CTGTTGTCCA	GCATCTGACA	CAGTTGGTTT	TATATTTTGT	CTGGTTTCTA	60
GTTATTAAGC	AGGTTAAGTC	TGGTTCCTGC	TGTTCTATAT	AGCAGGAAGC	AAAGGTTCTC	120
TCATGAATTT	TTAGCATAAT	AACATAAGCG	TGGATTCCAA	AAATTCATTA	CACAGATCCT	180
GGAAATCTGT	TTACTATGTT	TTATACATTC	TGTGAAAGCT	GGAGAATATA	TATTTGTTTT	240
ACTATGTGTA	TCGCAAATAA	AATATCAATT	TCATGTGCCA	GAGAATTGAA	TACATTATCA	300
AAGGGTCAAC	TCGAG					315

- (2) INFORMATION FOR SEQ ID NO:1493:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

GGGACAACAA	GCCCATCTGG	ATGCACGCAG	AGGAGCGGGA	GGAAAGCAAG	GATAAGCGCC	60
GGGACAGCGC	CCCCTATGGG	GAATACGGCA	GCTGGTACAA	GGCCTGTAAA	GTAGACAGCC	120
CCACAGTCAA	CACCACCCTG	CGCAGCTTGG	GGGCCCTATA	CCGGCGCCAG	GGCAAGCTGG	180
AAGCCGCGCA	CACACTAGAG	GACTGTGCCA	GCCGTAACCG	CAAGCAGGGT	TTGGACCCCG	240
CAAGCCAGAC	CAAGGTGGTA	GAACTGCTGA	AAGATGGCAG	TGGCAGGCGG	GGAGACCGCC	300
GCAGCAGCCG	AGACATGGCT	GGGGGTGCCG	GGCCTCGGTC	TGAGTCTGAC	CTCGAG	356

- (2) INFORMATION FOR SEQ ID NO:1494:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:

GAATTCGGCC	TTCATGGCCT	AGTAAAGGGA	TTTATAATAA	CATTAAAAAT	TTCGTTAGAT	60
			CTTTAATCTC			120
TTCCTAATCC	TCTCAATGCC	ATGCAGATTT	TGTGGATCAA	TATTATTATG	GATGGACCCC	180
CAGCTCAGAG	CCTTGGAGTA	GAACCAGTGG	ATAAAGATGT	CATTCGTAAA	CCTCCTCGCA	240
ACTGGAAAGA	CAGCATTTTG	ACTAAAAACT	TGATACTTAA	AATACTTGTT	TCATCAATAA	300
TCATTGTTTG	TGGGACTTTG	TTTGTCTTCT	GGCGTGAGCT	ACGAGACAAT	GTGATTACAC	360
CTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:1495:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

GCTCGAGCGT	TGAGGTCAAC	ACTTCCTCCA	GGGAAAAGGA	TTCCATTAAT	AGATTTGAAA	60
AGTATTTCAT	AGTCTTTCTC	TGTAAGATCC	AGCCTTACTG	GTACAACTCT	CGCACCTGCA	120
GACTCCAAGT	ACTTTACATA	GGACGCAGCA	ATATAGTATC	TTCCATAGTT	TTTCATGACT	180
TTATTACGGC	ATTTTTGCAT	TAATATTCCG	ATGATGGGCT	TCTTGGCGGT	GTCGCCGTGG	240
GGTCTAGACT	ATCTCGAG					258

- (2) INFORMATION FOR SEQ ID NO:1496:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

GAATTCGGCT	TCATGGCCTA	CTCTCTTTCT	CCATGTTAAA	CCCCTTGGCA	TGAATGAAAG	60
GCTTTCCCCT	TTATCCTTGC	TGTGTTTATT	CATTGTGTCC	AATGAGCTTC	TGAAGGTAGG	120
AGTAACTTTG	CACATTTTGC	TGTGTGGGCT	GCTGCATCTC	TGCCAAAAGG	TTTATGGGAT	180
	GAGATCCAGG					240
AGGTACAGAA	ACATGTTGGA	GATCTTGAGC	CTCAAGGTGC	TTGCTTCAGA	ATTTTCCTGA	300
	CCAGACCTAT					360
	GGAGCTGGAA					420
GACTCCTCAC						437

- (2) INFORMATION FOR SEQ ID NO:1497:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

GAATTCGGCC	TTCATGGCCT	AGTGCAGGTC	CTGGTGCTTG	ATGGTCGAGG	CCATCTCCTG	60
GGCCGCCTGG	CGGCCATCGT	GGCTAAACAG	GTACTGCTGG	GCCGGAAGGT	GGTGGTCGTA	120
CGCTGTGAAG	GCATCAACAT	TTCTGGCAAT	TTCTACAGAA	ACAAGTTGAA	GTACCTGGCT	180
TTCCTCCGCA	AGCGGATGAA	CACCAACCCT	TCCCGAGGCC	CCTACCACTT	CCGGGCCCCC	240
AGCCGCATCT	TCTGGCGGAC	CGTGCGAGGT	ATGCTGCCCC	ACAAAACCAA	GCGAGGCCAG	300
GCCGCTCTGG	ACCGTCTCAA	GGTGTTTGAC	GGCATCCCAC	CGCCCTACGA	CAAGAAAAAG	360
CGGATGGTGG	TTCCTGCTGC	CCTCAAGGTC	GTGCGTCTGA	AGCCTACAAG	AAAGTTTGCC	420
TATCTGGGGC	GCCTGGCTCA	CGAGGTTGGC	TGGAAGTACC	AGGCAGTGAC	AGCCACCCTG	480
GAGGAGAAGA	GGAAAGAGAA	AGCCAAGAAC	CTCGAG			516

- (2) INFORMATION FCR SEQ ID NO:1498:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 329 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

GCGAGCTCCT	GACCTCAGGT	GATCTACCCG	CCTCAGCCTC	CCAAAGTGTT	AGGATTACAG	60
GCGTGAGCCA	CCGCACCTGG	CACCCCCCC	CTTTTTTTT	AATATAAATG	ATCAGTCTTA	120
ACTCCCTAGG	TTATCAGGTT	GAGGGGGTGG	GGATGAGGCT	GGGGGACAGA	TTGTTTTCCT	180
GGCTTCTAGC	TCGGTGTTCT	TTCTGCCTCT	GTGCACAACA	AGGTATGCGT	GTATTGTGGT	240
TGTGGACTGT	GGTTGTGGAC	TGCCTATTCA	CAAGTGGCTA	TGAGGCCCAT	CTGCTGATGC	300
TTTTGGATGC	ACTTGGCGAT	GAACTCGAG				329

- (2) INFORMATION FOR SEQ ID NO:1499:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

GAATTCGGCC	TTCATGGCCT	AGGAGCGCGG	TGGCCACGGA	ACGCTGCCCG	GAGCCGCGCG	60
AGGGAGGACC	CGACGCGCGG	CGTTTACCCA	GCGCAGCGTT	CCACCGCTCG	GGTTTGGCTG	120
GATAAAATAA	AAAATGGGGA	TATTGACCTC	CTGTCACTAC	TGCATGGACT	TTGATGGTTT	180
CCAATCATTA	CTTTCTCCTC	TGTGTCAATC	TGCCTCTTCG	AGAAATTCAT	ACTCCTGAAT	240
AGCTCTCCAG	ACCCCCAGCT	GGCCATGTGG	TGAGTTCAGG	GCCCAAATCA	AGTAGTACCA	300
GCAATCAGGG	AACTCCTATC	TGTTTTGAAT	GGATTCACAC	CAGCCACAAG	CCTGGAAAGA	360
TGGTGTCACA	ATCTACAGTC	AGGCAGGATT	CTCCTGTGGA	GCCCTGGGAA	GGGATCAGCG ·	420
ATCACTCGAG						430

(2) INFORMATION FOR SEQ ID NO:1500:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

GAATTCGGCC	TTCATGGCCT	AGCCAAGTCT	GGGAAGCCTT	AAGGAAAGGA	GTGCCCGTCG	60
GCGTCTTGGT	CCTCCTGTCC	CTGCTGCAGG	GGCTGGGGCC	TCCGGAGCTG	CTGCGGGCTC	120
CCCTCAGGCT	CTGCTTCGTG	ACCCGTGACC	CATGACCCAC	AGTGCTGGCC	TCCTGTGGGG	180
CCACTATAGC	AGCCACCAGA	AGCCGCGAGG	CCCTCAGGGA	AGCCCAAGGC	CTGCAGAAGC	240
CTCCTGGCCT	GGCTGTGTCT	TCCCCACCCA	GCTCTCCCCT	GCGCCCCTGT	CTTTGTAAAT	300
TGACCCTTCT	GGAGTGGGG	GCGGCGGCA	GGGCTGCTTT	TCTTAGTCTG	ATACCAAGCA	360
AGGCCTTTTC	TCGAG					375

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEO ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145,

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NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500; or a complement of said sequence.

2. An isolated polynucleotide consisting of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEO ID NO:22, SEO ID NO:23, SEO ID NO:24, SEO ID NO:25, SEO ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEO ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEO ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID

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3. An isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ

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NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID
NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID
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NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID
NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID
NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID
NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;
```

or a complement of said sequence.

4. An isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ

ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEO ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEO ID NO:100. SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEO ID NO:118. SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEO ID NO:136. SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEO ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID

NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185. SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID

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NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500; or to a complement of said sequence.

- 5. An isolated protein encoded by an isolated polynucleotide of claim 1.
- 6. An isolated protein encoded by an isolated polynucleotide of claim 2.
- 7. An isolated protein encoded by an isolated polynucleotide of claim 3.
- 8. An isolated protein encoded by an isolated polynucleotide of claim 4.

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- (57) Abstract

Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.

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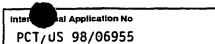
INTERNATIONAL SEARCH REPORT

PCT/US 98/06955

A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12N15/12 C12 C12N5/10 C07K14/47 C12Q1/68 A61K38/17 According to International Patent Classification (IPC) or to both national classification and IPC **B. FIELDS SEARCHED** Minimum documentation searched (classification system followed by classification symbols) IPC 6 C12N C07K C12Q A61K Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practical, search terms used) C. DOCUMENTS CONSIDERED TO BE RELEVANT Category ° Citation of document, with indication, where appropriate, of the relevant passages Relevant to claim No. Α WO 97 07198 A (GENETICS INSTITUT) 27 1-8 February 1997 see the whole document WO 97 04097 A (GENETICS INST) 6 February Α 1-8 1997 Α ADAMS M D ET AL: "3,400 NEW EXPRESSED 1-8 SEQUENCE TAGS IDENTIFY DIVERSITY OF TRANSCRIPTS IN HUMAN BRAIN" NATURE GENETICS. vol. 4, no. 3, July 1993, pages 256-267, XP000611495 see the whole document -/--X Further documents are listed in the continuation of box C. X Patent family members are listed in annex. Special categories of cited documents : *T* later document published after the international filing date or priority date and not in conflict with the application but "A" document defining the general state of the art which is not considered to be of particular relevance cited to understand the principle or theory underlying the invention "E" earlier document but published on or after the international "X" document of particular relevance; the claimed invention filing date cannot be considered novel or cannot be considered to "L" document which may throw doubts on priority claim(s) or involve an inventive step when the document is taken alone which is cited to establish the publication date of another citation or other special reason (as specified) "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such docudocument referring to an oral disclosure, use, exhibition or other means ments, such combination being obvious to a person skilled in the art. document published prior to the international filing date but later than the priority date claimed "&" document member of the same patent family Date of the actual completion of the international search Date of mailing of the international search report 3 July 1998 3 0, 09, 98 Name and mailing address of the ISA Authorized officer European Patent Office, P.B. 5818 Patentiaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, HORNIG H. Fax: (+31-70) 340-3016

Form PCT/ISA/210 (second sheet) (July 1992)





		PCT/US 98/0695) <u> </u>
C.(Continua	ation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant	t to claim No.
A	US 5 536 637 A (JACOBS KENNETH) 16 July 1996 cited in the application see the whole document	1	1-8
A	JACOBS K ET AL: "A NOVEL METHOD FOR ISOLATING EUKARYOTIC CDNA CLONES ENCODING SECRETED PROTEINS" JOURNAL OF CELLULAR BIOCHEMISTRY - SUPPLEMENT, vol. 21A, 10 March 1995, page 19 XP002027246 see abstract		l-8
A	WO 90 14432 A (GENETICS INST) 29 November 1990 see the whole document	1	L-8
Α	WO 96 17925 A (IMMUNEX CORP) 13 June 1996 see the whole document]	1-8
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Form PCT/ISA/210 (continuation of second sheet) (July 1992)



ational application No.

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INTERNATIONAL SEARCH REPORT

Box I Observati ns where certain claims wer f und unsearchable (Continuati n of item 1 of first sheet)
This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows:
see further information sheet
As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. X No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: see further information sheet, subject 1.
Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

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FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1. Claims: (1-8) partially

An isolated polynucleotide comprising a nucleotide sequence selected from SEQ ID no.1, consisting of a nucleotide sequence selected from SEQ ID no.1, consisting essentially of a nucleotide sequence selected from SEQ ID no.1; an isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence consisting of SEQ ID no.1; an isolated protein encoded by said isolated polynucleotides;

Inventions 2 to 1500. Claims: (1-8) partially

Idem as subject 1 but limited to SEQ ID nos.2 to 1500 respectively clone ID nos. BV34 to BK517. (Invention 2 is limited to SEQ ID. no. 2; Invention 3 is limited to SEQ ID no. 3;.....Invention 1500 is limited to SEQ ID no. 1500);

INTERNATIONAL SEARCH REPORT mation on patent family members

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Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9707198 A	27-02-97	US 5707829 A AU 6712396 A AU 6768596 A EP 0839196 A EP 0851875 A WO 9704097 A	13-01-98 18-02-97 12-03-97 06-05-98 08-07-98 06-02-97
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